US 20090042291A1

(19) United States

(12) Patent Application Publication

(10) Pub. No.: US 2009/0042291 A1

(43) Pub. Date: Feb. 12, 2009

Chu et al.

(54) **OPTIMIZED FC VARIANTS**

(75) Inventors: **Seung Yup Chu**, Cypress, CA (US); **John R. Desjarlais**, Pasadena, CA (US); **Sher Bahadur Karki**, Pomona, CA (US); **Gregory Alan Lazar**, Arcadia, CA (US); **Gregory L. Moore**, Monrovia, CA (US); **Igor Vostiar**, Monrovia, CA (US)

Correspondence Address:
DORSEY & WHITNEY, LLP
INTELLECTUAL PROPERTY DEPARTMENT
370 SEVENTEENTH STREET, SUITE 4700
DENVER, CO 80202-5647 (US)

(73) Assignee: **Xencor, Inc.**, Monrovia, CA (US)

(21) Appl. No.: **12/156,184**

(22) Filed: **May 30, 2008**

Related U.S. Application Data

(63) Continuation-in-part of application No. 11/124,620, filed on May 5, 2005, which is a continuation-in-part of application No. 10/822,231, filed on Mar. 26, 2004, now Pat. No. 7,317,091, which is a continuation-in-part of application No. 10/672,280, filed on Sep. 26, 2003, which is a continuation-in-part of application No. 10/379,392, filed on Mar. 3, 2003, now abandoned.

(60) Provisional application No. 60/940,776, filed on May 30, 2007, provisional application No. 60/953,174, filed on Jul. 31, 2007, provisional application No. 60/970,413, filed on Sep. 6, 2007, provisional application No. 60/976,279, filed on Sep. 28, 2007, provisional application No. 60/990,509, filed on Nov. 27, 2007, provisional application No. 61/012,035, filed on Dec. 6, 2007, provisional application No. 61/013,775, filed on Dec. 14, 2007, provisional application No. 61/019,395, filed on Jan. 7, 2008, provisional application No. 61/032,059, filed on Feb. 27, 2008, provisional application No. 61/043,585, filed on Apr. 9, 2008, provisional application No. 61/046,397, filed on Apr. 18, 2008, provisional application No. 60/568,440, filed on May 5, 2004, provisional application No. 60/589,906, filed on Jul. 20, 2004, provisional application No. 60/627,026, filed on Nov. 9, 2004, provisional application No. 60/626,991, filed on Nov. 10, 2004, provisional application No. 60/627,774, filed on Nov. 12, 2004, provisional application No. 60/477,839, filed on Jun. 12, 2003, provisional application No. 60/467,606, filed on May 2, 2003, provisional application No. 60/477,839, filed on Jun. 12, 2003, provisional application No. 60/467,606, filed on May 2, 2003, provisional application No. 60/414,433, filed on Sep. 27, 2002, provisional application No. 60/442,301, filed on Jan. 23, 2003, provisional application No. 60/360,843, filed on Mar. 1, 2002, provisional application No. 60/384,197, filed on May 29, 2002, provisional application No. 60/414,433, filed on Sep. 27, 2002.

Publication Classification

(51) **Int. Cl.**
C12N 5/00 (2006.01)

(52) **U.S. Cl.** **435/375**

(57) **ABSTRACT**

The present invention relates to optimized Fc variants, methods for their generation, Fc polypeptides comprising optimized Fc variants, and methods for using optimized Fc variants.

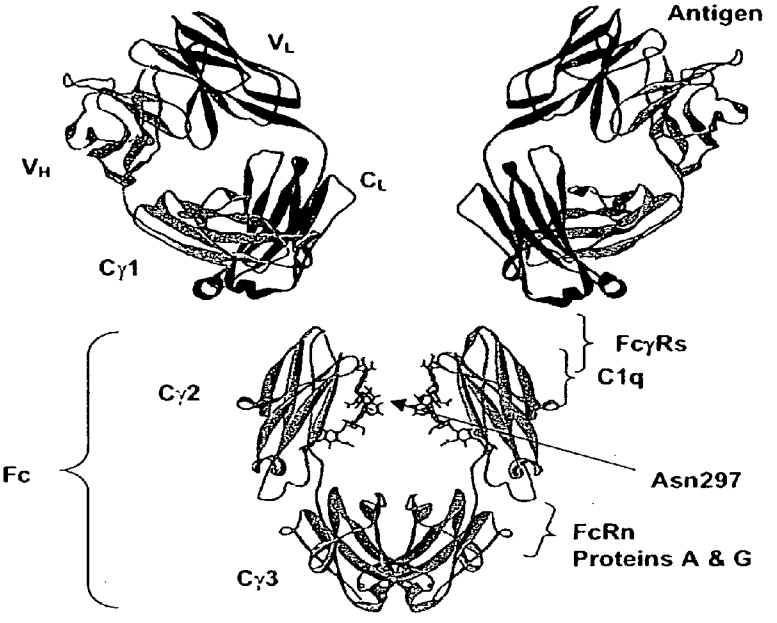


Figure 1

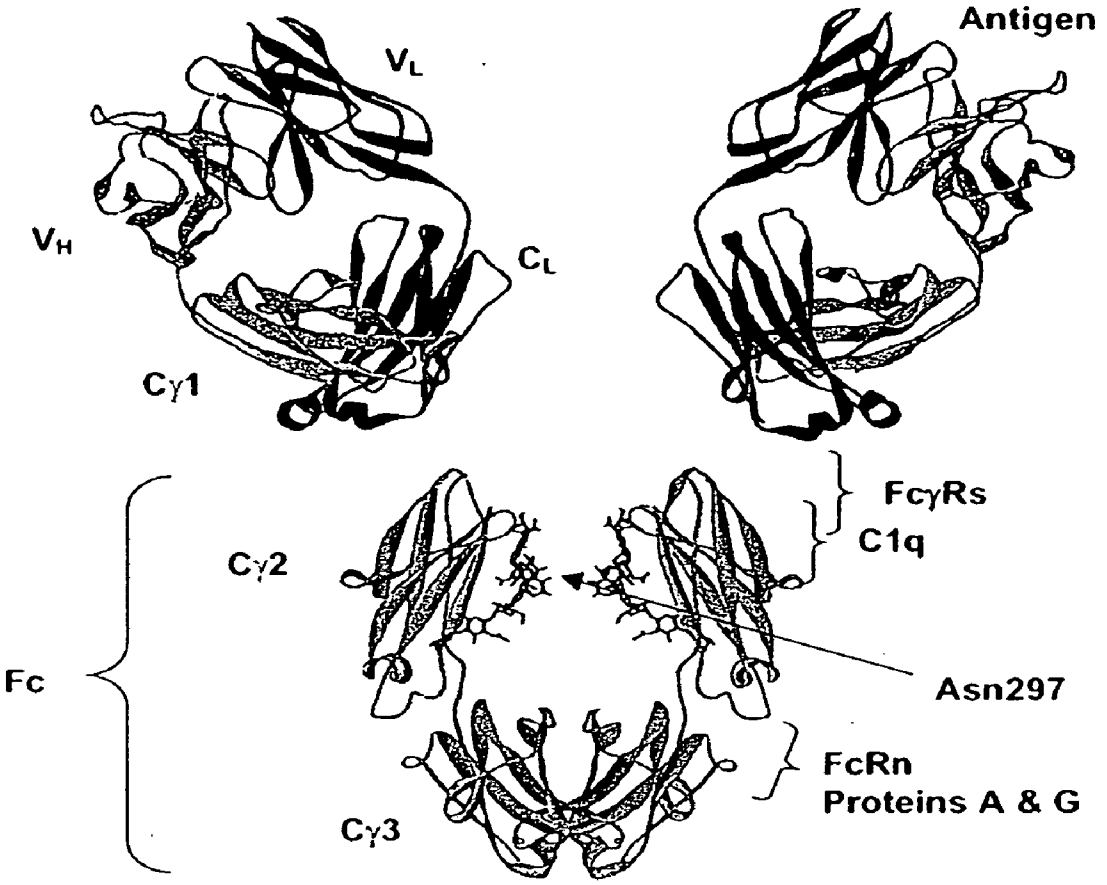

Antigen
V_L
V_H
C_L
$C\gamma1$
$C\gamma2$
$C\gamma3$
Fc
FcγRs
C1q
Asn297
FcRn
Proteins A & G

Figure 2

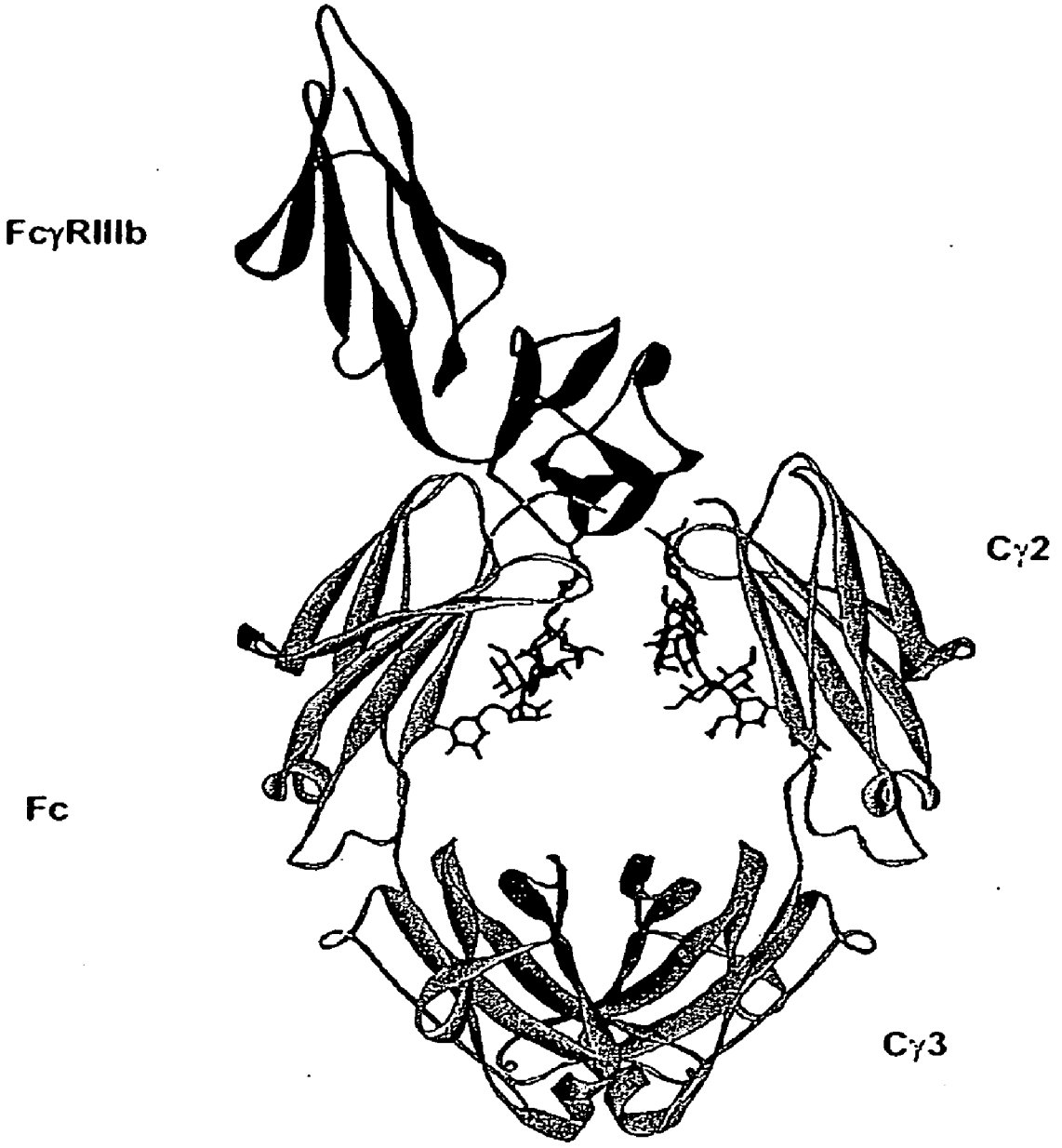


Figure 3a

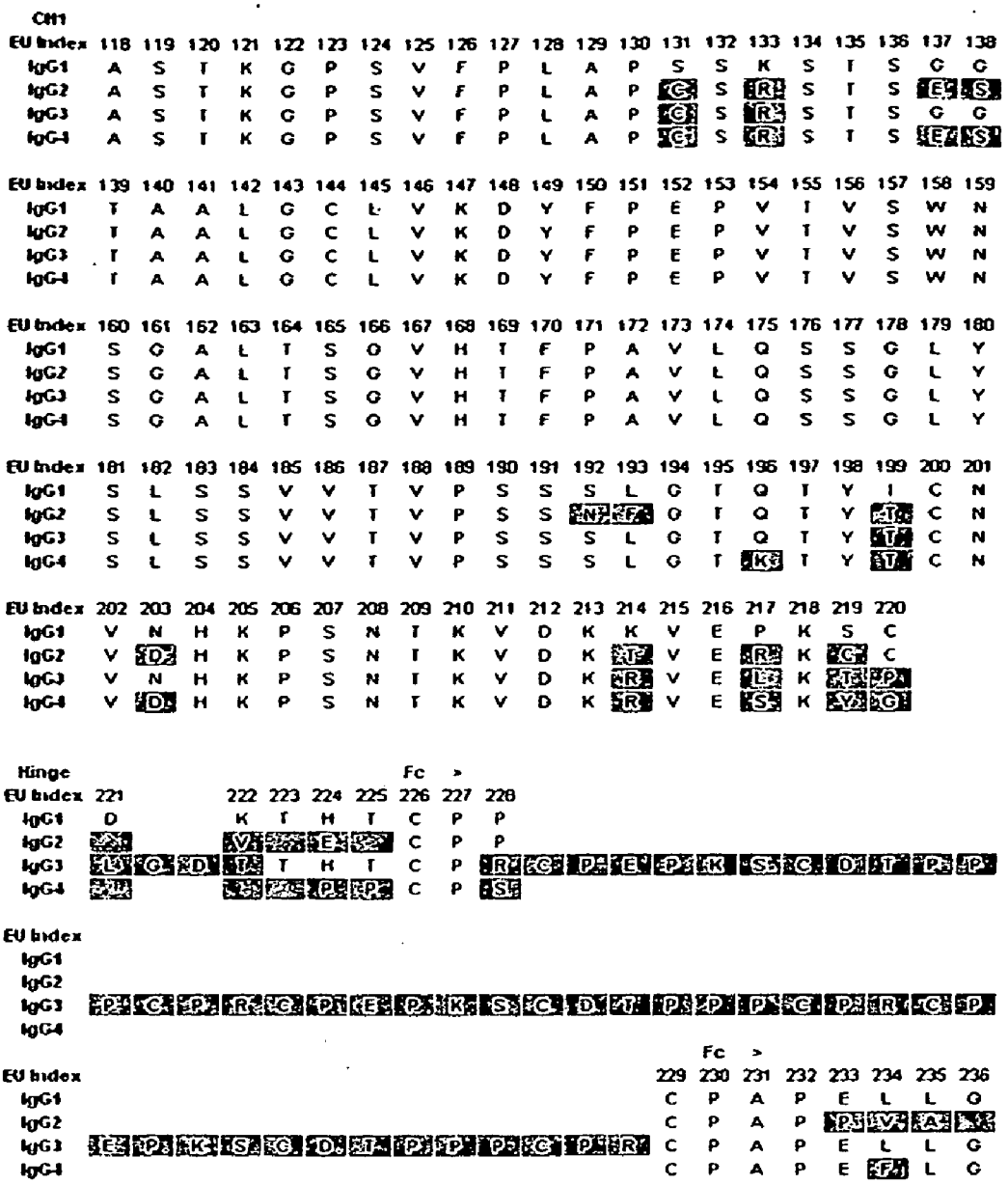

CH1
EU Index 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138
IgG1 A S T K G P S V F P L A P S S K S T S G G
IgG2 A S T K G P S V F P L A P C S R S T S E S
IgG3 A S T K G P S V F P L A P C S R S T S G G
IgG4 A S T K G P S V F P L A P C S R S T S E S
EU Index 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159
IgG1 T A A L G C L V K D Y F P E P V T V S W N
IgG2 T A A L G C L V K D Y F P E P V T V S W N
IgG3 T A A L G C L V K D Y F P E P V T V S W N
IgG4 T A A L G C L V K D Y F P E P V T V S W N
EU Index 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
IgG1 S G A L T S G V H T F P A V L Q S S G L Y
IgG2 S G A L T S G V H T F P A V L Q S S G L Y
IgG3 S G A L T S G V H T F P A V L Q S S G L Y
IgG4 S G A L T S G V H T F P A V L Q S S G L Y
EU Index 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201
IgG1 S L S S V V T V P S S S L G T Q T Y I C N
IgG2 S L S S V V T V P S S NF F G T Q T Y IC C N
IgG3 S L S S V V T V P S S S L G T Q T Y T C N
IgG4 S L S S V V T V P S S S L G T K T Y T C N
EU Index 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220
IgG1 V N H K P S N T K V D K K V E P K S C
IgG2 V D H K P S N T K V D K NF V E R K C C
IgG3 V N H K P S N T K V D K R V E L K T P A
IgG4 V D H K P S N T K V D K R V E S K Y G
Hinge
Fc >
EU Index 221 222 223 224 225 226 227 228
IgG1 D K T H T C P P
IgG2 V T E C P P
IgG3 L D T T H T C P R C P E P K S C D T P P P
IgG4 P S P P C P S
EU Index
IgG1
IgG2
IgG3 P K P R C P E P K S C D T P P P C P R C P
IgG4
Fc >
EU Index 229 230 231 232 233 234 235 236
IgG1 C P A P E L L G
IgG2 C P A P P V A A
IgG3 E P K S C D T P P P C P R C P E L L G
IgG4 C P A P E F L G

Figure 3b

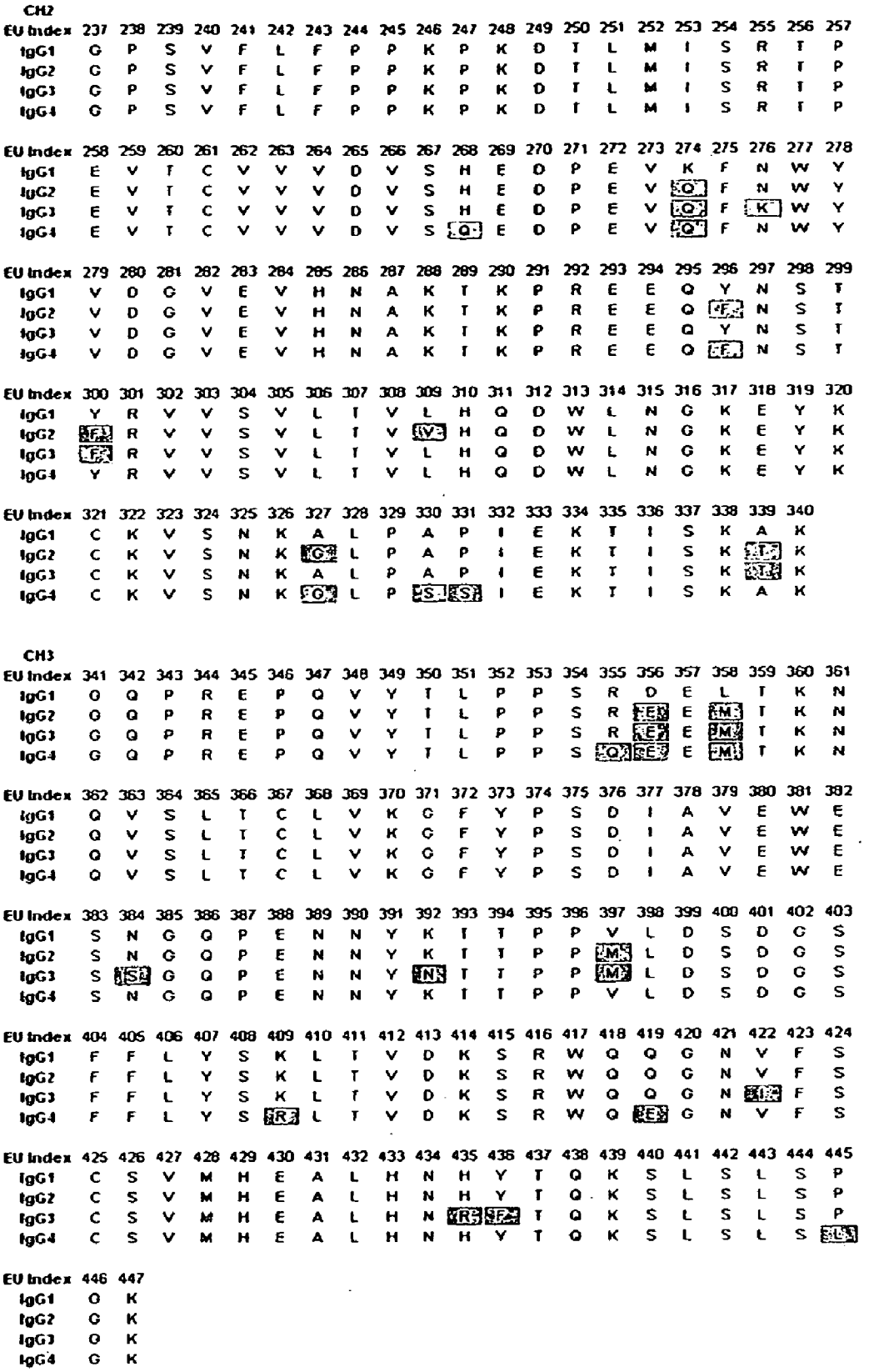

CH2
EU Index 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257
IgG1 G P S V F L F P P K P K D T L M I S R T P
IgG2 G P S V F L F P P K P K D T L M I S R T P
IgG3 G P S V F L F P P K P K D T L M I S R T P
IgG4 G P S V F L F P P K P K D T L M I S R T P
EU Index 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278
IgG1 E V T C V V V D V S H E D P E V K F N W Y
IgG2 E V T C V V V D V S H E D P E V Q F N W Y
IgG3 E V T C V V V D V S H E D P E V Q F K W Y
IgG4 E V T C V V V D V S Q E D P E V Q F N W Y
EU Index 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299
IgG1 V D G V E V H N A K T K P R E E Q Y N S T
IgG2 V D G V E V H N A K T K P R E E Q F N S T
IgG3 V D G V E V H N A K T K P R E E Q Y N S T
IgG4 V D G V E V H N A K T K P R E E Q F N S T
EU Index 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320
IgG1 Y R V V S V L T V L H Q D W L N G K E Y K
IgG2 F R V V S V L T V V H Q D W L N G K E Y K
IgG3 F R V V S V L T V L H Q D W L N G K E Y K
IgG4 Y R V V S V L T V L H Q D W L N G K E Y K
EU Index 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340
IgG1 C K V S N K A L P A P I E K T I S K A K
IgG2 C K V S N K G L P A P I E K T I S K T K
IgG3 C K V S N K A L P A P I E K T I S K T K
IgG4 C K V S N K G L P S S I E K T I S K A K
CH3
EU Index 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361
IgG1 Q Q P R E P Q V Y T L P P S R D E L T K N
IgG2 Q Q P R E P Q V Y T L P P S R E E M T K N
IgG3 Q Q P R E P Q V Y T L P P S R E E M T K N
IgG4 Q Q P R E P Q V Y T L P P S Q E E M T K N
EU Index 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382
IgG1 Q V S L T C L V K G F Y P S D I A V E W E
IgG2 Q V S L T C L V K G F Y P S D I A V E W E
IgG3 Q V S L T C L V K G F Y P S D I A V E W E
IgG4 Q V S L T C L V K G F Y P S D I A V E W E
EU Index 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403
IgG1 S N G Q P E N N Y K T T P P V L D S D G S
IgG2 S N G Q P E N N Y K T T P P M L D S D G S
IgG3 S S G Q P E N N Y N T T P P M L D S D G S
IgG4 S N G Q P E N N Y K T T P P V L D S D G S
EU Index 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424
IgG1 F F L Y S K L T V D K S R W Q Q G N V F S
IgG2 F F L Y S K L T V D K S R W Q Q G N V F S
IgG3 F F L Y S K L T V D K S R W Q Q G N R F S
IgG4 F F L Y S R L T V D K S R W Q E G N V F S
EU Index 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445
IgG1 C S V M H E A L H N H Y T Q K S L S L S P
IgG2 C S V M H E A L H N H Y T Q K S L S L S P
IgG3 C S V M H E A L H N R S T Q K S L S L S P
IgG4 C S V M H E A L H N H Y T Q K S L S L S L
EU Index 446 447
IgG1 G K
IgG2 G K
IgG3 G K
IgG4 G K

Figure 4

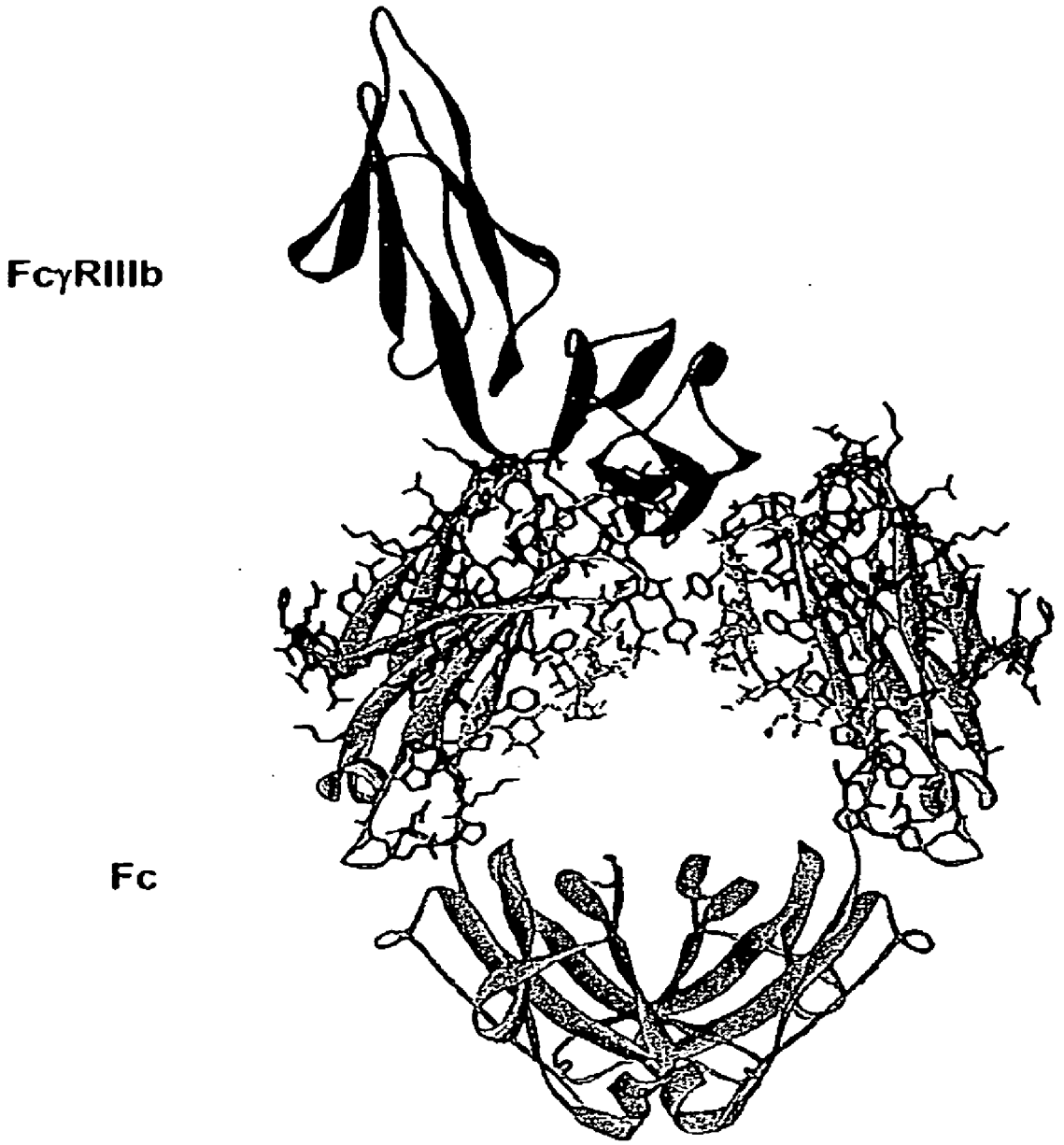


Figure 5

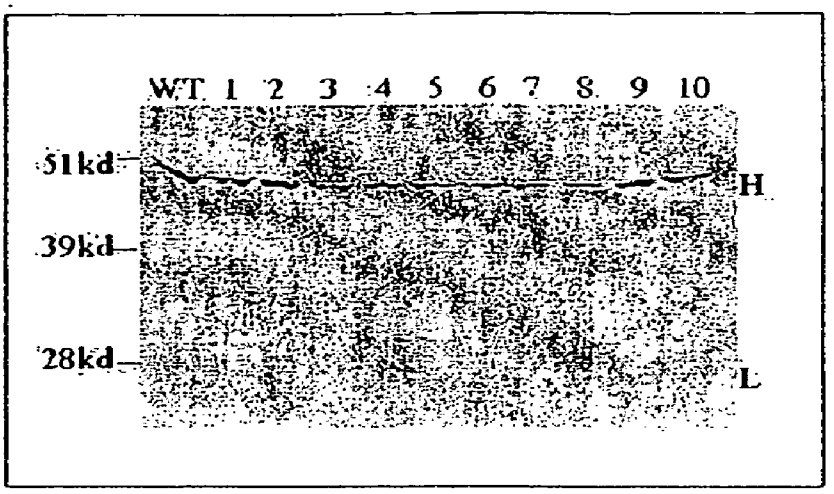


Figure 6

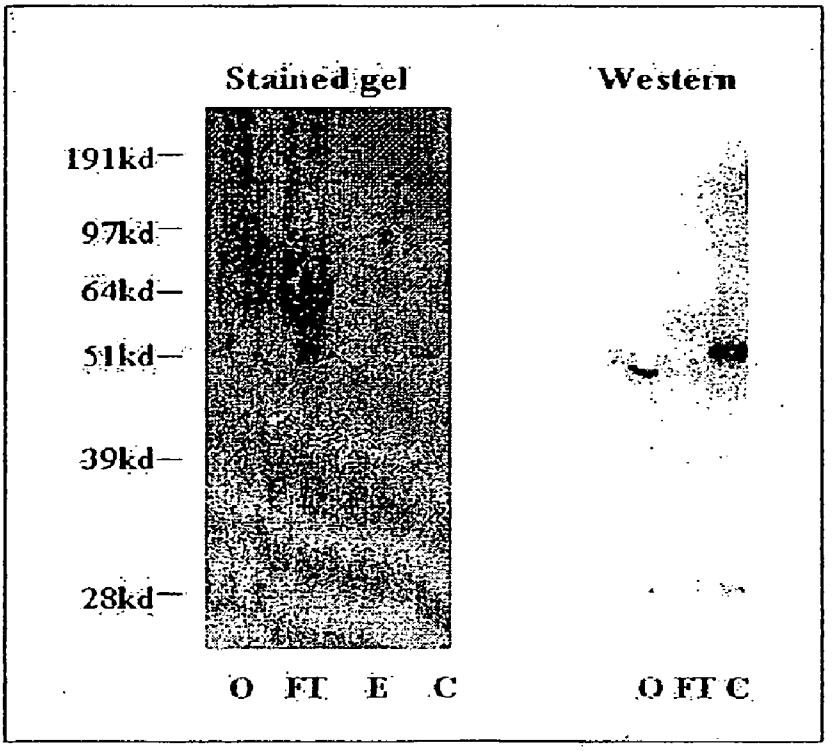


Figure 7

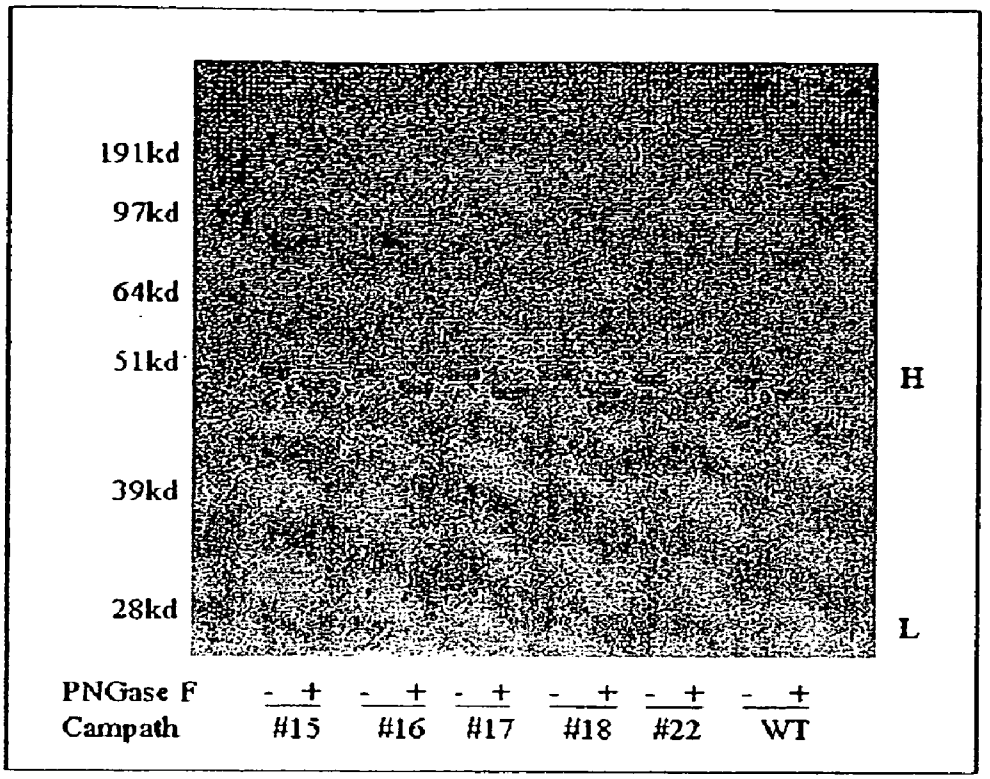


Figure 8

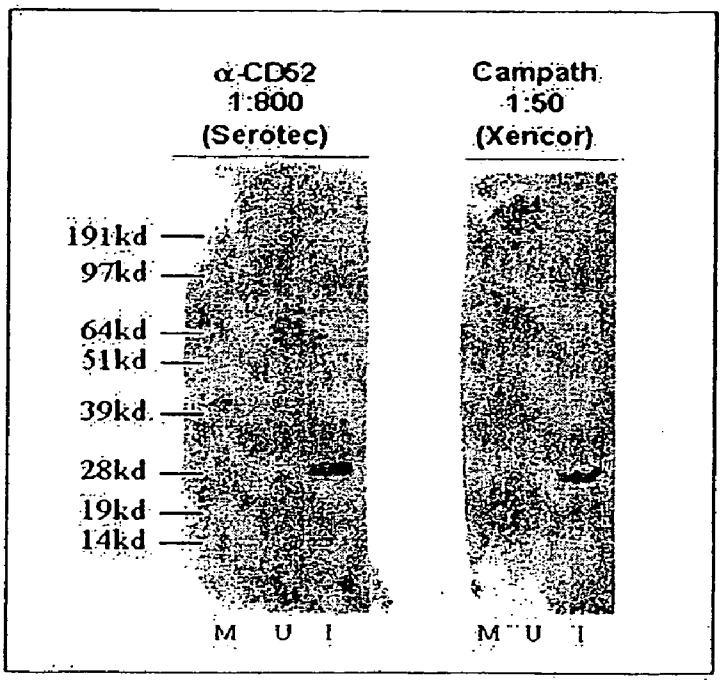


Figure 9

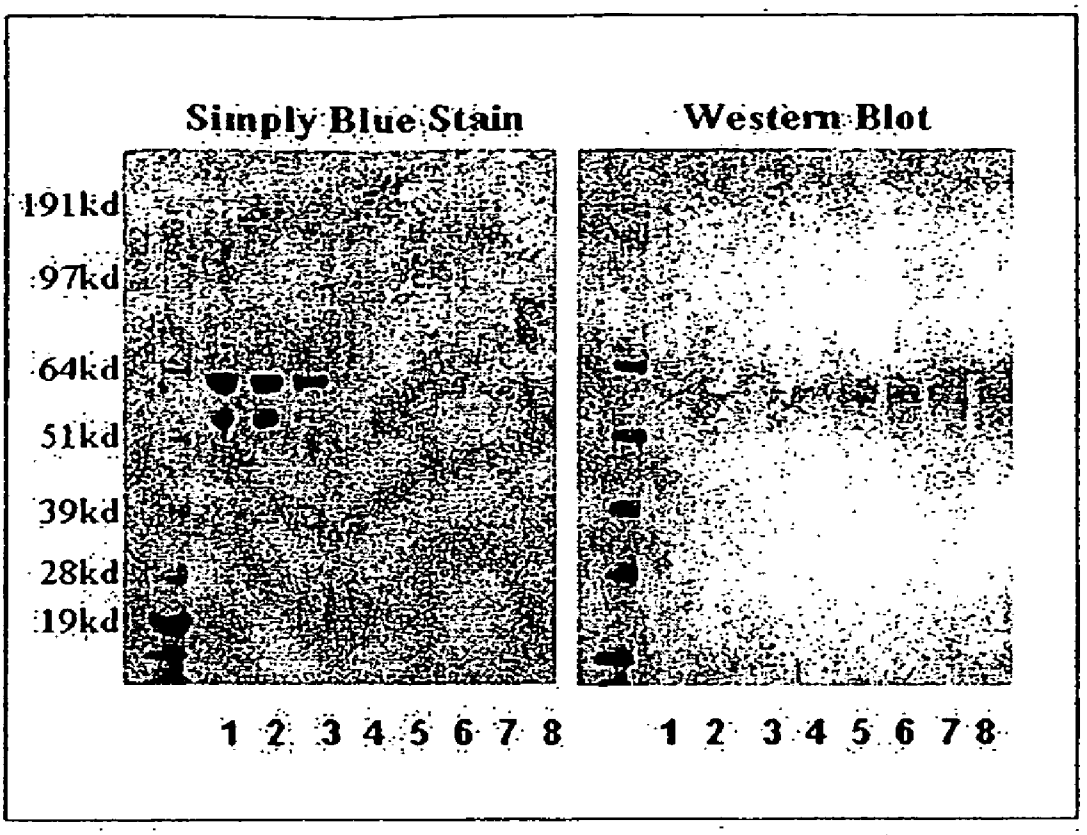

Simply Blue Stain
Western Blot
191kd
97kd
64kd
51kd
39kd
28kd
19kd
1 2 3 4 5 6 7 8
1 2 3 4 5 6 7 8

Figure 10

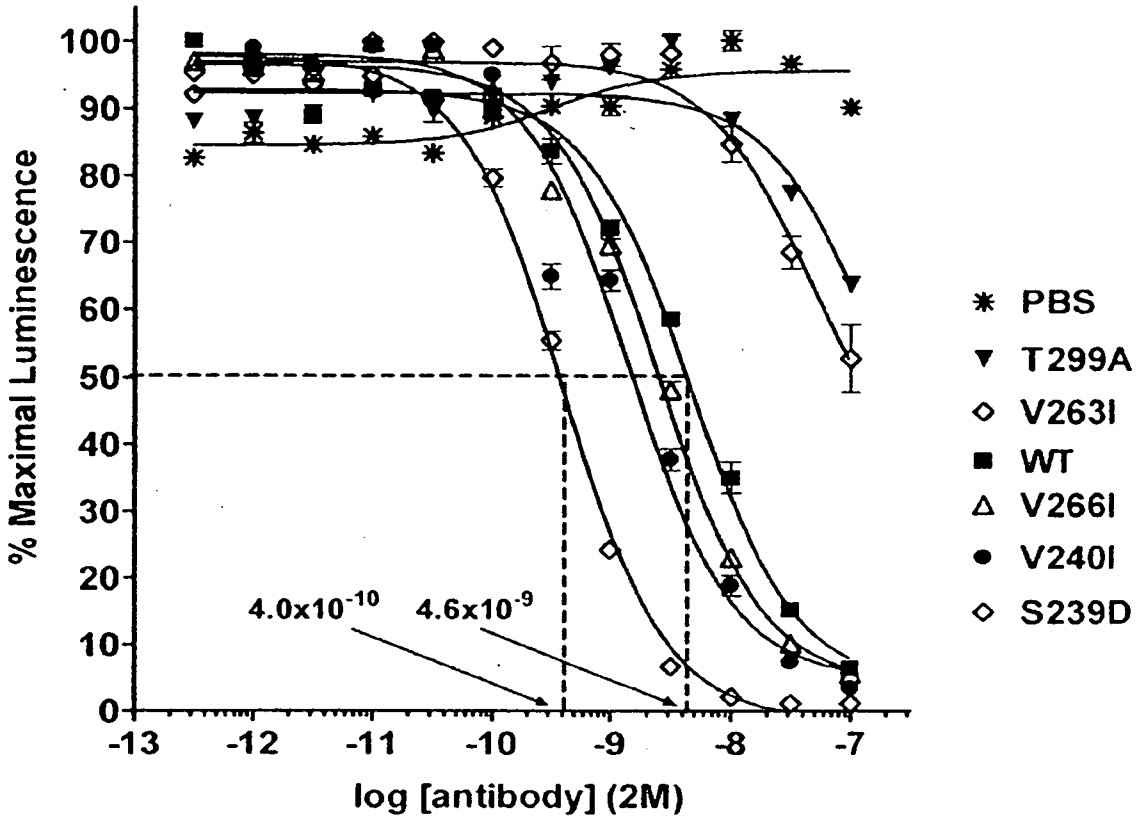

% Maximal Luminescence
100
90
80
70
60
50
40
30
20
10
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
4.0x10-10
4.6x10-9
PBS
T299A
V263I
WT
V266I
V240I
S239D

Figure 11a

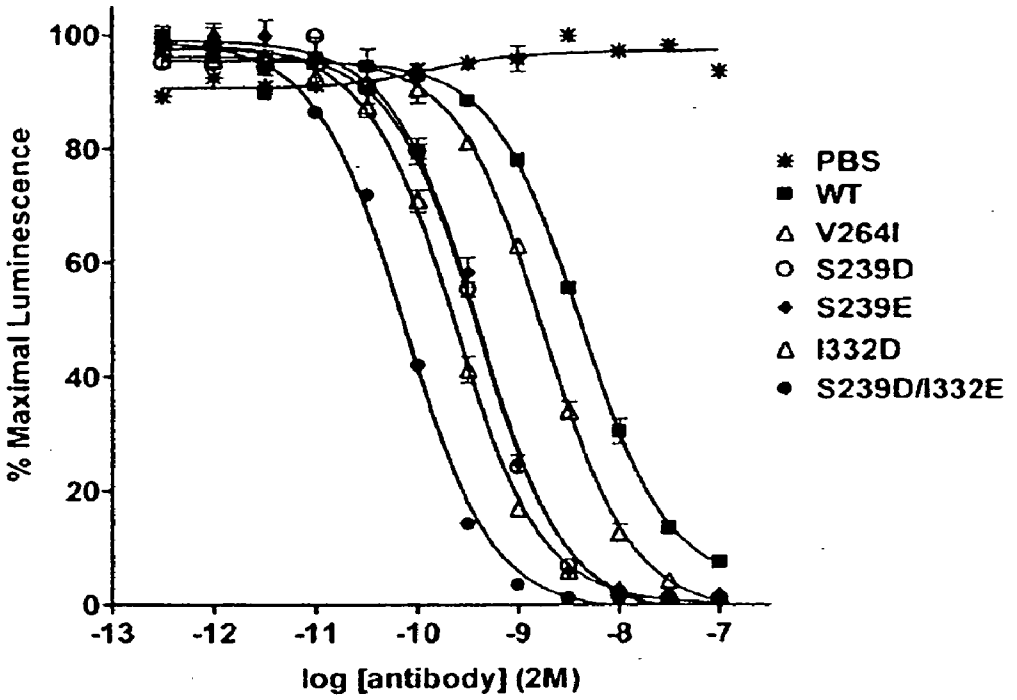


Figure 11b

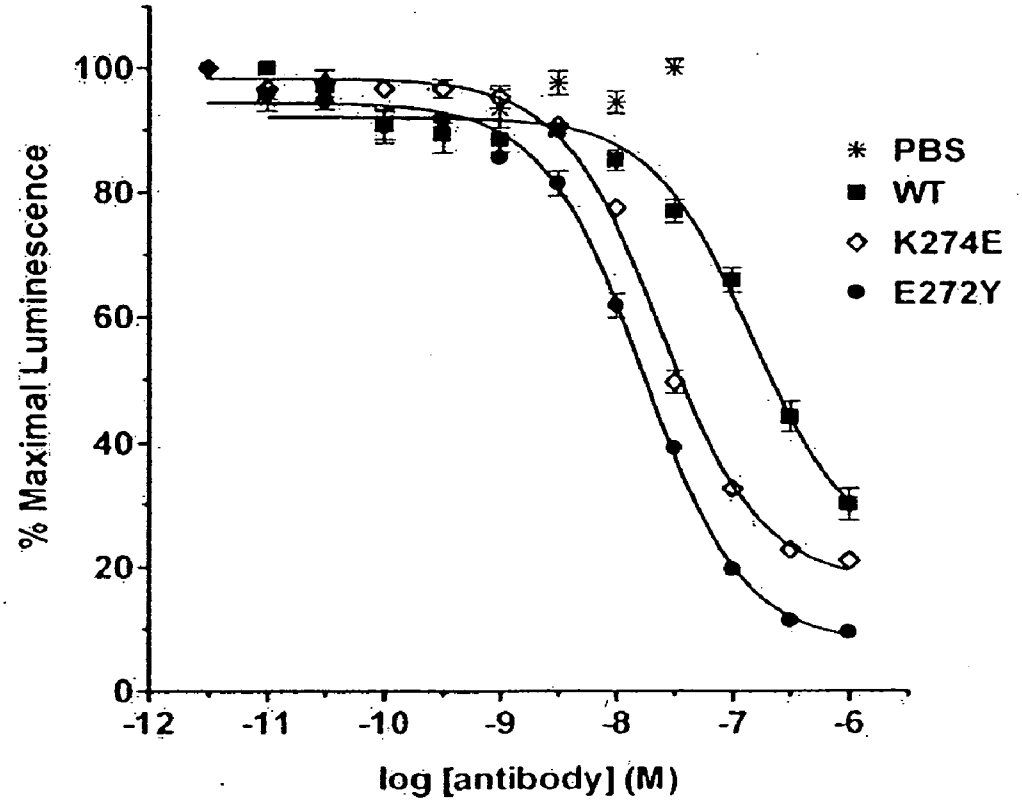


Figure 12

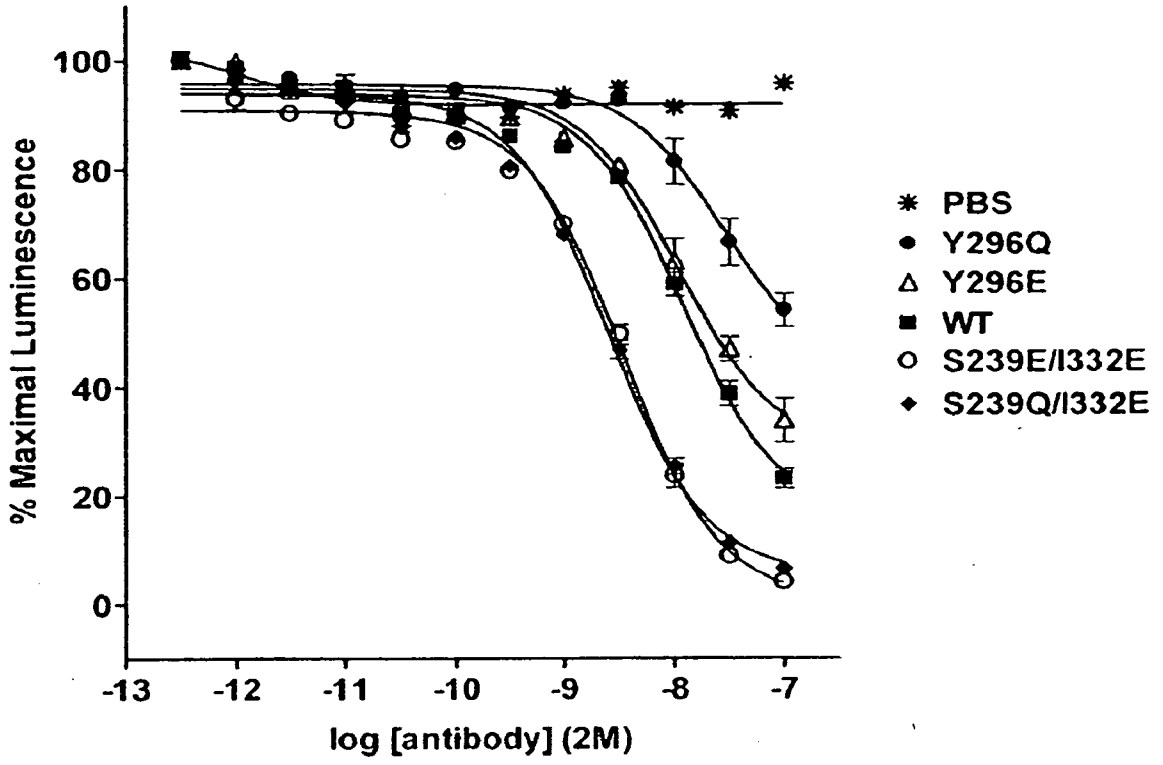

100
80
60
40
20
0
% Maximal Luminescence
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
PBS
Y296Q
Y296E
WT
S239E/I332E
S239Q/I332E

Figure 13

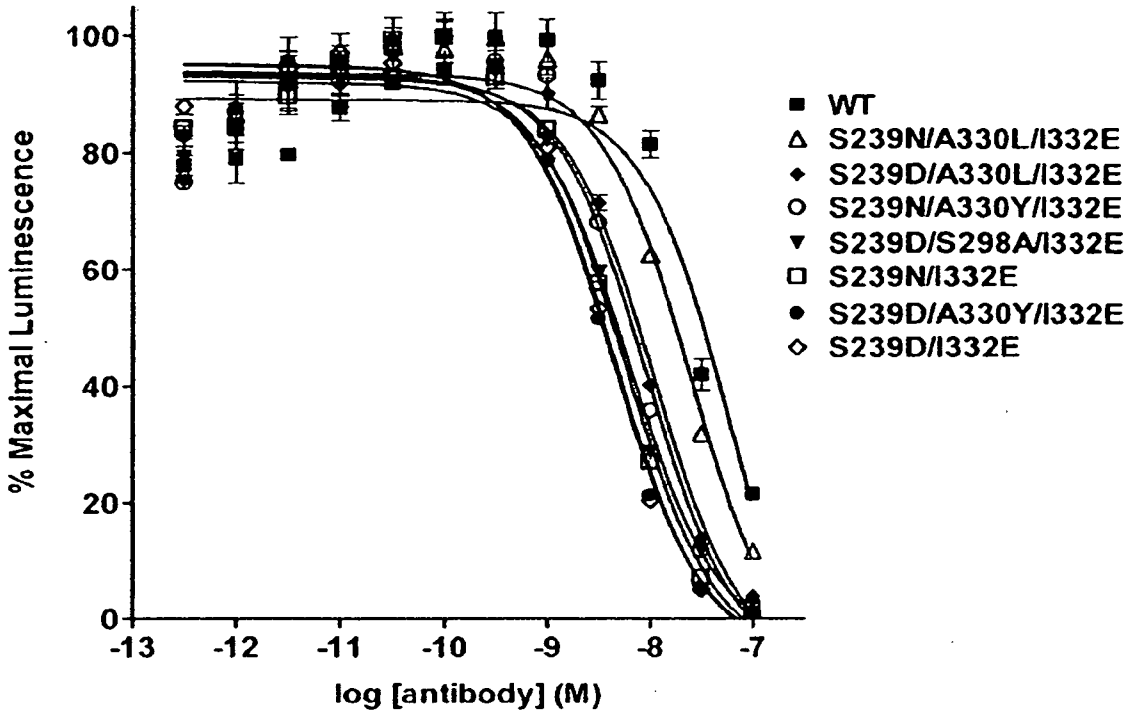

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (M)
WT
S239N/A330L/I332E
S239D/A330L/I332E
S239N/A330Y/I332E
S239D/S298A/I332E
S239N/I332E
S239D/A330Y/I332E
S239D/I332E

Figure 14

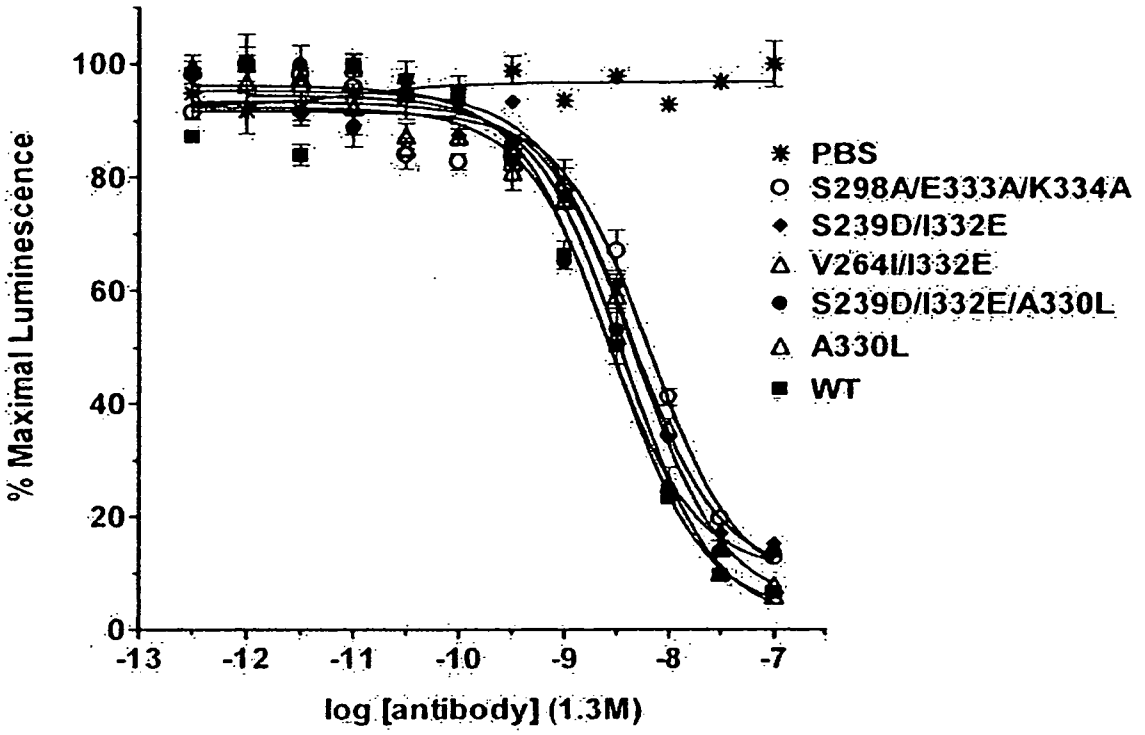

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (1.3M)
PBS
S298A/E333A/K334A
S239D/I332E
V264I/I332E
S239D/I332E/A330L
A330L
WT

Figure 15

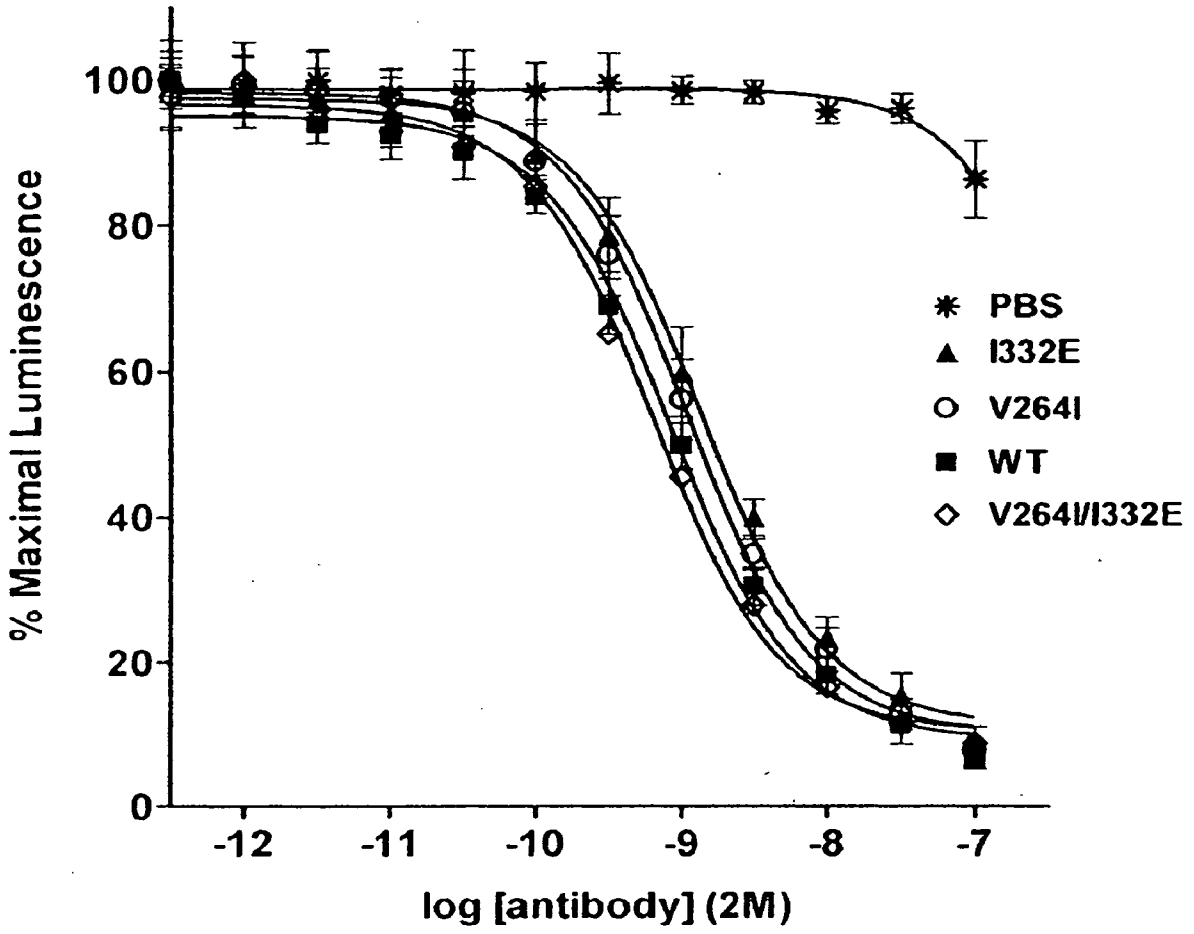

% Maximal Luminescence
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
PBS
I332E
V264I
WT
V264I/I332E

Figure 16a

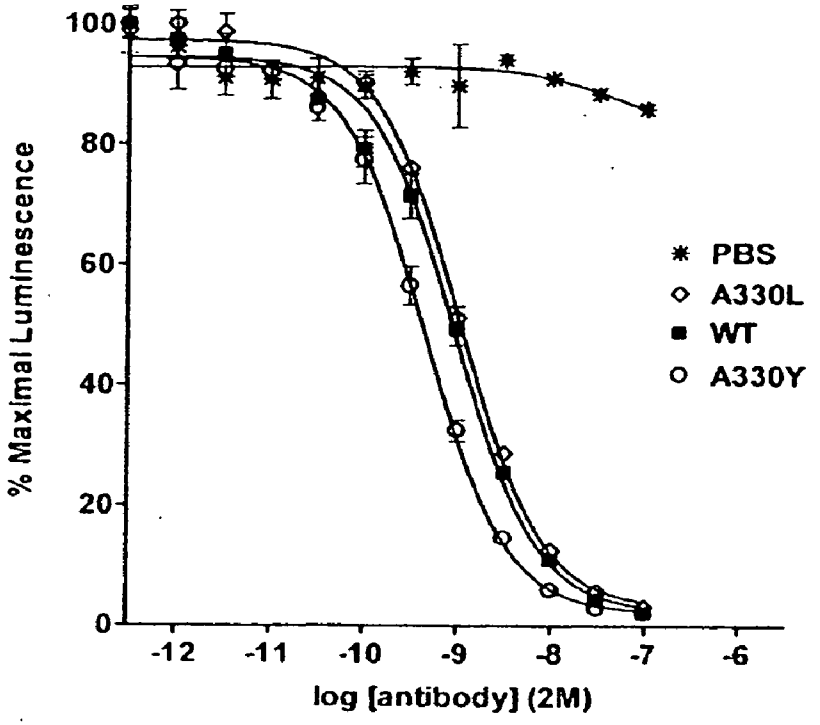


Figure 16b

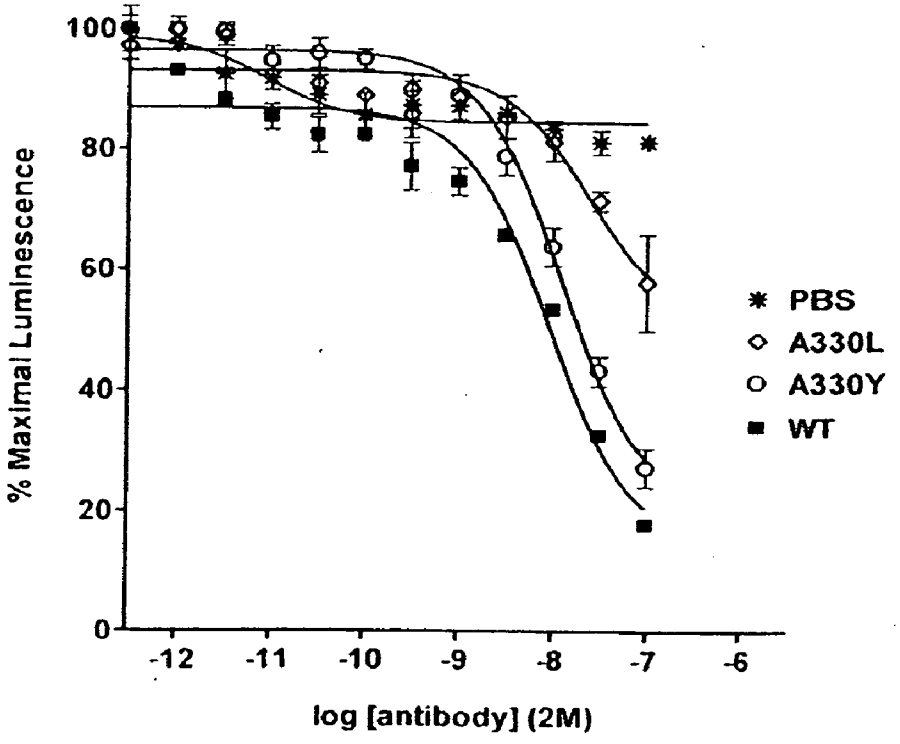


Figure 17a

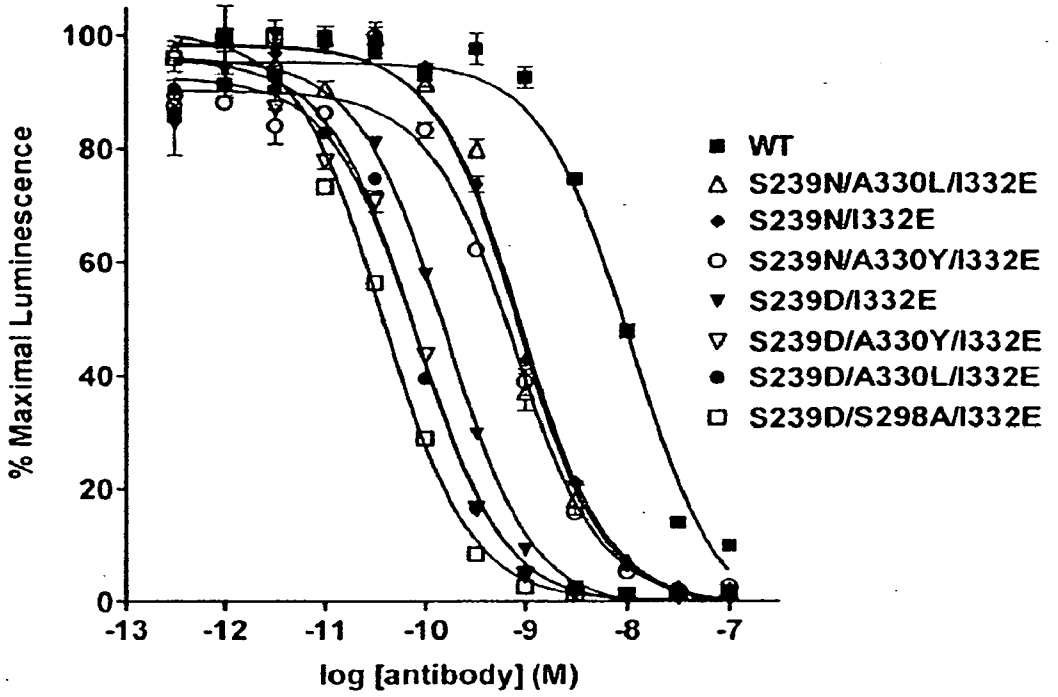


Figure 17b

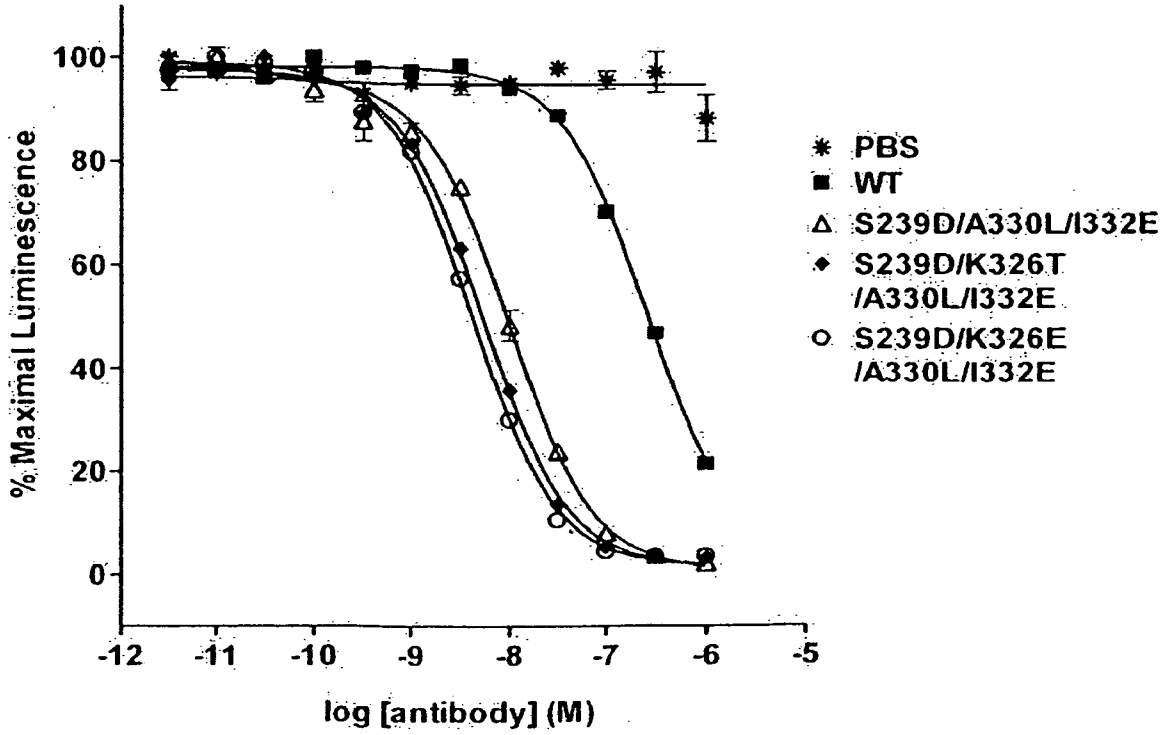


Figure 17c

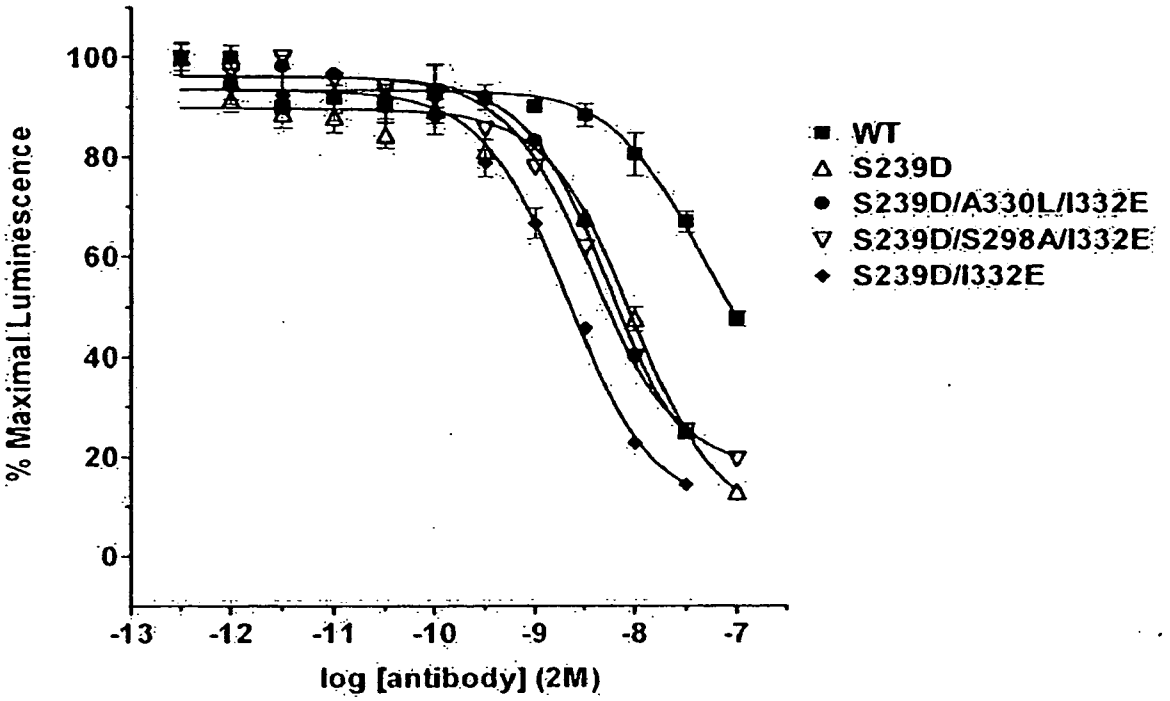

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
WT
S239D
S239D/A330L/I332E
S239D/S298A/I332E
S239D/I332E

Figure 18

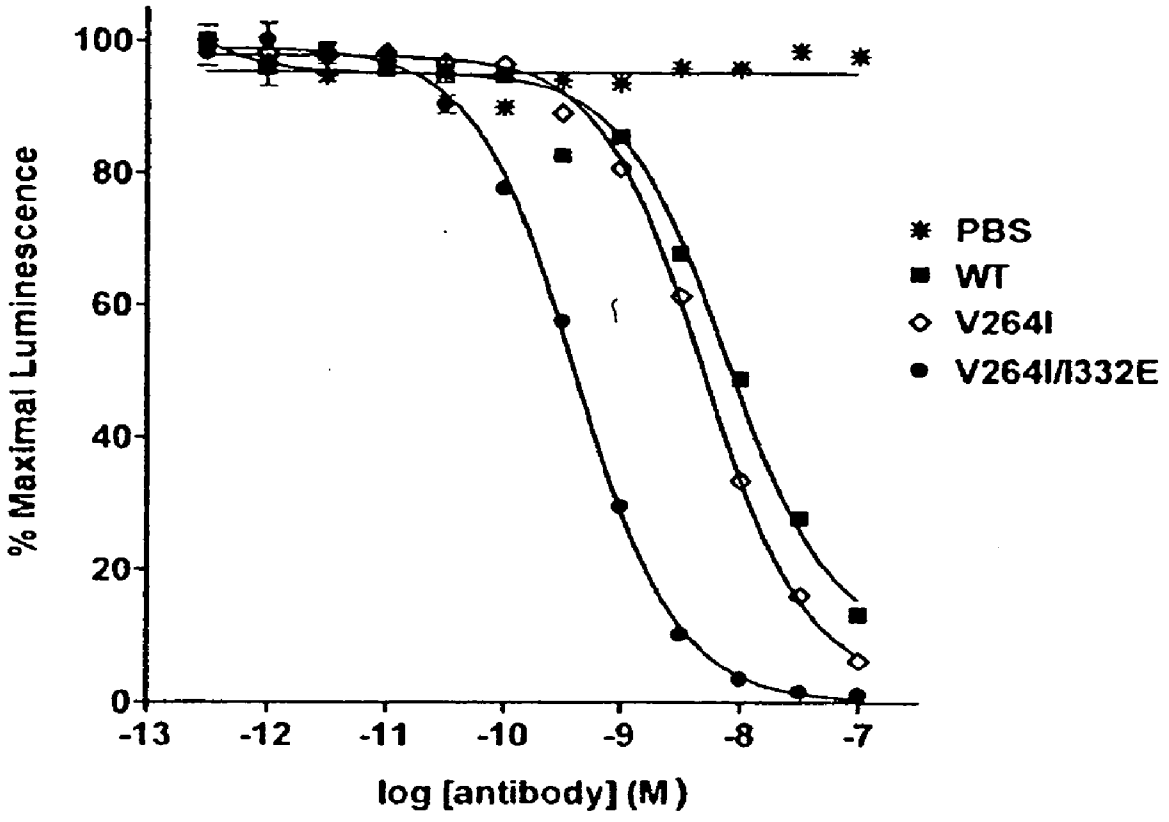

100
80
60
40
20
0
% Maximal Luminescence
-13
-12
-11
-10
-9
-8
-7
log [antibody] (M)
PBS
WT
V264I
V264I/I332E

Figure 19

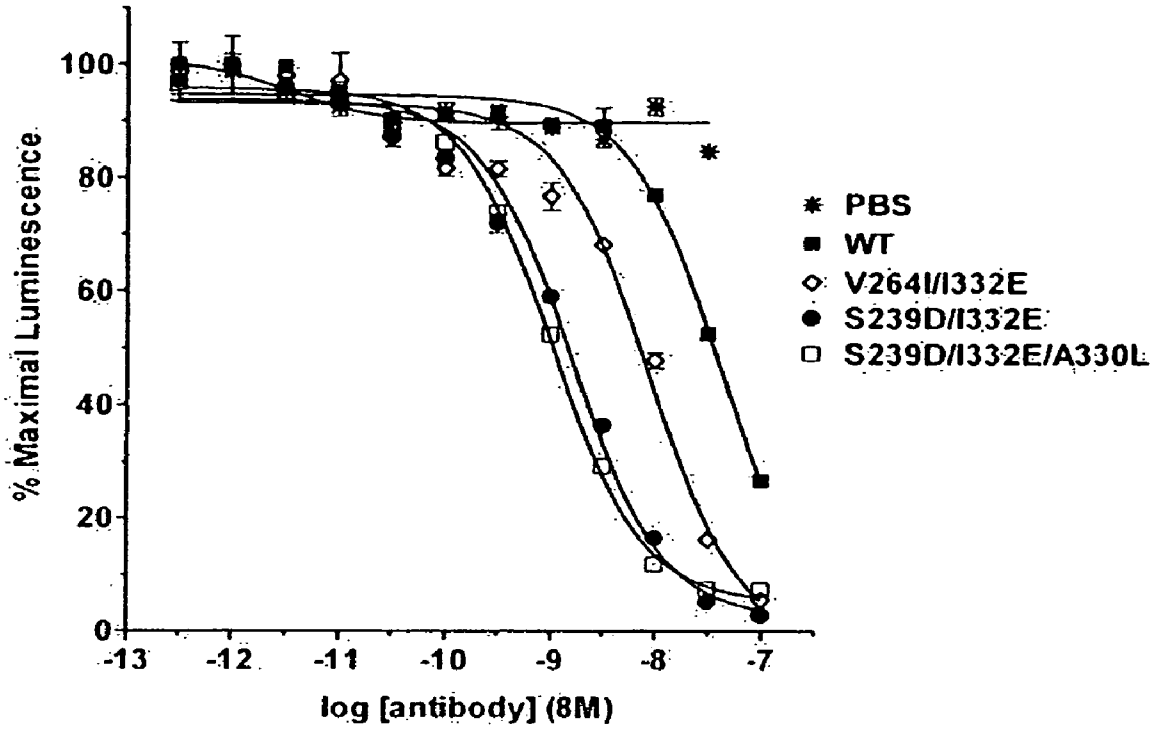

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (8M)
PBS
WT
V264I/I332E
S239D/I332E
S239D/I332E/A330L

Figure 20a

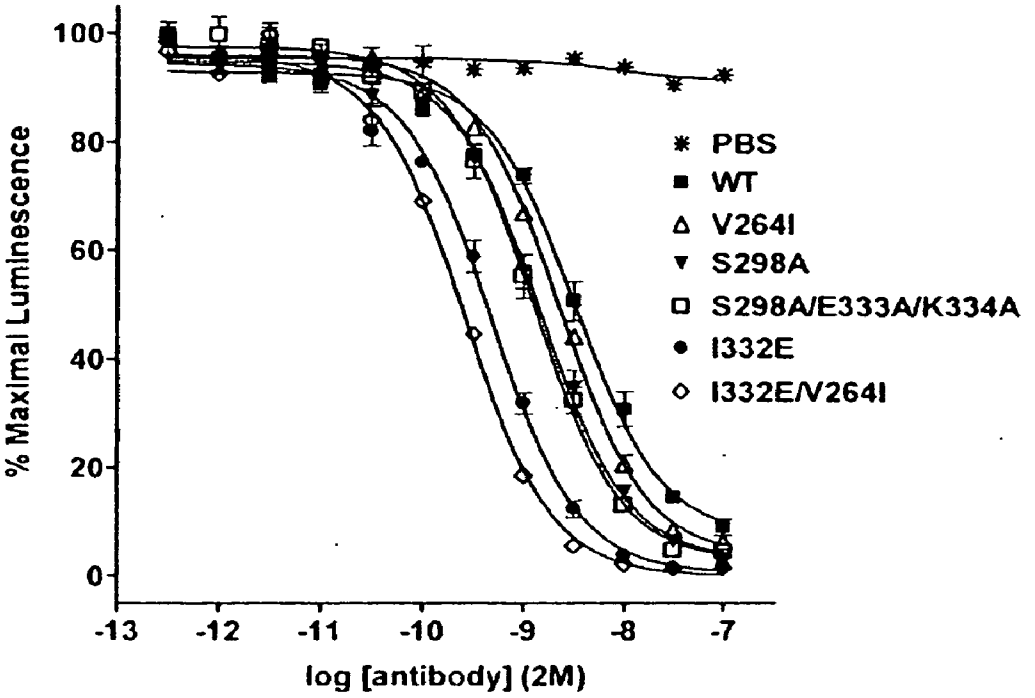


Figure 20b

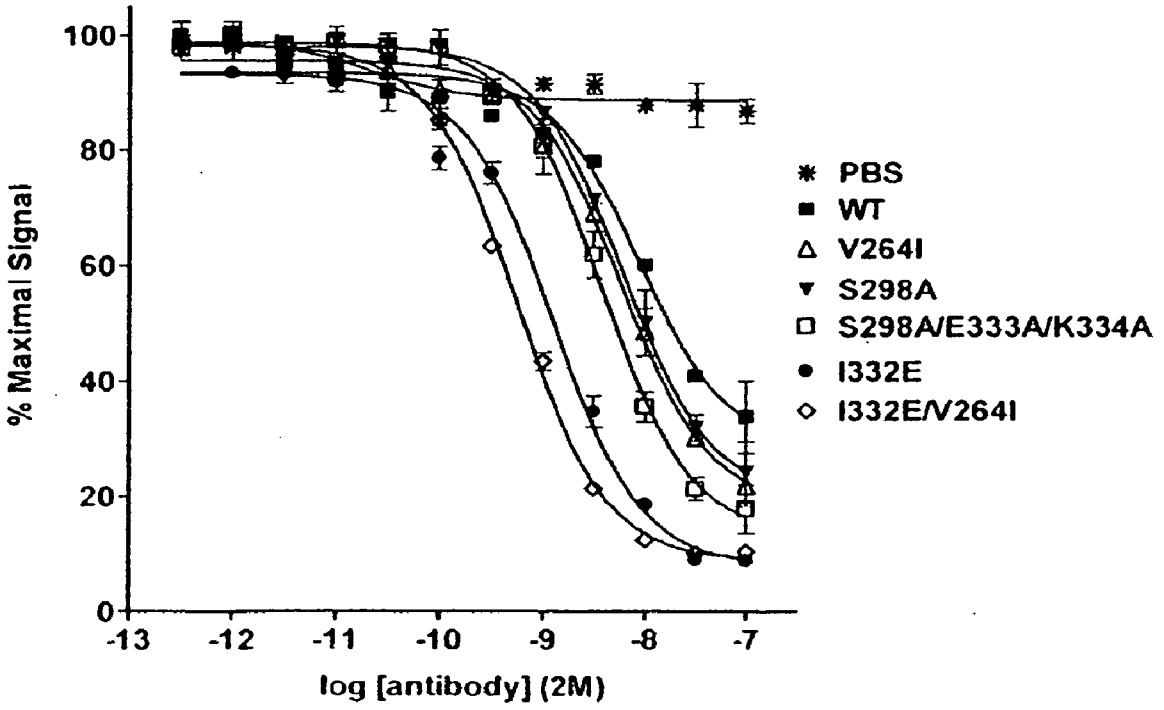


Figure 21a

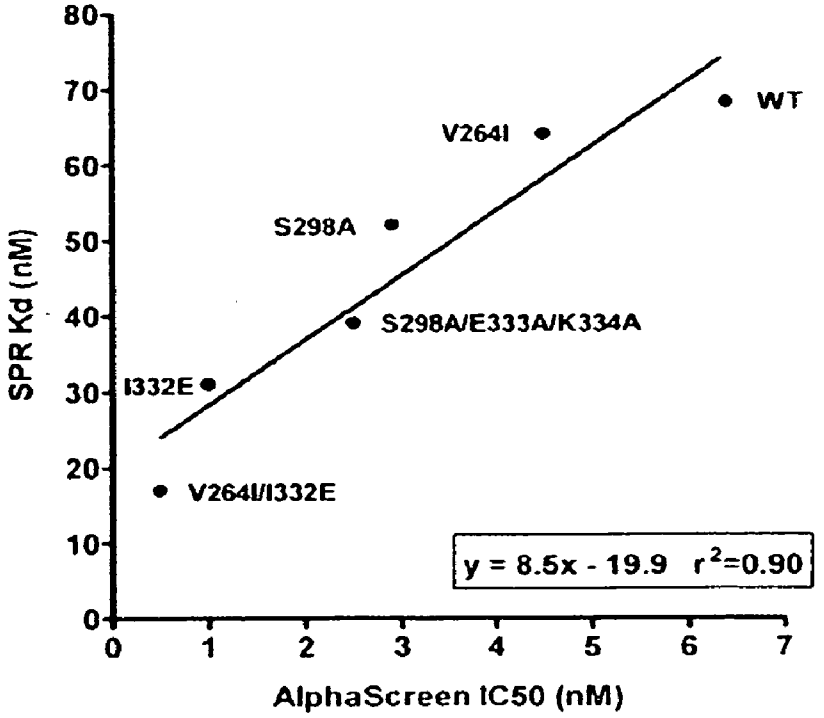


Figure 21b

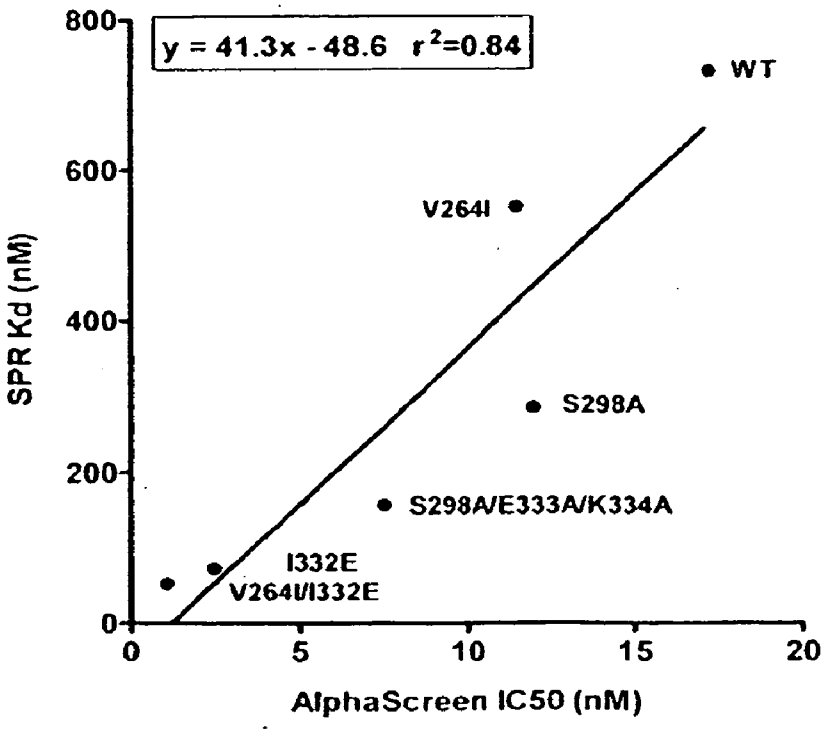


Figure 21c

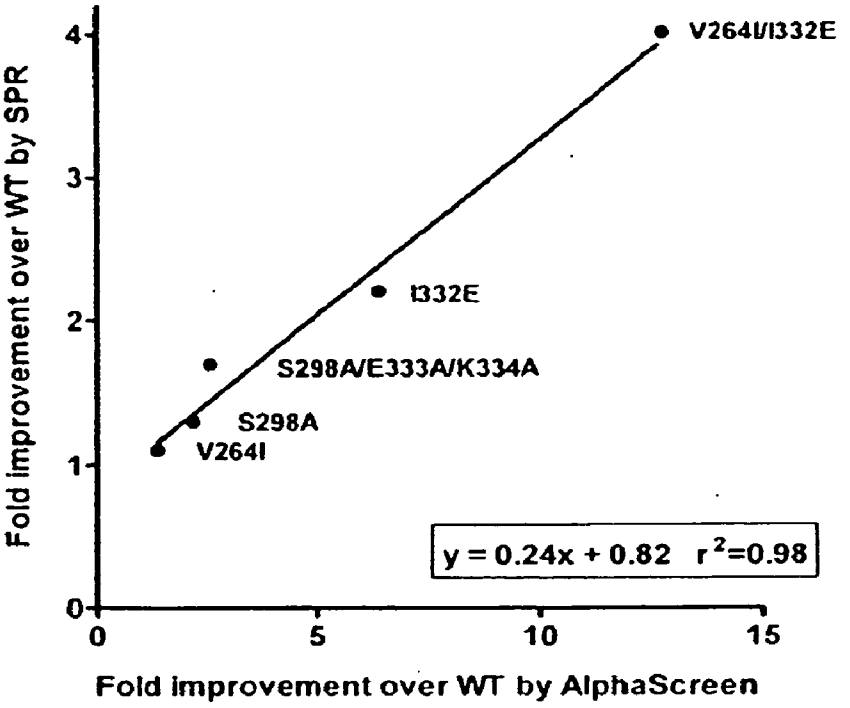


Figure 21d

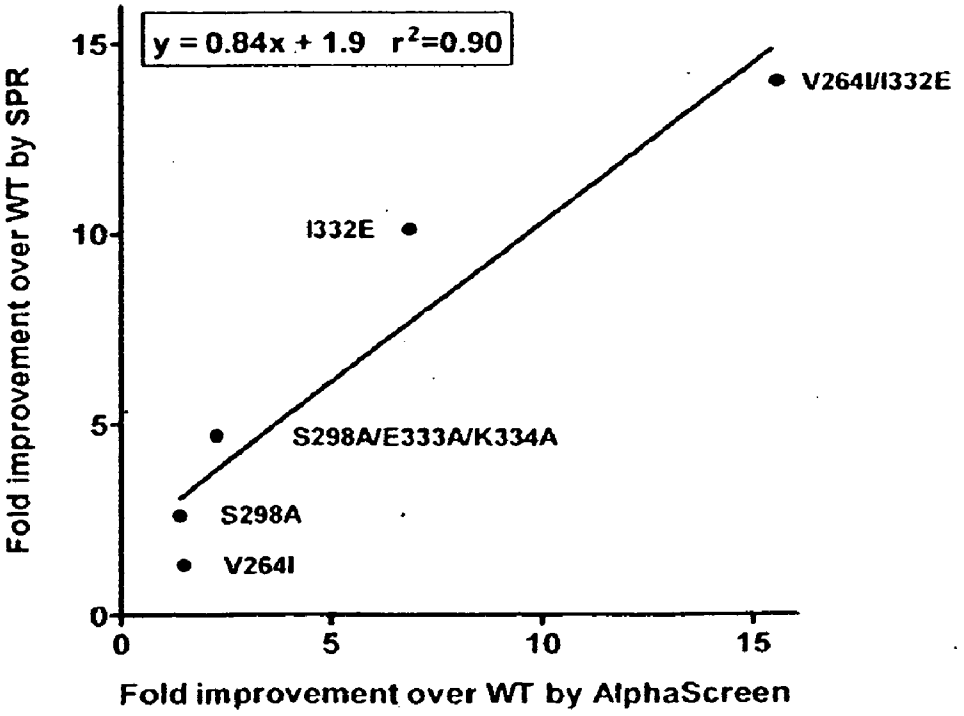


Figure 22a

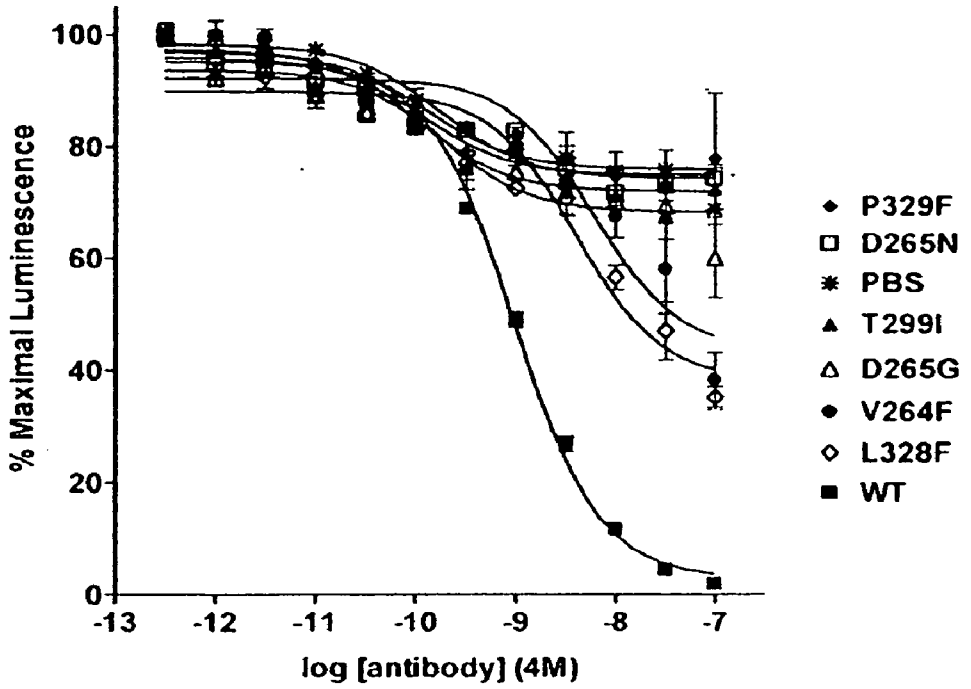


Figure 22b

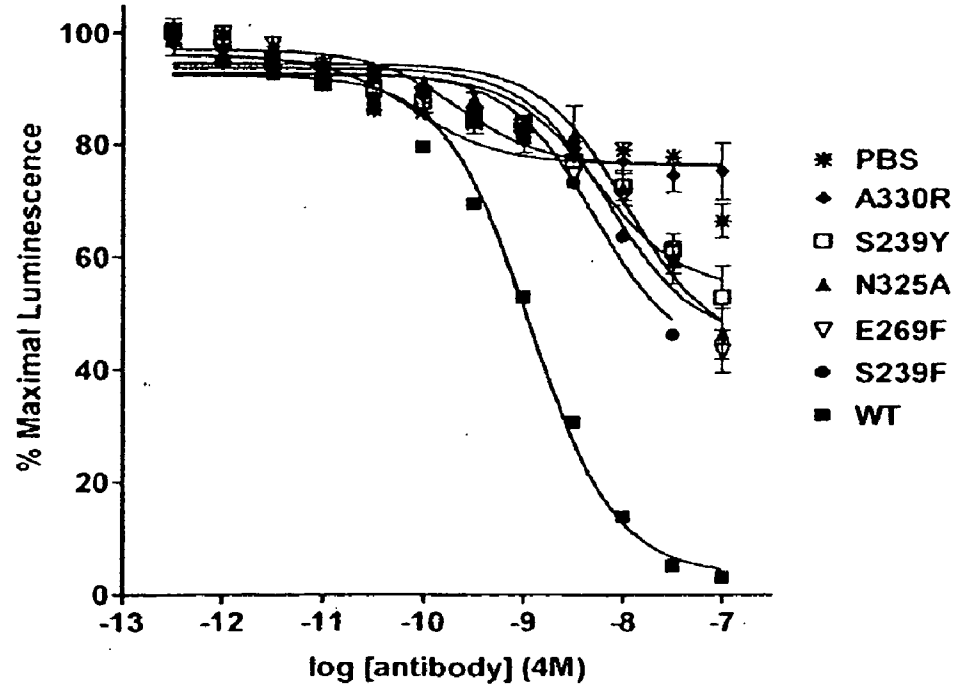


Figure 23a

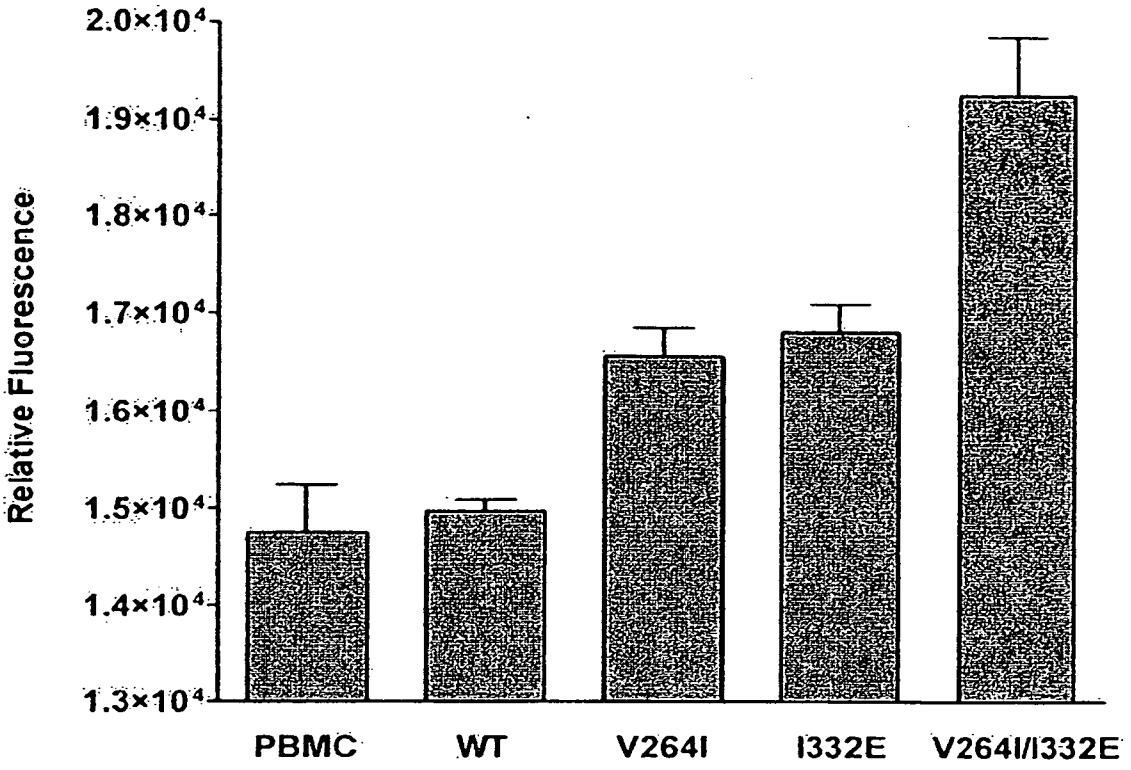

Relative Fluorescence
2.0×10⁴
1.9×10⁴
1.8×10⁴
1.7×10⁴
1.6×10⁴
1.5×10⁴
1.4×10⁴
1.3×10⁴
PBMC
WT
V264I
I332E
V264I/I332E

Figure 23b

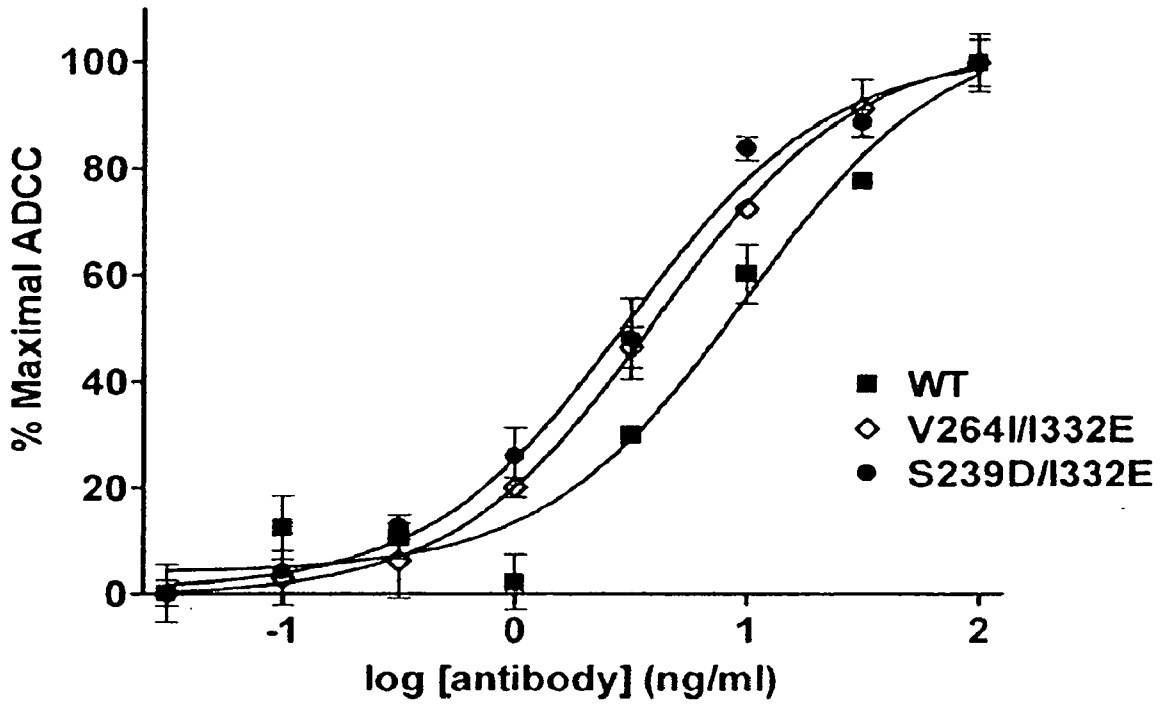

% Maximal ADCC
100
80
60
40
20
0
-1
0
1
2
log [antibody] (ng/ml)
WT
V264I/I332E
S239D/I332E

Figure 24a

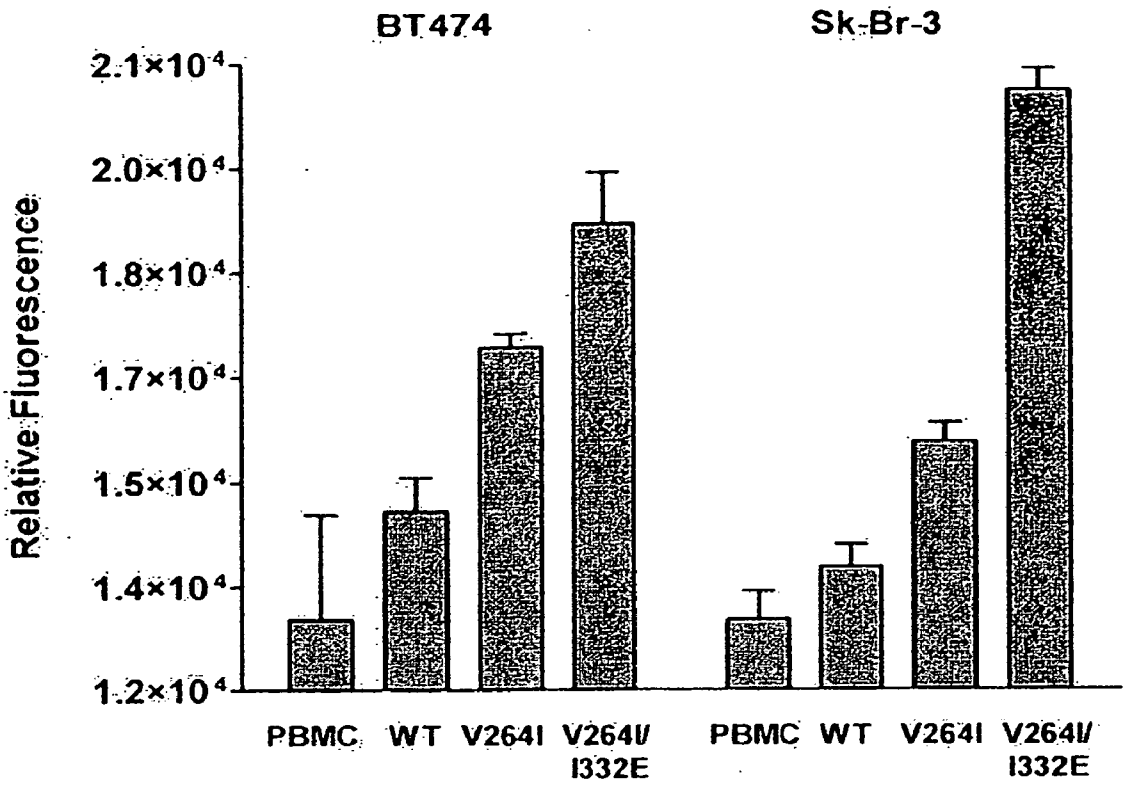

BT474
Sk-Br-3
Relative Fluorescence
2.1×10⁴
2.0×10⁴
1.8×10⁴
1.7×10⁴
1.5×10⁴
1.4×10⁴
1.2×10⁴
PBMC
WT
V264I
V264I/ I332E
PBMC
WT
V264I
V264I/ I332E

Figure 24b

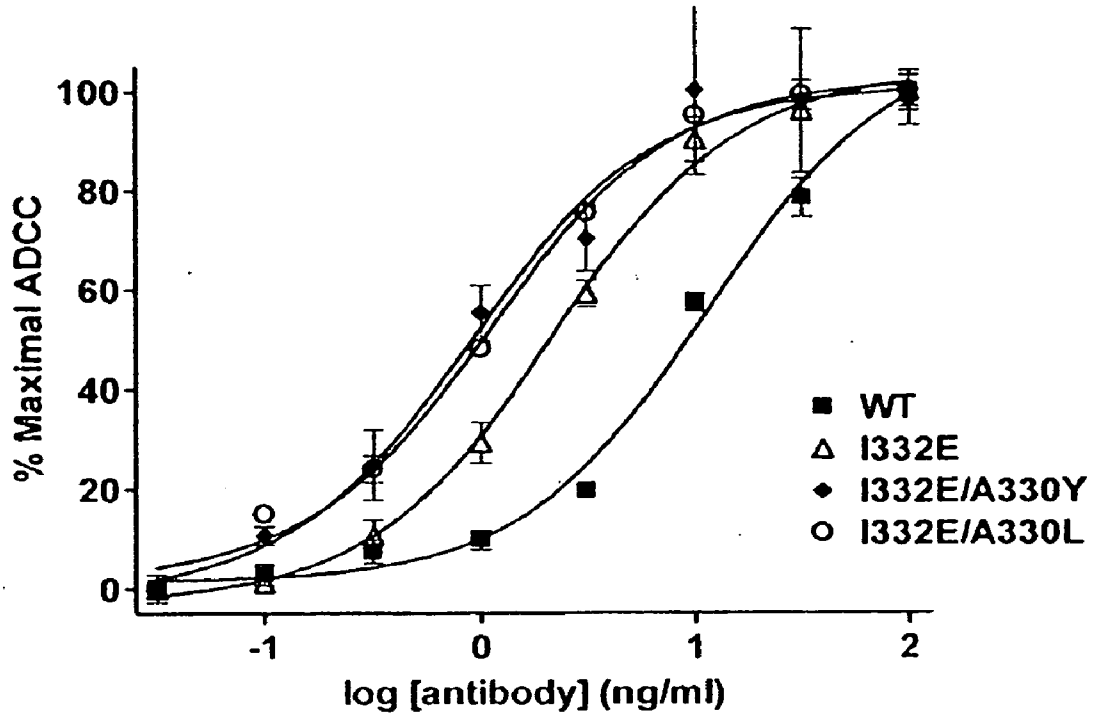


Figure 24c

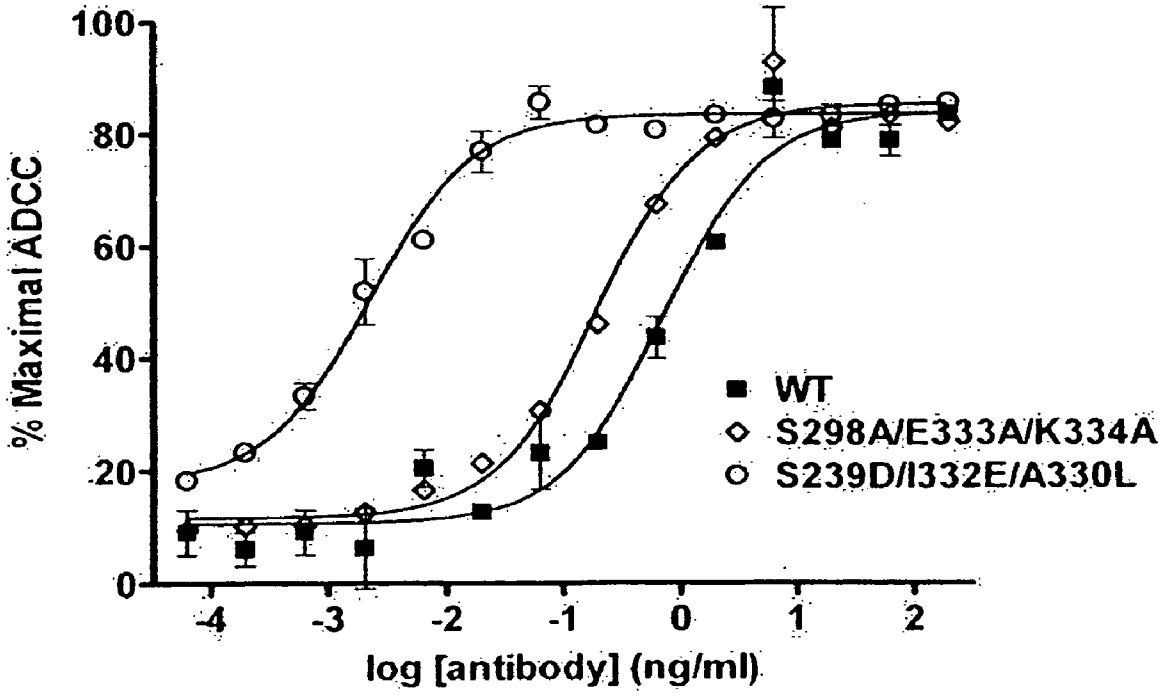


Figure 25a

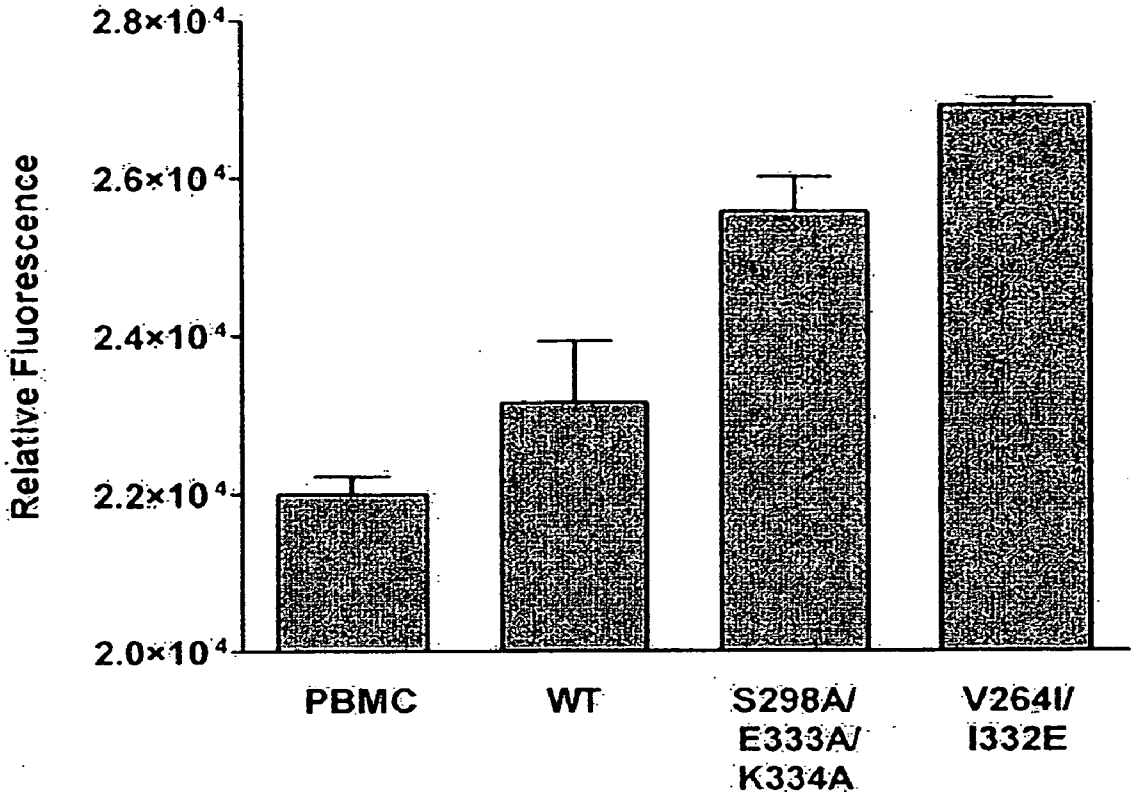

Relative Fluorescence
2.8×10⁴
2.6×10⁴
2.4×10⁴
2.2×10⁴
2.0×10⁴
PBMC
WT
S298A/ E333A/ K334A
V264I/ I332E

Figure 25b

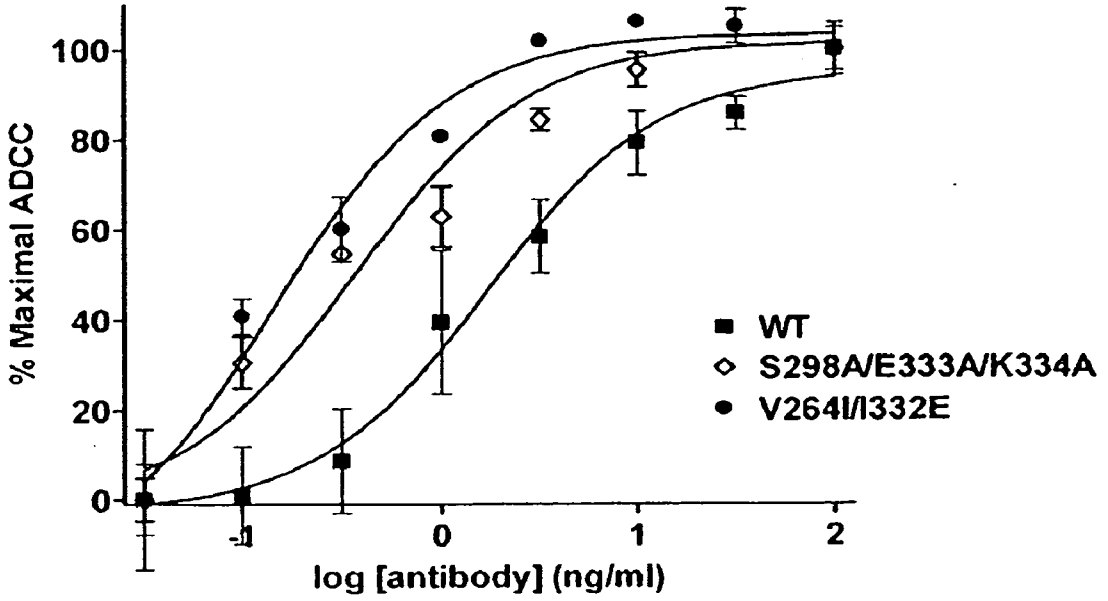


Figure 25c

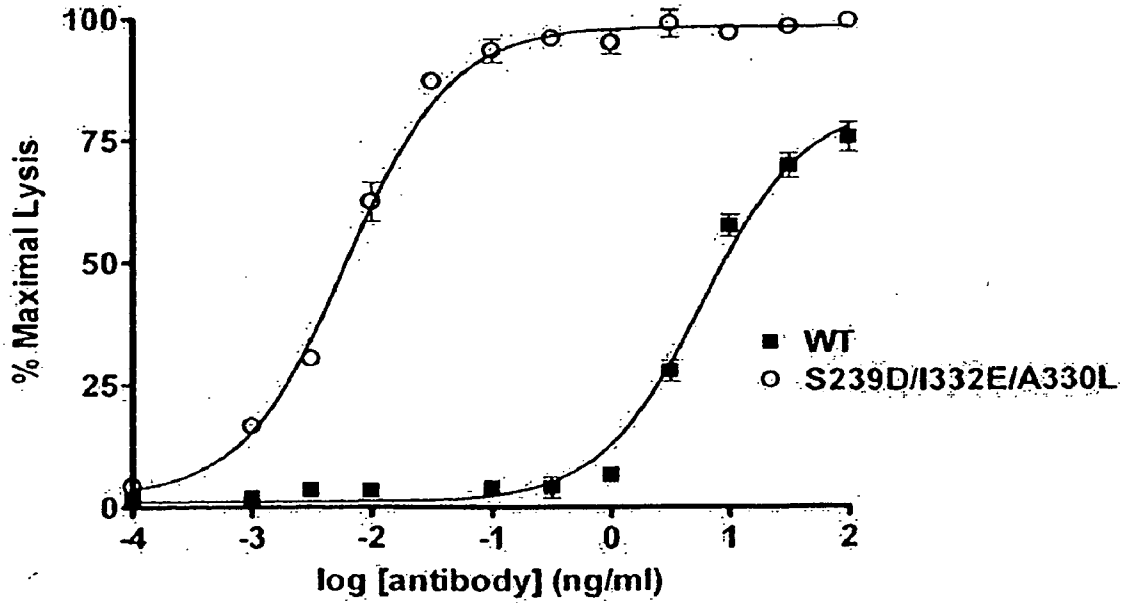


Figure 26a

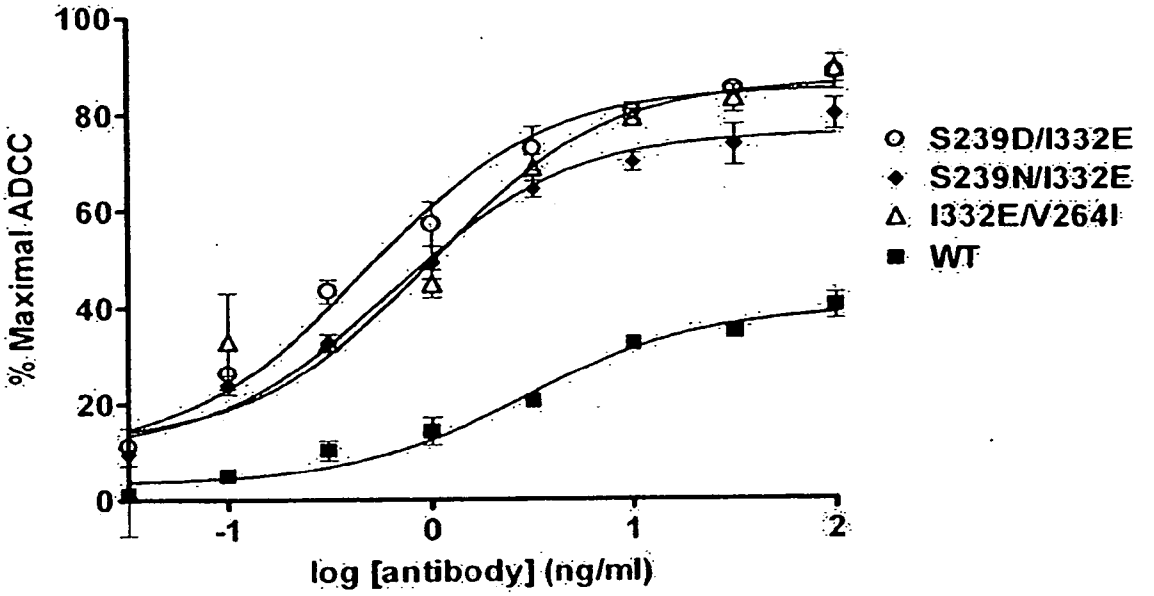


Figure 26b

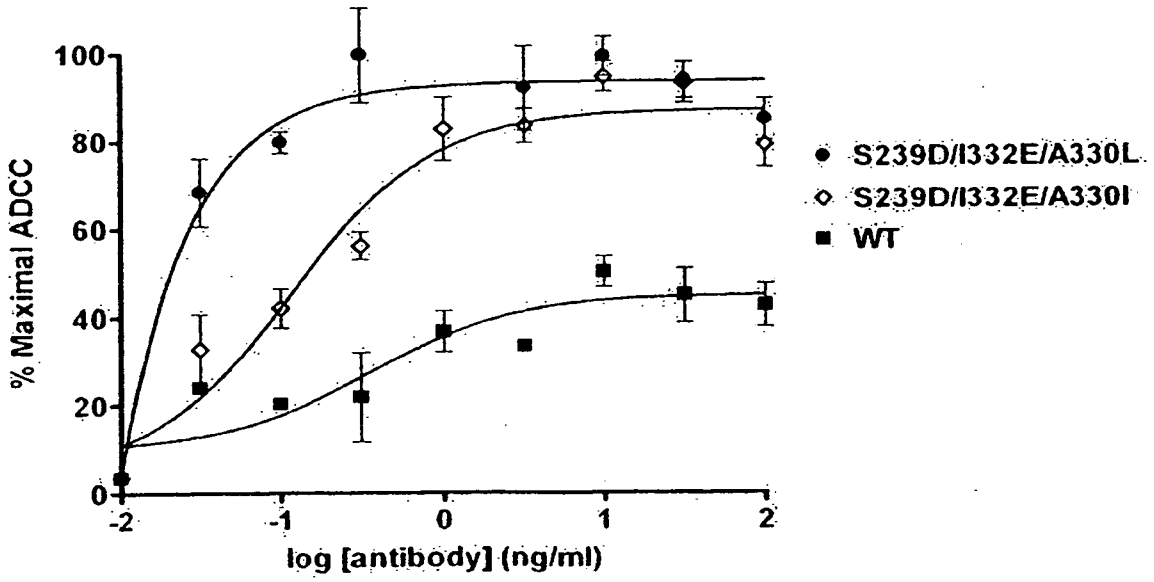


Figure 27

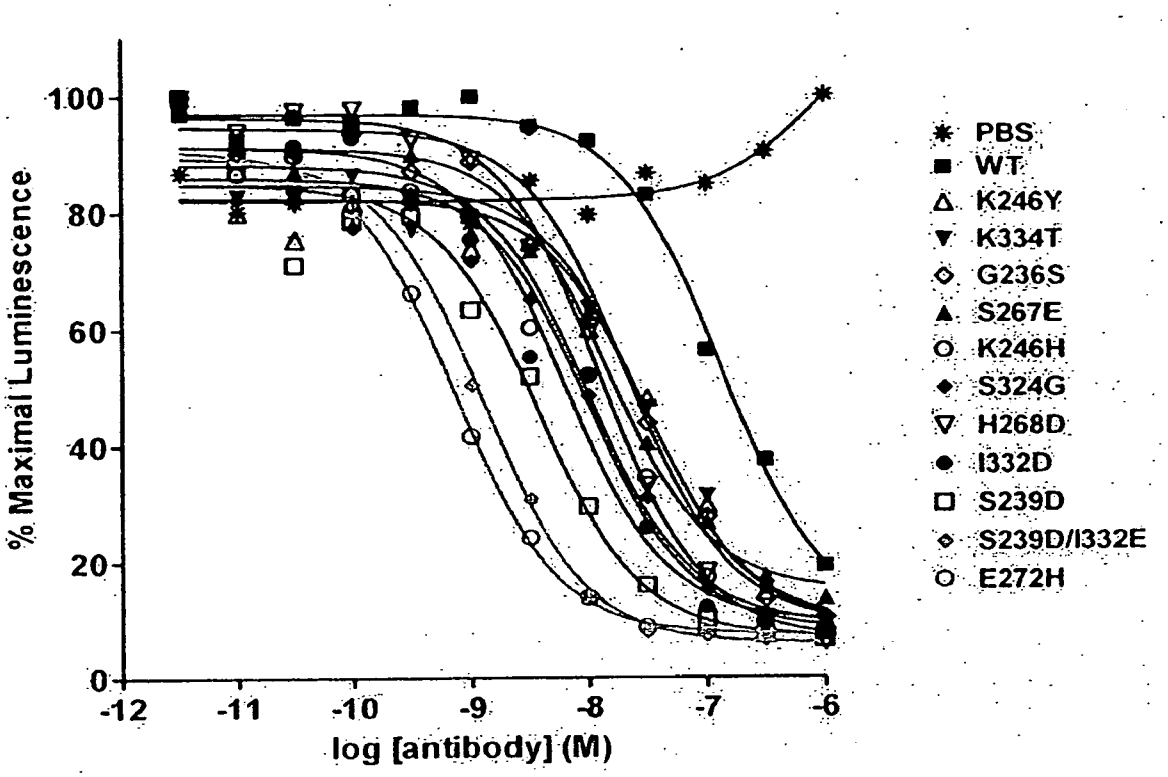

% Maximal Luminescence
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
log [antibody] (M)
PBS
WT
K246Y
K334T
G236S
S267E
K246H
S324G
H268D
I332D
S239D
S239D/I332E
E272H

Figure 28

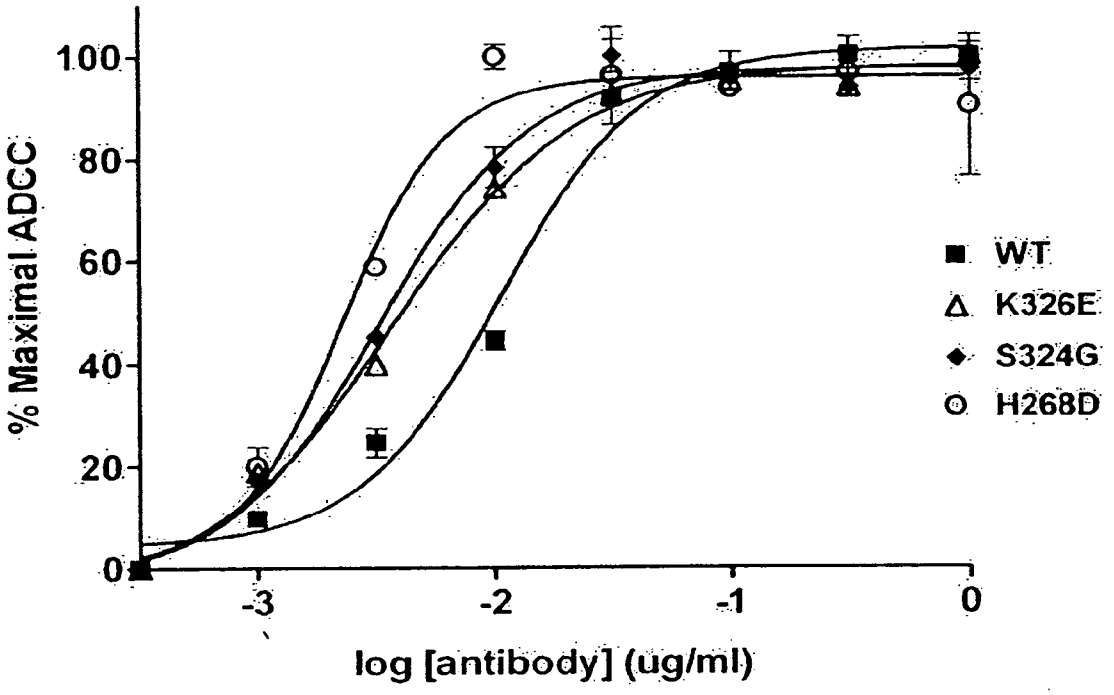

% Maximal ADCC
100
80
60
40
20
0
-3
-2
-1
0
log [antibody] (ug/ml)
WT
K326E
S324G
H268D

Figure 29a

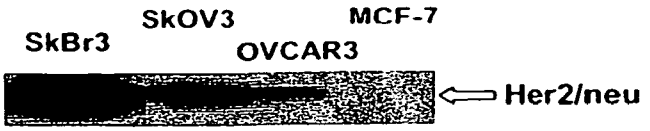


Figure 29b

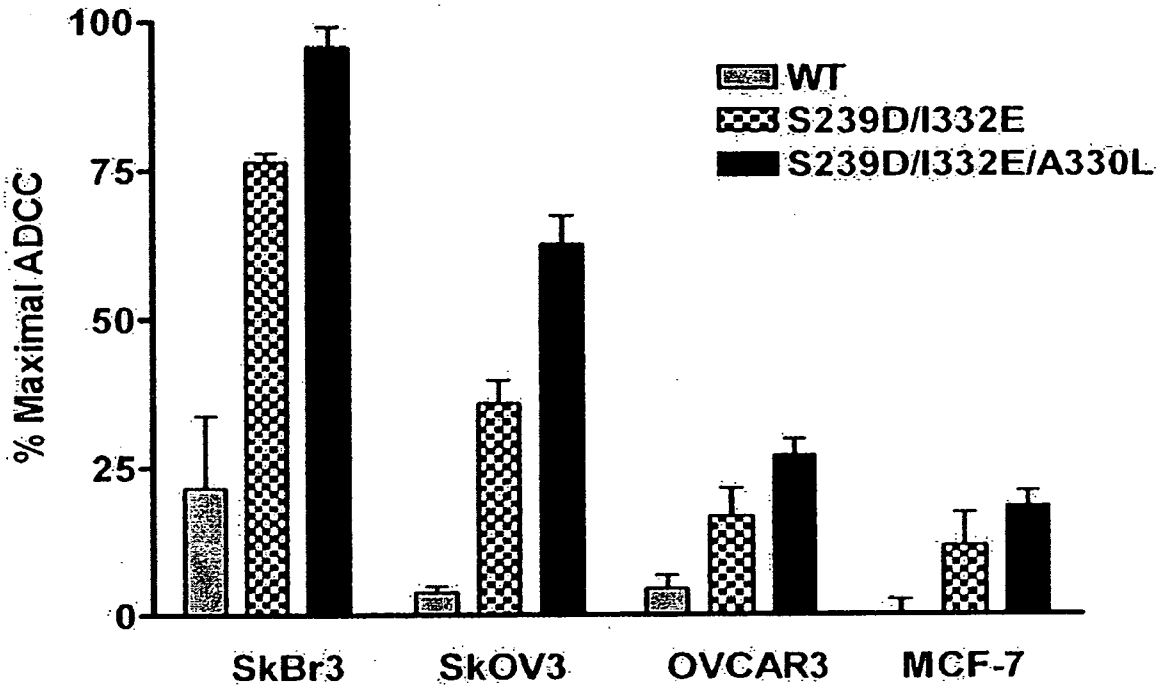


Figure 30

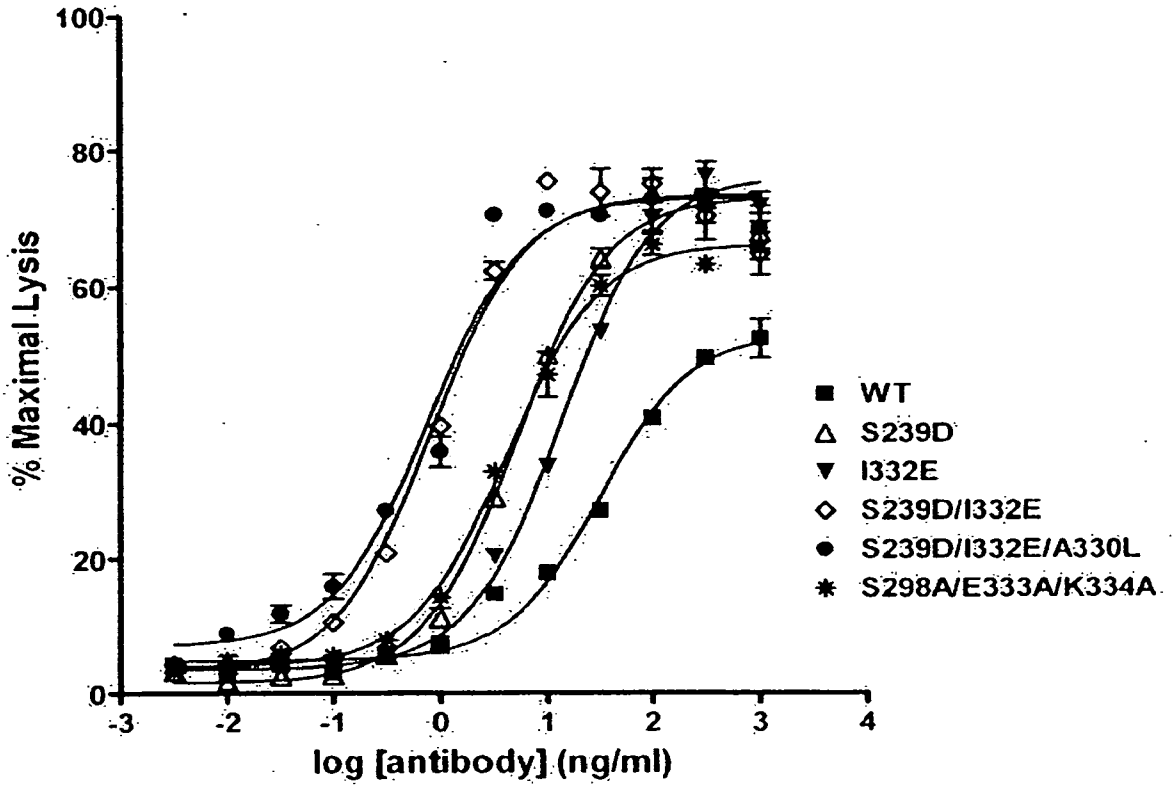

100
80
60
40
20
0
% Maximal Lysis
-3
-2
-1
0
1
2
3
4
log [antibody] (ng/ml)
WT
S239D
I332E
S239D/I332E
S239D/I332E/A330L
S298A/E333A/K334A

Figure 31

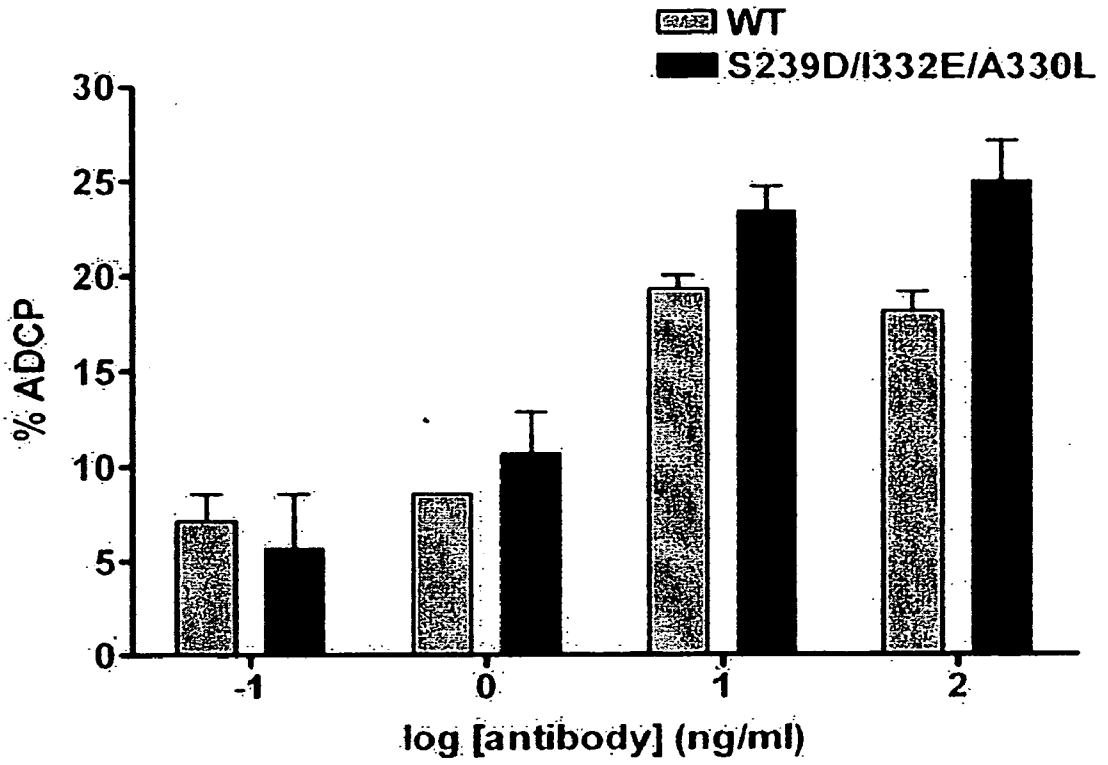

WT
S239D/I332E/A330L
% ADCP
30
25
20
15
10
5
0
-1
0
1
2
log [antibody] (ng/ml)

Figure 32a

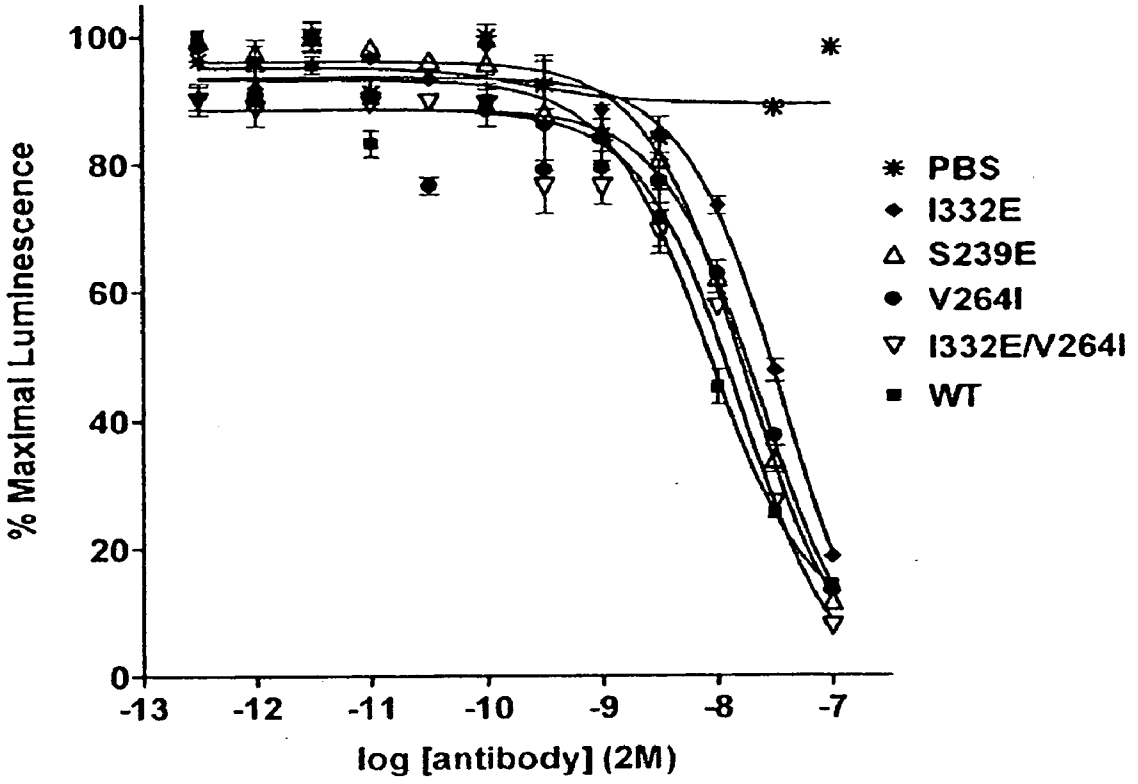

100
80
60
40
20
0
% Maximal Luminescence
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
PBS
I332E
S239E
V264I
I332E/V264I
WT

Figure 32b

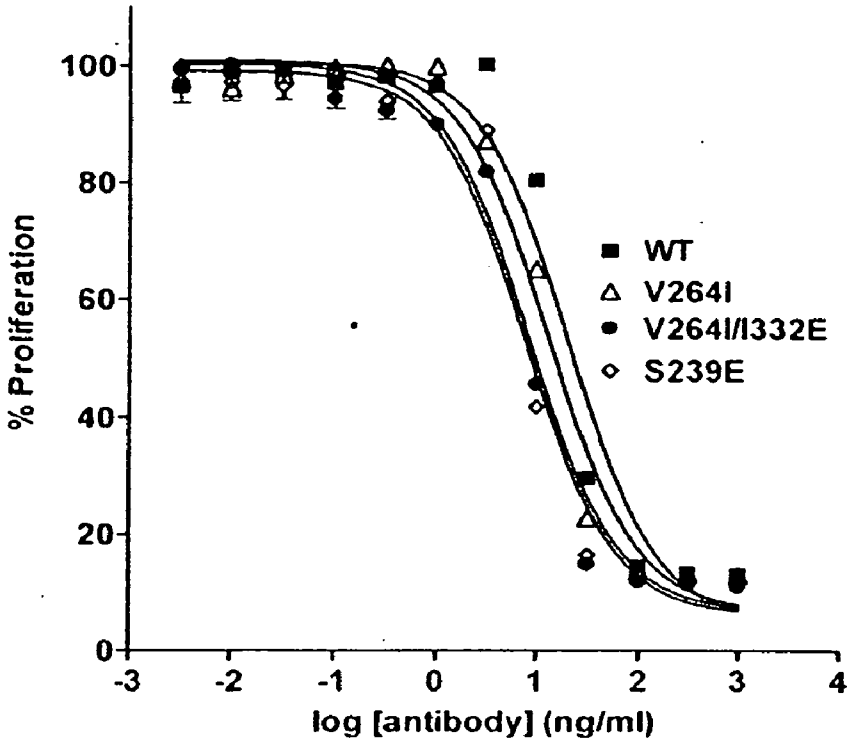


Figure 32c

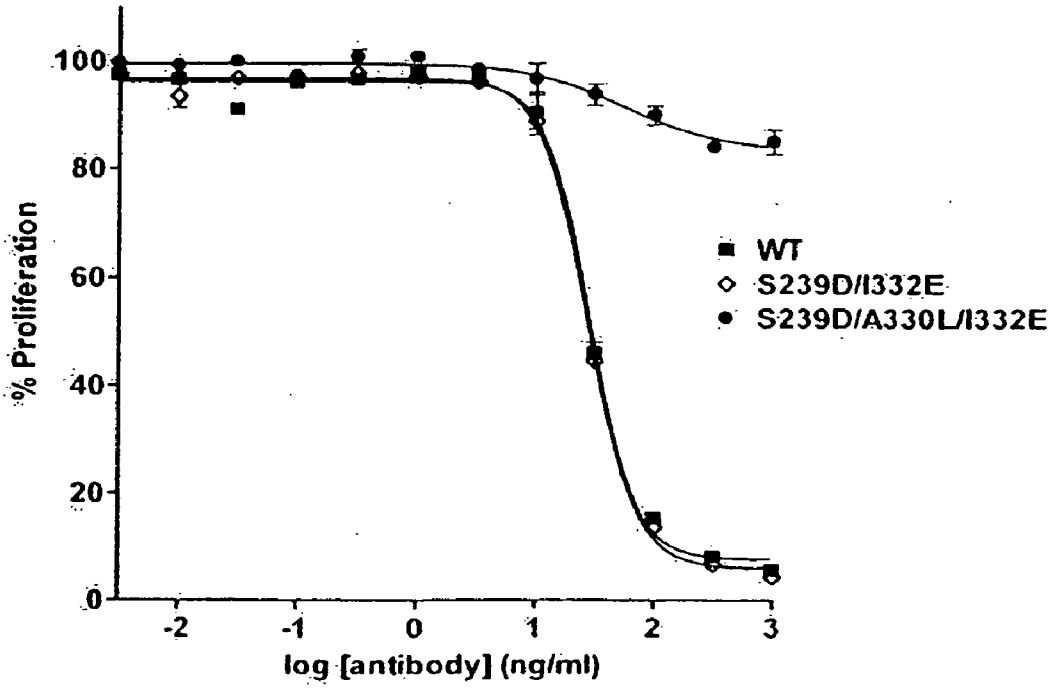


Figure 33a

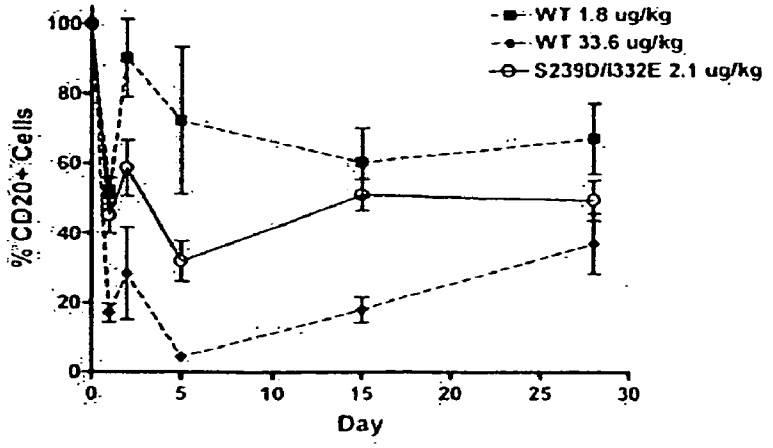


Figure 33b

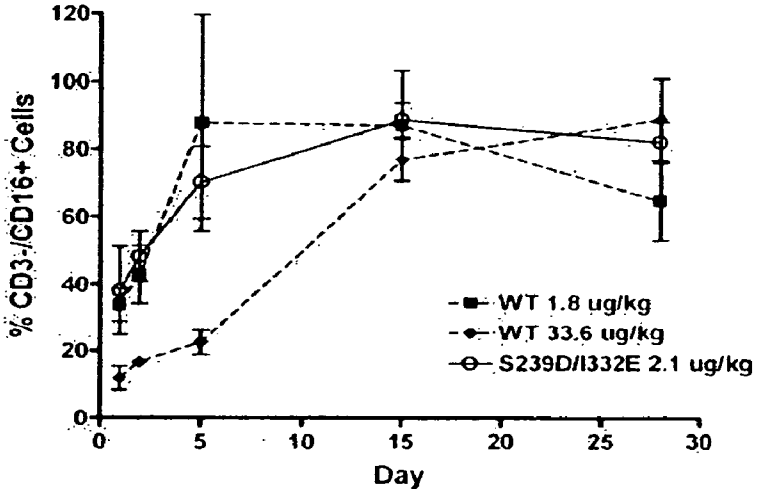


Figure 33c

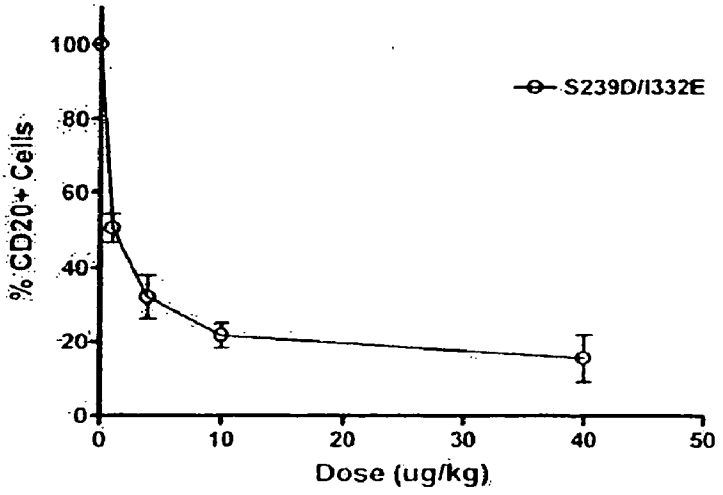


Figure 34a

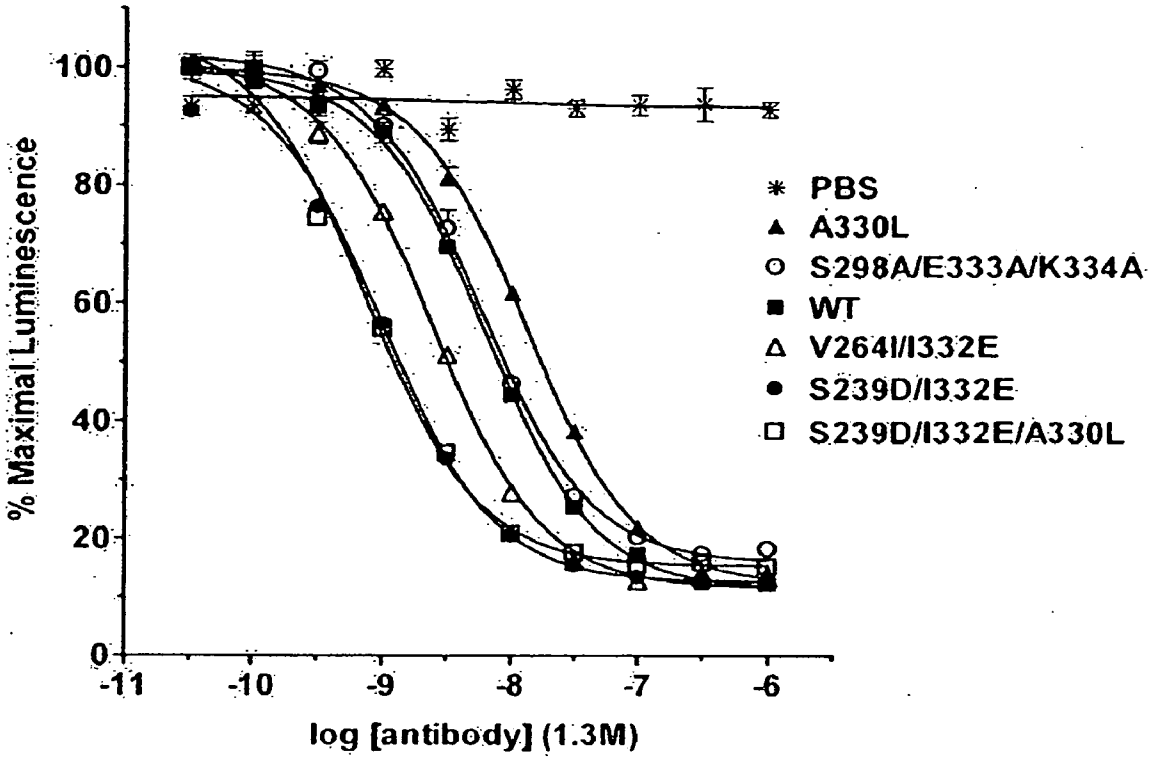

100
80
60
40
20
0
% Maximal Luminescence
-11
-10
-9
-8
-7
-6
log [antibody] (1.3M)
PBS
A330L
S298A/E333A/K334A
WT
V264I/I332E
S239D/I332E
S239D/I332E/A330L

Figure 34b

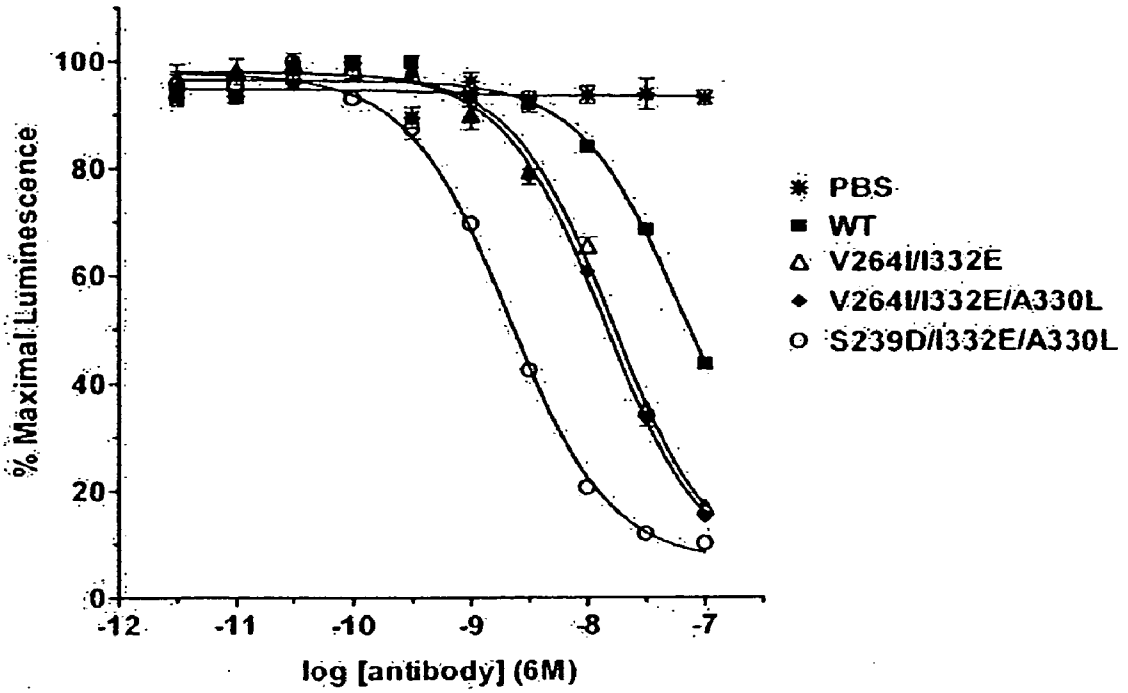


Figure 35c

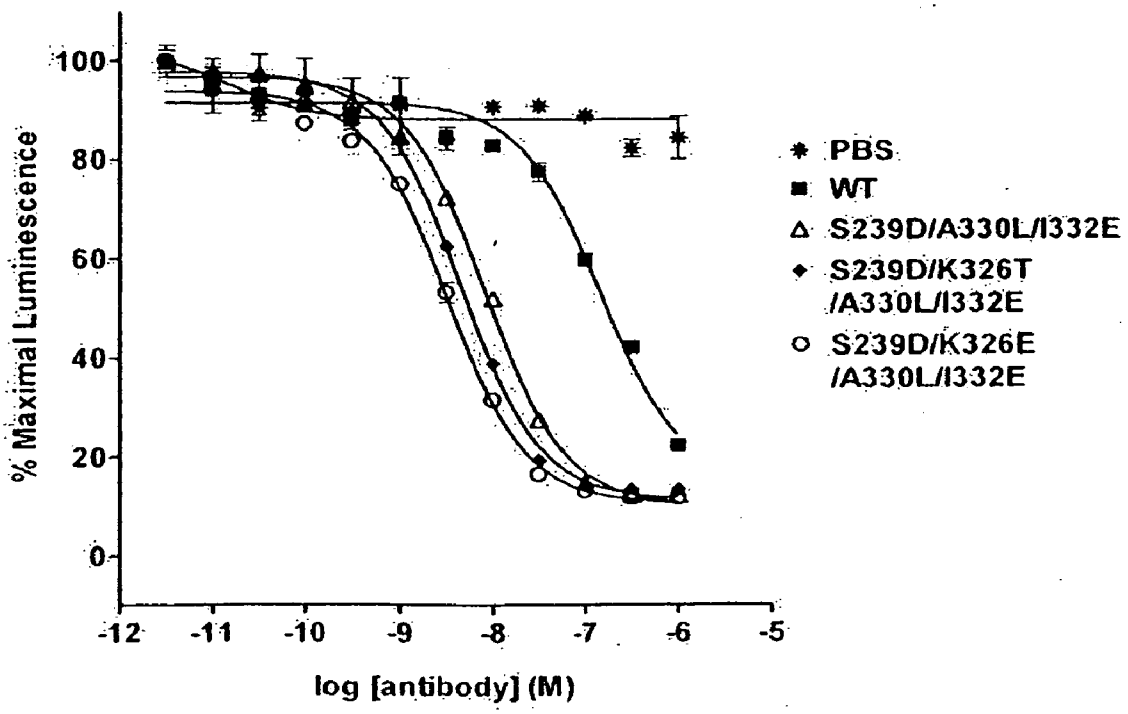


Figure 35

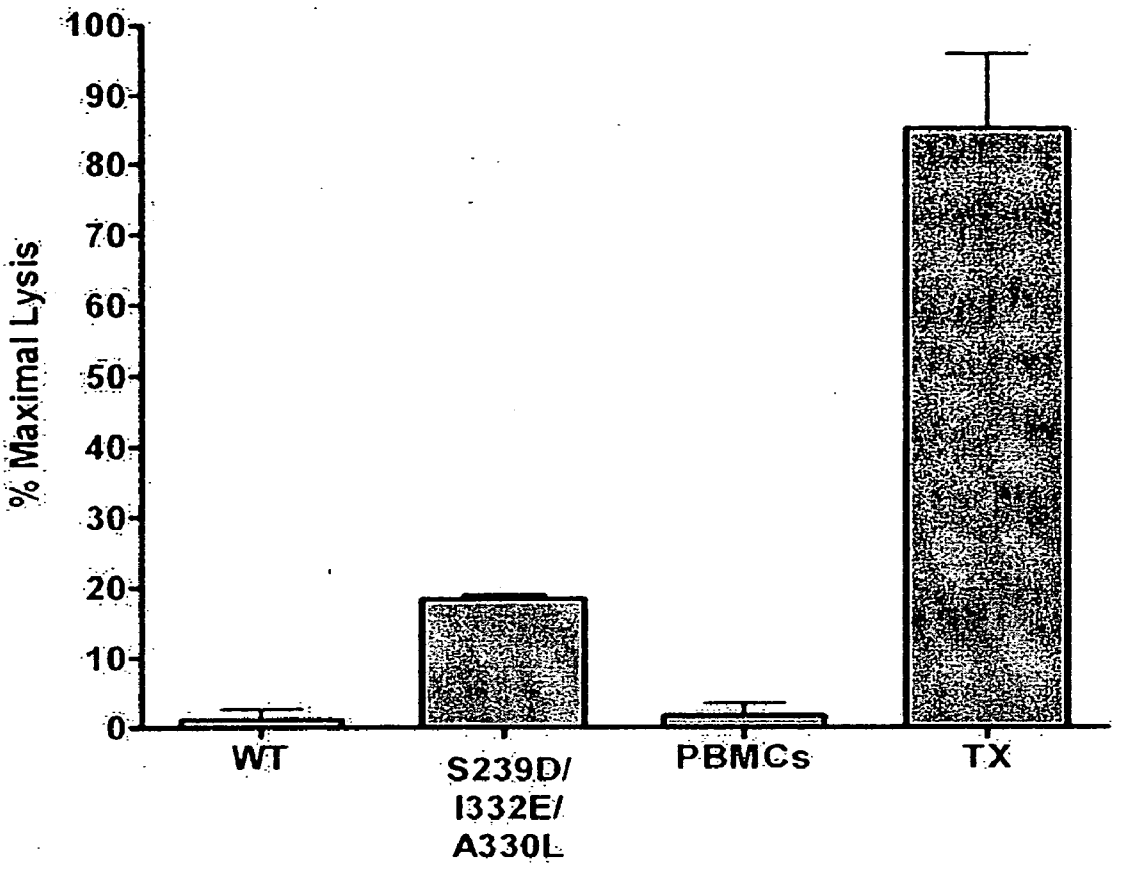

% Maximal Lysis
100
90
80
70
60
50
40
30
20
10
0
WT
S239D/
I332E/
A330L
PBMCs
TX

Figure 36

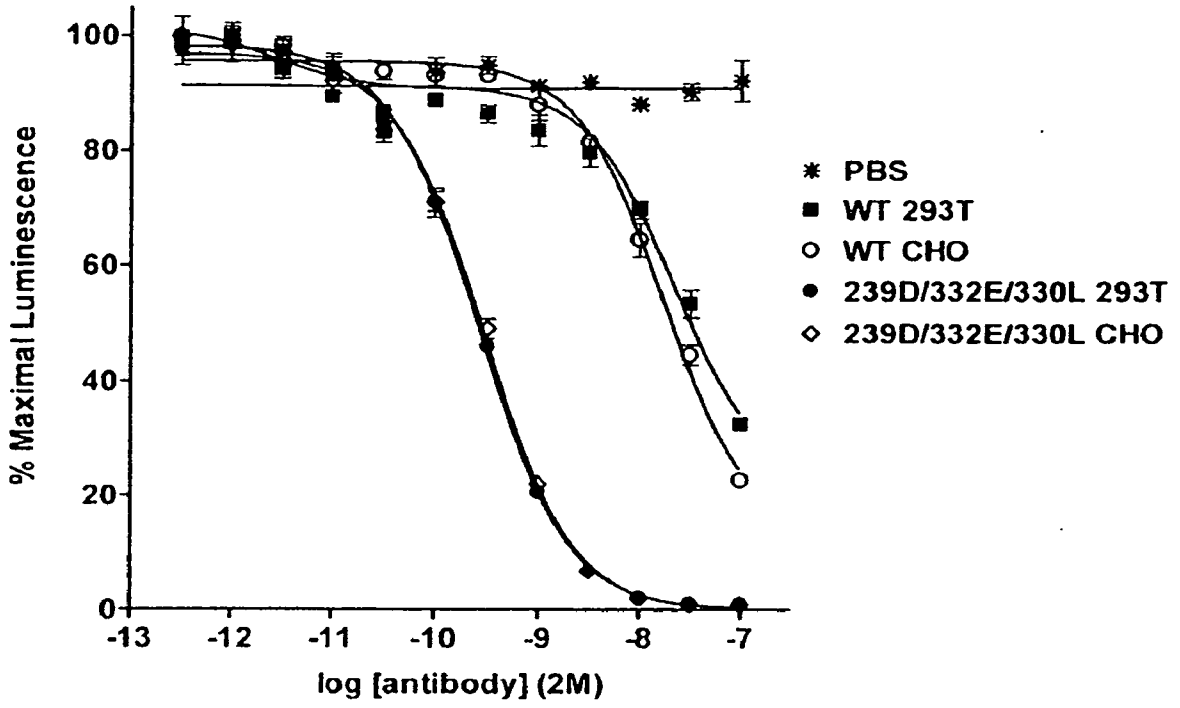

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2M)
PBS
WT 293T
WT CHO
239D/332E/330L 293T
239D/332E/330L CHO

Figure 37a

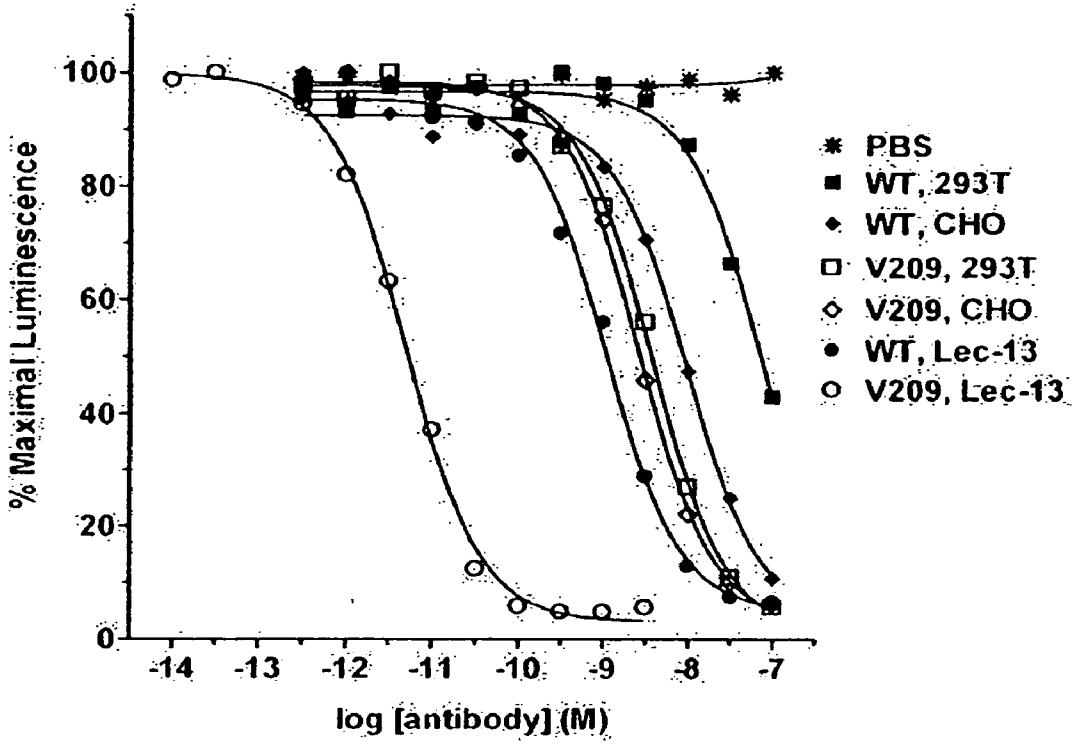


Figure 37b

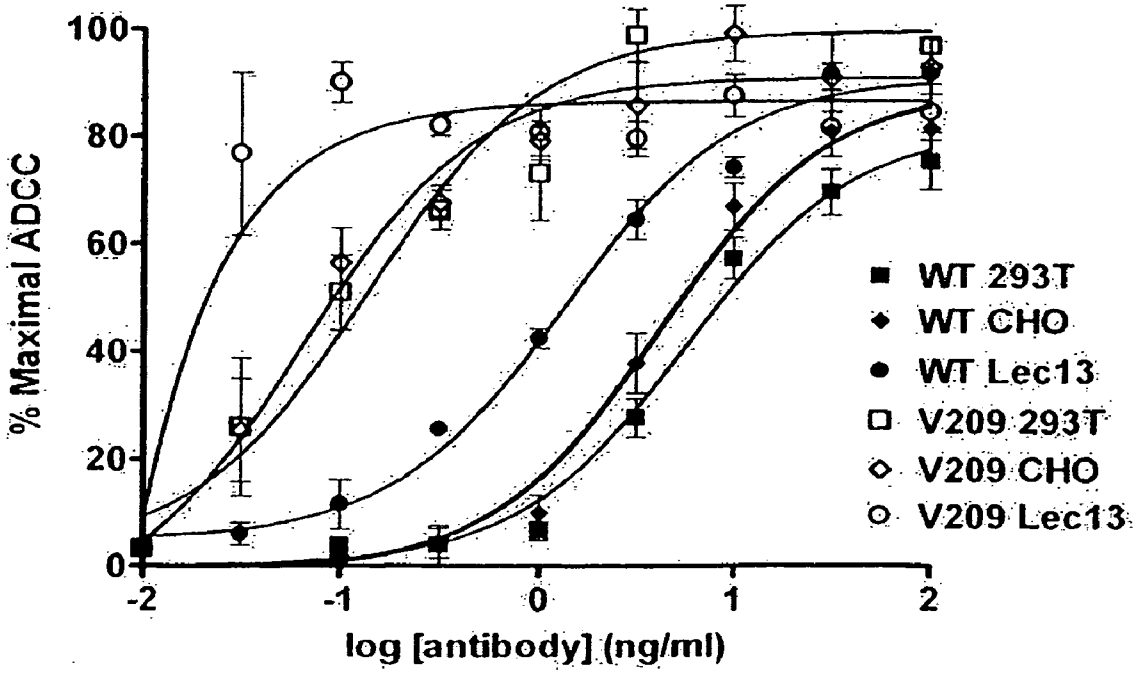


Figure 38

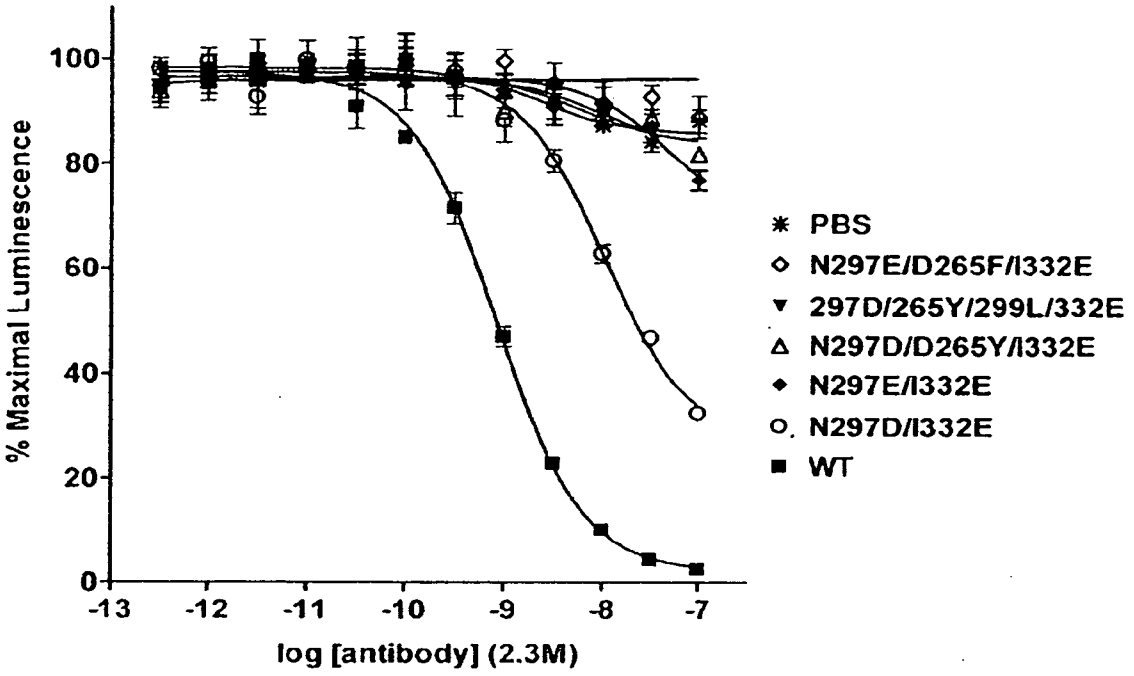

% Maximal Luminescence
100
80
60
40
20
0
-13
-12
-11
-10
-9
-8
-7
log [antibody] (2.3M)
PBS
N297E/D265F/I332E
297D/265Y/299L/332E
N297D/D265Y/I332E
N297E/I332E
N297D/I332E
WT

Figure 39

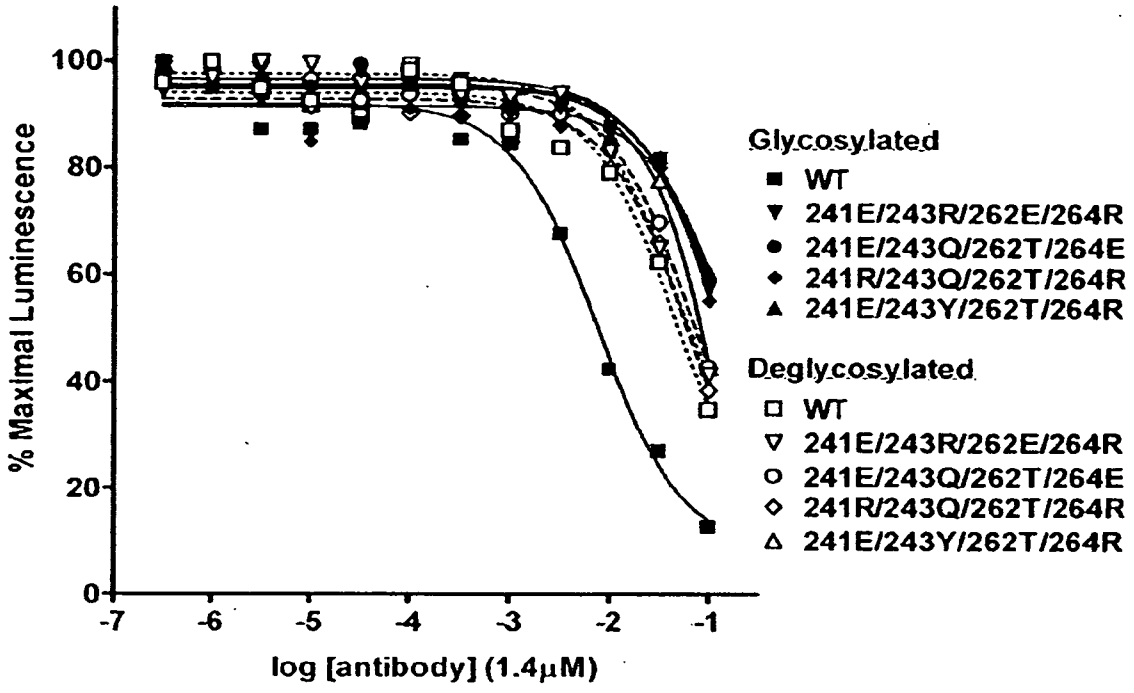

% Maximal Luminescence
100
80
60
40
20
0
-7
-6
-5
-4
-3
-2
-1
log [antibody] (1.4μM)
Glycosylated
WT
241E/243R/262E/264R
241E/243Q/262T/264E
241R/243Q/262T/264R
241E/243Y/262T/264R
Deglycosylated
WT
241E/243R/262E/264R
241E/243Q/262T/264E
241R/243Q/262T/264R
241E/243Y/262T/264R

Figure 40a

Anti-CD20 heavy chain comprising possible Fc variants

QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFK
GKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSAASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPX_1X_2FLFPPKPKDTLMISRTPEVTC
VVX_3DVSX_4EDPX_5VX_6FNWYVDGVEVHNAKTKPREEQYX_7Z_1TYRVVSVLTVLHQDWLNGKEYKCKV
SNZ_2ALPX_8PX_9EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Position	WT	Possible Substitutions
X_1	S	D, E, N, Q, T
X_2	V	I, M
X_3	V	I, T, Y
X_4	H	D, E
X_5	E	Y
X_6	K	E
X_7	N	D
X_8	A	Y, L, I
X_9	I	D, E, N, Q
Z_1	S	A D
Z_2	K	E, T

Figure 40b

Anti-CD20 light chain

QIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVRFSGSGSG
TSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL
NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS
SPVTKSFNRGEC

Figure 40c

Anti-CD20 heavy chain

QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKFK
GKATLTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSAASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLG
TQTYICNVNHKPSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 41

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
1	V264A	a	0.67	0.06	0.32	0.69	1.03	0.40	0.91	0.57	0.14	0.25	2.16	0.23	1.12	0.18	0.13
2	V264L	a	0.76	0.07	0.43	0.67	1.17	0.33	0.90	0.56	0.53 0.22	0.31	1.44	0.21	0.81	0.17	0.19
3	V264I	a r r	1.35	0.05	0.70	0.57	1.28	0.33	1.05	0.51	0.56 0.84	0.22	8.58	0.56	1.32	0.18	0.66
4	F241W	a	1.59	0.13	0.68	0.62	1.10	0.34	0.85	0.57	1.43 0.32	0.23	3.68	0.21	1.70	0.25	0.29
5	F241L	a	0.84	0.25	0.77	0.57	1.20	0.34	1.12	0.50	0.29 0.24	0.27	3.24	0.30	1.99	0.48	0.20
6	F243W	a	1.61	0.23	1.71	0.58	1.44	0.34	1.11	0.45	0.26 1.12	0.18	2.88	0.24	4.63	0.26	0.78
7	F243L	a	0.51	0.07	0.31	0.63	1.00	0.44	0.72	0.72	0.51 0.43	0.26	2.47	0.21	0.64	0.12	0.43
8	F241L/F243L/V262I/V264I	a	0.80 0.51	0.21 0.10	0.10	0.36	0.49	24.05 0.57	8.39	6.19	0.51 0.06 0.05	0.66 0.48	1.24	0.20	0.44	0.19	0.10
9	F241W/F243W	a	1.13	0.07	0.81	0.59	1.39	0.38	0.96	0.54	0.09 0.28	0.21	1.88	0.27	1.12	0.12	0.20
10	F241W/F243W/V262A/V264A	a	0.50	0.12	0.28	0.58	1.33	0.32	1.06	0.53	0.07 0.19	0.23	2.13	0.19	1.91	0.15	0.15
11	F241L/V262I	a	1.30	0.10	0.27	0.59	0.75	0.36			0.04 0.17 0.06	0.25	5.29	0.63	1.37	0.17	0.23
12	F243L/V264I	a	1.02	0.12	0.34	0.68	0.69	0.38			0.72	0.21	3.94	0.30	0.71	0.34	1.04
13	F243L/V262W/V264W	a	0.32 0.30	0.26 0.18	0.12 0.24	0.31 195	0.91	24.05 0.44	15.82 1.05	5.78 28.03	1.23 0.03 0.55	0.51 0.24	3.72	0.62	1.35	0.42	0.60
14	F241Y/F243Y/V262T/V264T	a	0.58 0.66	0.19 0.23	0.18 0.25	0.32 1.97	1.17	24.04 0.35	30.49 1.01	5.72 9.71	0.02 0.06 0.47	0.42 0.19	1.19	0.36	1.89	0.57	0.40
15	F241E/F243R/V262E/V264R	a	0.05 0.06	0.39 0.11	0.04	0.61	0.69	24.05 0.52	10.73 0.67	5.99 1.52	0.05 0.48	0.24	1.51	0.18	0.28	0.16	0.70
16	F241E/F243Q/V262T/V264E	a	0.02 0.01	0.31 0.27	0.10	0.99	0.36	24.07 0.67	5.62	6.06	0.05 0.07	0.30	1.34	0.24	0.24	0.23	0.19
17	F241R/F243Q/V262T/V264R	a	0.01 0.16	0.63 0.11	0.07 0.21	0.51 521	1.00	24.06 0.35	17.05 0.71	5.77 0.80	0.07 0.80	54.64 0.19	1.58	0.22	0.45	0.27	0.79
18	F241E/F243Y/V262T/V264R	a	0.17 0.12	0.24 0.18	0.08 0.18	0.30 63.41	0.94	24.05 0.38	17.48 0.83	5.79 1.39	0.02 0.02 0.51	1.23 0.19	1.24	0.19	0.54	0.29	0.55
19	L328M	a	2.07 1.33	5407 0.07	0.47 0.85	0.35 0.56	1.90	24.04 0.32	0.19 1.29	9.68 0.46	0.05 0.62	0.28 0.22	5.40	0.57	0.84	0.21	0.32
20	L328E	a	2.17 1.23	0.17 0.10	0.07 0.23	0.34 124	1.90	24.04 0.33	1.07	0.54	0.21 0.07 0.72	0.34 0.21	2.55	0.36	0.73	0.31	0.38
21	L328F	a	1.38 0.99	0.17 0.18	0.13 0.25	0.30 2.89	5.14	24.05 0.33	71.81 4.13	5.62 0.45	0.12 0.00	4.94	2.48	0.35	2.06	0.46	
22	I332E	a r p	3.97 2.08	0.19 0.13	1.09 1.26	0.60 0.21	1.92 2.37	0.33 0.37	1.27 2.64	0.49 0.34	0.24 3.57 1.22	0.19 2.82	4.28	0.56	1.32 0.78	0.44 0.41	1.86 0.52
23	L328M/I332E	a	0.30	0.19	0.28	0.35	3.93 0.90	0.12	0.82	0.12	6.72 0.21	0.15	0.05	0.64			1.71 0.24
24	P244H	a	1.05	0.34	0.53	0.67	1.02	0.42	0.79	0.68	2.6 0.64	0.23	1.42	0.26	0.46	0.14	0.62
25	P245A	a	0.84	0.11	0.46	0.65	0.70	0.52			0.83 0.45	0.22	2.00	0.26	0.44	0.27	0.64
26	P247V	a	1.06	0.12	0.99	0.58	1.34	0.48	0.88	0.54	0.25 0.62 0.53	0.20	1.45	0.31	0.43	0.24	0.46
27	W313F	a	0.82	0.11	0.38	0.65	0.64	0.39			0.24	0.20	1.36	0.19	0.47	0.25	0.38
28	P244H/P245A/P247V	a	0.98	0.09	0.68	0.57	0.73	0.32			0.88 0.52	0.23	4.95	0.54	0.52	0.25	0.71
29	P247G	a	1.57	0.20	0.35	0.70	0.69	0.40	0.83	8.15	0.93 0.28 0.54	0.22	1.72	0.24	0.68	0.45	0.41
30	V264I/I332E	a r r c	1.65 4.58	0.18 0.20	0.79 0.89	0.54 0.23	2.13 5.08	0.36 0.40	1.41 2.80	0.49 0.31	4.80 3.00	0.19 2.82	4.07	0.38	1.70 0.89	0.61 0.38	2.25 0.59
							1.57				12.5						7.96

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
31	F241E/F243R/V262E/V264R/A332E	a									0.19						
32	F241E/F243Q/V262T/V264E/A332E	a															
33	F241R/F243Q/V262T/V264R/A332E	a															
34	F241E/F243Y/V262T/V264R/A332E	a									0.1						
35	S298A	a									2.21						
36	S298A/A332E	a									21.7						
37	S298A/E333A/K334A	a t r p									2.56						
41	S239E/A332E	a	3.64	0.21	3.22	0.13	8.73	0.11	8.29	0.17	88.98	0.33	0.76	0.29	1.34	0.31	10.19
							3.49				5.8						1.66
42	S239Q/A332E	a	2.08	0.23	1.91	0.14	3.68	0.13	3.64	0.18	13.85	0.42	1.67	0.20	1.33	0.37	3.77
							4.68				6.6						1.41
43	S239E	a t	2.17	0.23	1.38	0.15	2.18	0.11	3.01	0.23	51.22	0.47	0.95	0.21	1.47	0.85	23.47
											10.2						
44	D265G	a	0.17	0.22	1.97	0.10	4.86	0.09	3.19	0.15	4.37	0.38	0.72	0.28	1.74	0.52	0.90
											<0.02						
45	D265N	a	0.02	0.31	0.95	0.14	0.90	0.14	0.58	0.18		1.30	0.55	0.31	0.48	0.28	
											<0.02						
46	S239E/D265G	a	0.11	0.42	0.75	0.12	0.93	0.11	0.95	0.22			1.15	0.22	0.50	0.34	
											<0.02						
47	S239E/D265N	a	0.12	0.26	0.61	0.12	1.39	0.09	1.11	0.15	1.51	0.38	0.63	0.25	0.52	0.35	1.08
											0.02						
48	S239E/D265Q	a	0.65	0.23	0.53	0.15	0.99	0.12	1.00	0.18			1.74	0.19	0.37	0.55	
											0.05						
49	Y296E	a	1.56	0.22	1.09	0.13	1.28	0.12	1.66	0.19	1.04	0.49	1.85	0.18	1.23	0.60	0.81
							1.11				0.73						0.66
50	Y296Q	a	0.81	0.23	1.18	0.19	2.49	0.15	2.45	0.19	2.13	0.37	1.18	0.22	0.31	0.50	0.85
							0.43				0.52						1.21
51	S298T	a	1.33	0.23	1.15	0.15	1.44	0.10	1.63	0.19	2.04	0.35	1.90	0.19	2.13	0.76	1.41
							<0.02				0.94						
52	S298N	a	0.59	0.24	0.80	0.14	1.27	0.13	0.91	0.17			1.28	0.21	0.94	0.31	
							<0.02				0.41						
53	T299I	a	0.13	0.22	0.90	0.13	1.26	0.11	0.57	0.17			0.80	0.24	0.34	0.36	
											<0.02						
54	A327S	a	0.39	0.26	0.64	0.12	0.89	0.10	1.15	0.24		3.86	0.47	0.25	0.13	0.44	
							0.39				0.23						0.59
55	A327N	a	1.25	0.32	0.77	0.16	1.07	0.10	1.31	0.17	0.61	0.40	0.66	0.32	0.88	0.38	0.57
							1.15				0.19						0.17
56	S267Q/A327S	a	0.44	0.22	0.52	0.11	1.14	0.16	1.08	0.18			0.88	0.22	0.71	0.51	
											0.03						
57	S267L/A327S	a	0.35	0.23	0.64	0.14	1.23	0.13	0.97	0.19	0.27	0.35	1.93	0.20	1.05	0.35	0.22
											<0.02						
58	A327L	a	0.53	0.28	0.55	0.21	1.21	0.19	0.97	0.29			0.89	0.25	1.55	0.52	
											0.05						
59	P329F	a	0.33	0.25	0.93	0.16	1.86	0.09	1.91	0.17	0.96	0.33	2.29	0.18	0.61	0.29	0.51
											<0.02						
60	A330L	a p	1.37	0.23	1.27	0.13	1.23	0.10	1.20	0.18	1.08	0.41	0.83	0.24	0.96	0.47	0.87
							0.38				0.73						1.92
61	A330Y	a p	1.18	0.23	1.08	0.15	1.62	0.09	1.11	0.20	1.04	0.47	2.00	0.24	0.94	0.41	0.64
							0.75				1.64						2.19
62	I332D	a	2.70	0.26	5.41	0.11	3.76	0.11	3.69	0.17	9.03	0.36	2.73	0.20	0.42	0.36	2.40
			3.95	0.10	8.79	0.23	8.32	0.39	7.11	0.29	2.85	2.82			1.75	0.39	0.34
							3.34				17.8						5.33
63	N297S	a	0.03	0.26	0.68	0.12	0.65	0.11	0.68	0.23			1.77	0.23	0.38	0.55	
											<0.02						
64	N297D	a	0.22	0.23	0.62	0.19	1.30	0.09	1.07	0.16	1.00	0.36	1.01	0.22	0.63	0.32	0.77
											<0.02						
65	N297S/A332E	a	0.18	0.24	0.52	0.24	0.89	0.13	0.69	0.20			0.89	0.19	0.19	0.52	
											<0.02						
66	N297D/A332E	a	1.41	0.23	0.60	0.23	0.94	0.20	0.80	0.29			0.97	0.23	0.96	0.82	
							<0.02				0.08						
67	N297E/A332E	a	0.45	0.24	0.54	0.15	0.96	0.17	0.76	0.24			0.65	0.22	0.58	0.31	
											<0.02						
68	D265Y/N297D/A332E	a	0.09	0.24	0.65	0.14	1.16	0.11	0.83	0.16	0.31	0.38	2.78	0.21	0.25	0.33	0.27
											<0.02						
69	D265Y/N297D/T299L/A332E	a	0.33	0.22	1.63	0.13	1.99	0.09	1.30	0.15	3.15	0.40	1.33	0.21	0.63	0.57	1.58
											<0.02						
70	D265F/N297E/A332E	a	0.01	0.29	0.79	0.13	0.65	0.13	0.87	0.20			1.56	0.18	0.31	0.47	
			0.37	0.36	0.80	0.26	1.68	0.32	2.64	0.29	5.65	0.71	1.00	0.46	1.38	0.75	3.37
											<0.02						
71	L328I/A332E	a	2.79	0.11	1.44	0.17	7.61	0.24	6.59	0.25	11.11	0.70	1.14	0.47	2.21	0.55	1.46
			3.95	0.13	1.22	0.23	11.60	0.27	7.87	0.94	12.61	0.12	2.63	0.31	0.82	0.34	1.09
											7.03						

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
72	L328Q/I332E	a	2.87	0.12	1.76	0.13	11.30	0.29	6.52	0.23	1.93	0.69	0.91	0.48	4.29	0.65	0.17
			2.15	0.14	1.05	0.16	15.13	0.29	7.38	0.93	1.69	0.22	1.90	0.31	0.88	0.33	0.11
73	I332N	a	1.64	0.20	2.96	0.14	1.43	0.32	1.82	0.26	1.54 1.70	0.71	0.98	0.52	3.20	0.54	1.19
			0.82	0.12	1.52	0.19	1.26	0.57		46.97	0.33	0.11	2.35	0.33	0.71	0.33	0.26
74	I332Q	a	1.49	0.33	2.70	0.16	1.10	0.28	1.10	0.29	0.39 0.67	0.70	1.10	0.49	1.07	0.51	0.61
			1.29	0.15	2.08	0.19	1.46	0.29	1.11	1.34	0.65	0.14	1.82	0.36	1.20	0.32	0.45
75	V264T	a	1.36	0.21	2.82	0.15	2.94	0.20	2.86	0.24	0.37 1.30	0.69	1.08	0.49	1.00	0.47	0.44
			1.25	0.15	2.50	0.16	4.84	0.21	6.12	1.16	1.73	0.10	1.42	0.33	1.66	0.35	0.36
76	V264F	a	0.35	0.17	0.14	0.43	0.96	0.56	0.47	0.82	2.73 0.16	0.79	1.16	0.50	0.82	0.51	0.17
			0.43	0.22	0.05	0.23	0.22	0.46			0.06	0.13	1.87	0.29	1.07	0.36	0.29
77	V240I	a	0.95	0.12	1.19	0.16	1.02	0.28	1.06	0.25	0.16 1.37	0.69			1.21	0.51	1.34
			1.17	0.14	0.38	22.08	1.04	0.22	0.86	0.91	0.87	0.10	2.02	0.33	1.28	0.34	0.84
78	V263I	a	1.39	0.31	0.61	0.21	0.68	0.60	0.94	0.42	3.25 0.15	0.71	1.11	0.49	2.71	0.73	0.22
79	V266I	a	1.64	0.12	1.63	0.24	3.66	0.36	3.85	1.17	0.1 1.41	0.15	1.25	0.31	1.17	0.32	0.39
80	T299A	a	0.01	0.18	0.10	0.25	0.56	0.48	72.84	6.18	1.86 0.06	0.37	2.31	0.32	0.82	0.33	0.11
81	T299S	a	0.80	0.19	0.16	0.24	2.01	0.81			0.03 0.19	0.20	1.52	0.32	0.86	0.31	0.09
82	T299V	a	0.02	0.20	0.14	0.20	0.21	0.50	19.44	7.11	0.15 0.21	0.14	1.92	0.41	0.35	0.31	1.03
83	N325Q	a	0.65	0.17	0.07	0.23	0.26	0.42	62.17	9.35	<0.02 0.04	0.57	1.92	0.34	0.69	0.34	0.16
84	N325L	a	0.42	0.25	0.04	0.42	1.46	0.39		18.73	<0.02 0.03	0.93	2.18	0.28	0.91	0.33	0.02
85	N325I	a	0.35	0.12	0.05	0.31	0.86	0.26	0.97	1.09	<0.02 0.09	0.13	2.05	0.33	0.89	0.33	0.11
86	S239Q	a|p	4.40	0.25	1.74	0.57	6.21	0.29	5.13	0.45	<0.02 6.29	0.20	3.54	0.42	1.73	0.48	1.01
			2.63	0.13	2.29	0.13	11.42	0.17	3.83	0.80	23.17	0.10	0.96	0.46	0.80	0.31	2.03
			1.86	0.13	2.17	0.22	9.04	0.37	10.98	0.28	2.55	2.82			1.07	0.41	0.28
							4.47*				11.6						2.60
87	S239N	a									<0.02						
88	S239F	a	0.28	0.17	0.02	1.14	0.33	0.68		51.36	0.10	0.24	0.95	0.43	0.85	0.34	0.30
							<0.02				0.22						
89	S239D/I332D	a	2.33	0.11	2.68	0.16	41.43	0.18	18.96	0.78	25.53	0.11	1.53	0.29	1.12	0.33	0.62
90	S239D/I332E	a|r|c|p	3.89	0.12	11.57	0.15	128	0.26	145	0.99	14.1 192	0.10	1.88	0.35	1.01	0.36	1.50
			9.42	0.13	15.46	0.19	70.44	0.37	84.57	0.29	27.74	2.82			1.22	0.36	0.39
							19.71*				56.1						2.85
91	S239D/I332N	a	1.97	0.12	4.95	0.16	14.13	0.20	8.14	0.82	10.79	0.12	1.16	0.35	0.76	0.31	0.76
92	S239D/I332Q	a	1.81	0.21	3.05	0.33	15.24	0.19	9.75	0.91	7.19 9.41	0.09	1.28	0.32	0.64	0.35	0.62
93	S239E/I332D	a	4.52	0.18	1.72	0.15	10.87	0.29	30.32	1.31	9.28 21.77	0.10	2.42	0.31	1.00	0.37	2.00
94	S239E/I332N	a	1.62	0.12	1.81	0.16	4.55	0.23	6.01	1.16	9.33 16.86	0.13	2.00	0.32	0.88	0.33	3.71
95	S239E/I332Q	a	1.66	0.19	0.93	0.11	2.52	0.34	1.41	0.97	11.9 3.21	0.10	1.78	0.29	0.64	0.31	1.28
96	S239N/I332D	a	2.01	0.21	2.40	0.16	11.11	0.32	8.21	0.91	3.8 9.89	0.12	2.09	0.27	0.73	0.34	0.89
97	S239N/I332E	a	1.93	0.12	1.64	0.16	29.42	0.24	8.44	0.81	3.08 19.80	0.12	1.38	0.29	0.73	0.33	0.67
98	S239N/I332N	a	0.55	0.18	0.67	0.21	1.88	0.46		13.55	14.2 0.55	0.15	1.08	0.33	0.84	0.35	0.29
99	S239N/I332Q	a	0.73	0.13	0.72	0.17	2.55	0.35	11.03	2.16	0.43 0.59	0.11	1.88	0.29	0.73	0.33	0.23
100	S239Q/I332D	a	1.40	0.13	1.08	0.14	5.76	0.36	5.76	1.05	0.56 2.33	0.11	1.89	0.29	0.74	0.35	0.40
101	S239Q/I332N	a	0.52	0.25	0.80	0.15	1.55	0.50		10.71	5.05 0.32	0.09	2.68	0.30	1.11	0.35	0.21
102	S239Q/I332Q	a	0.86	0.22	0.69	0.12	1.51	0.42			0.39 0.42 0.59	0.21	1.41	0.21	1.04	0.14	0.28

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
103	K326E	ap	3.17	0.17	1.55	0.13	4.15	0.47			8.07	0.34	0.96	0.18			1.95
			3.41	0.11	0.79	0.24	4.99	0.41	3.68	0.31	0.25	2.82			0.82	0.38	0.05
104	Y296D	a	1.28	0.18	0.88	0.10	1.28	0.55			3.85 0.86	0.21	0.83	0.21	0.50	0.09	0.67
105	Y296N	a	0.84	0.23	0.68	0.13	1.30	0.41			0.62 0.21	0.21	0.67	0.20	0.26	0.14	0.16
106	F241Y/F243Y/V262T/ V264T/N297D/I332E	a	0.38	0.25	0.11	0.23					0.29 0.25	0.23	1.35	0.22	0.25	0.09	
107	A330Y/I332E	a	4.49	0.18	4.81	0.13	10.81	0.36			0.15 68.79	0.20	0.74	0.18	1.53	0.09	6.37
108	V264I/A330Y/I332E	a	3.89	0.19	1.17	0.07	4.4 4.18	0.35			12 22.76	0.20	0.61	0.17	0.85	0.08	2.73 5.44
109	A330L/I332E	a	4.94	0.17	1.28	0.09	3.54 3.15	0.35			12 55.42	0.20	0.72	0.18	1.50	0.20	3.39 17.59
110	V264I/A330L/I332E	a	4.31	0.22	0.66	0.08	2.03 2.73	0.34			10.3 24.96	0.20	1.12	0.21	1.13	0.17	5.09 9.13
111	L234D	a	0.36	0.30	0.40	0.13	1.79 4.95	0.35			11.2 3.89	0.21	0.96	0.21	1.54	0.16	6.23 0.79
112	L234E	a	0.42	0.29	0.24	0.08	4.78	0.36			0.21 1.86	0.21	1.19	0.21	1.25	0.11	0.39
113	L234N	a	0.10	0.32	0.19	0.11	2.21 2.05	0.41			1.34 0.49	0.22	1.18	0.33	1.06	0.13	0.61 0.24
114	L234Q	a	0.28	0.27	0.28	0.09	1.39 3.53	0.38			0.56 0.52	0.20	0.94	0.18	0.97	0.11	0.40 0.15
115	L234T	a	0.49	0.26	0.20	0.10	1.79	0.43			0.37 0.26	0.22	0.56	0.21	0.99	0.08	0.14
116	L234H	a	0.11	0.34	0.29	0.08	1.56	0.49			0.35 0.27	0.21	0.65	0.19	1.48	0.08	0.18
117	L234Y	ap	1.45	0.24	0.51	0.09	1.93	0.39			0.33 0.80	0.21	0.99	0.22	1.90	0.21	0.41
118	L234I	a	1.20	0.27	0.78	0.08	1.08 2.57 1.14	0.40			1.42 1.30 1.55	0.21	1.28	0.28	1.26	0.12	1.31 0.50 1.36
119	L234V	a	1.66	0.26	0.78	0.08	3.94	0.35			1.61	0.22	0.64	0.18	1.45	0.13	0.41
120	L234F	a	0.74	0.26	0.47	0.07	2.36	0.37			0.38 0.37	0.21	0.72	0.21	1.46	0.13	0.15
121	L235D	ap			0.76	0.09	5.48	0.37			0.3 1.61	0.20	1.05	0.17	0.90	0.15	0.29
122	L235S	a			0.27	0.08	3.63 2.99	0.37			1.66 0.95	0.21	0.66	0.21	1.51	0.09	0.46 0.32
123	L235N	a	0.06	0.37	0.21	0.15	1.59	0.46			1.25 0.37	0.22	0.70	0.20	1.32	0.09	0.23
124	L235Q	a	0.09	0.28	0.30	0.10	1.40	0.44			0.4 1.02	0.21	0.85	0.22	1.67	0.14	0.73
125	L235T	a	0.13	0.26	0.53	0.11	3.55	0.34			0.51 2.15	0.21	1.06	0.23	1.65	0.38	0.60
126	L235H	a	0.06	0.37	0.51	0.09	1.77	0.37			0.52 0.30	0.23	0.54	0.19	0.96	0.14	0.17
127	L235Y	ap	0.24	0.31	3.32	0.08	4.44	0.35			0.41 1.74	0.23	0.86	0.22	1.02	0.10	0.39
			0.02	0.55	0.70	0.20	1.39	0.64	1.15	0.38	0.05	2.82			0.78	0.39	0.04
128	L235I	a	0.16	0.26	0.67	0.10	10.15 1.24	0.55			1.19 1.47	0.26	0.68	0.21	0.81	0.10	0.12 1.18
129	L235V	a	0.16	0.31	0.43	0.10	0.94				1.1 0.58	0.22	0.94	0.26	1.31	0.17	1.17
			0.11	0.21	0.23	0.22	0.76	0.52	0.57	1.26	0.05	2.82			0.86	0.45	0.07
130	L235F	a			1.25	0.17	1.62	0.45			0.48 0.56	0.22	0.71	0.21	0.80	0.11	0.35
131	S239I	a	0.88	0.17	0.91	0.13	3.53 1.47	0.52			0.73 0.90	0.21	0.84	0.25	1.12	0.10	0.21 0.61
132	S239H	a	0.08	0.10	0.11	0.38	0.20	0.65	0.23	1.24	1.34 0.2	2.04	0.88	0.24	0.72	0.11	
133	S239Y	a	0.19	0.12	0.12	0.34	0.69	0.48	1.88	0.42			1.70	0.23	1.08	0.13	
134	V240A	a	0.80	0.10	0.62	0.28	1.45	0.39	1.02	0.44	0.21 1.49	0.20	0.91	0.22	0.93	0.11	1.03
135	V240T	a	0.92	0.12	0.67	0.30	0.14 1.20	0.46	0.13	0.97	0.7 1.16	0.16	0.78	0.23	0.46	0.69	5.00 0.96
136	V240M	a	1.60	0.07	0.67	0.30	0.94 1.38	0.55	0.68	0.68	0.86 2.06	0.22	0.74	0.21	0.93	0.09	0.92 1.49
137	V263A	a	1.05	0.14	0.45	0.31	0.04	1.64			0.54	0.26	1.35	0.25	0.91	0.09	12.93
138	V263T	a	1.00	0.08	1.57	0.27	1.20	0.39	1.02	0.67	2.67 0.43	0.32	0.59	0.20	0.93	0.15	2.23

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
139	V263M	a	0.69	0.07	0.41	0.26	1.69	0.41	1.65	0.38		3.66	1.32	0.26	0.58	0.19	
140	V264M	a	0.64	0.08	0.30	0.29	0.83	0.44	0.94	0.87	0.05 0.21	0.41	0.73	0.21	0.63	0.11	0.25
141	V264Y	a	0.51	0.08	0.32	0.29	0.57 0.27	0.44	0.81	0.59	0.26 0.30 1.02	0.29	1.19	0.22	0.75	0.12	0.52 3.78
142	V266A	a	0.61	0.12	0.30	0.28	0.76	0.64	0.05	1.67	0.61 <0.02	0.25	0.95	0.22	0.71	0.12	0.80
143	V266T	a	0.28	0.12	0.10	0.32	1.16	0.48	0.18	1.05	0.45		1.21	0.24	0.53	0.14	
144	V266M	a	1.32 1.11	0.09 0.15	0.43 0.19	0.29 0.23	16.45 2.63	0.45 0.40	3.32 2.57	0.45 0.30	0.01 0.62	7.83 2.84	0.83	0.21	0.71 0.86	0.11 0.45	0.01
145	E269H	a	0.16	0.13	0.18	0.31	0.07	1.25	0.28	0.92	<0.02	5.90	1.11	0.25	0.72	0.12	
146	E269Y	a	0.51	0.07	0.48	0.30	0.79	0.54	0.37	0.94	0.27 0.12	0.25	0.79	0.29	0.76	0.11	0.34
147	E269F	a	0.21	0.07	0.20	0.30	0.48	0.56	0.51	1.33	0.16		0.94	0.26	0.74	0.15	
148	E269R	a	0.07	0.11	0.07	0.28	0.13	1.73	0.06	2.21	0.05	1.97	1.15	0.26	0.72	0.15	
149	Y296S	a	0.63	0.08	0.71	0.28	0.51	0.49	0.64	1.31	0.12		1.21	0.26	0.67	0.13	
150	Y296T	a	0.72	0.09	0.71	0.25	0.97	0.39	0.58	0.80	<0.02	3.07	1.07	0.26	0.60	0.15	
151	Y296L	a	0.81	0.10	0.41	0.29	1.15	0.43	0.17	1.20	1.24 0.22	0.19	0.53	0.20	0.62	0.12	1.08
152	Y296I	a	0.87	0.11	0.43	0.27	0.52	0.85	0.20	1.02	0.35 0.09	0.24	1.51	0.26	0.56	0.11	0.67
153	S298H	a	0.58	0.10	0.23	0.31	0.09	1.22	0.18	0.86	0.27		1.22	0.25	0.60	0.10	
154	T299H	a	0.03	0.09	0.16	0.29	0.44	0.48	0.33	1.23	<0.02	1.02	1.65	0.22	0.57	0.15	
155	A330V	ap	1.12	0.09	0.41	0.28	0.37	0.58	0.79	1.13	0.55 0.43	0.20	0.81	0.26	0.75	0.16	1.47
156	A330I	ap	1.14	0.09	0.35	0.28	0.21 0.02	0.68	0.27	0.74	0.40 1.71	0.19	1.33	0.28	0.61	0.19	1.90 85.50
157	A330F	a	1.65	0.12	0.89	0.29	1.19	0.47	0.32	0.87	2.02 0.6	0.19	1.59	0.28	0.98	0.12	1.70
158	A330R	a	0.45 0.46	0.09 0.14	1.42 1.16	0.36 0.22	1.01 1.05	0.53 0.39	0.90 1.63	0.45 0.35	0.45 0.07 <0.02	0.22 2.82	0.74	0.22	0.58 0.95	0.14 0.42	0.45 0.07
159	A330H	ap	1.09	0.12	1.16	0.33	2.09	0.41	1.62	0.48	1.41 0.52	0.16	0.81	0.20	0.91	0.14	0.67
160	N325D	a	1.20 0.87	0.11 0.12	0.14 0.14	0.34 3.34	0.38 1.62	0.99 0.44	0.63	0.54	0.02 0.41	2.82	0.79	0.24	0.68 0.78	0.11 0.39	0.01
161	N325E	a	1.34	0.10	0.09	0.38	0.05	1.35	0.03	2.06	<0.02	7.72	0.86	0.23	0.55	0.11	
162	N325A	a	0.31	0.06					0.05	3.84	0.11		1.27	0.14	0.74	0.08	
163	N325T	a	0.83	0.05	0.41	0.37			0.13	3.68	0.93 1.1	0.18	1.35	0.16	1.23	0.08	
164	N325V	a	0.61	0.08	0.42	0.36			0.16	3.68	0.66 0.48	0.17	1.24	0.15	1.29	0.08	
165	N325H	a	0.52	0.08	0.25	2.55			0.13	3.68	0.64 0.73	0.22	1.28	0.15	0.03	1.97	
166	L328D/I332E	a	3.56	0.05	1.64	0.29			1.38	3.69	2.01 1.34	0.37	1.97	0.20	1.54	0.10	
167	L328E/I332E	a	2.02	0.15	0.94	0.34			1.39	3.66	0.95 0.2	0.37	2.59	0.20	1.44	0.11	
168	L328N/I332E	a	2.69	0.05	0.32	0.33			2.29	3.69	10.24 <0.02	0.24	1.12	0.16	1.18	0.14	
169	L328Q/I332E	a									0.7						
170	L328V/I332E	a	3.12	0.07	0.91	0.32			8.43	3.69	17.20 2.06	0.23	1.34	0.15	0.93	0.10	
171	L328T/I332E	a	2.70	0.07	1.46	0.35			14.23	3.66	19.76 1.1	10.55	2.36	0.39	0.99	0.15	
172	L328H/I332E	a	1.26	0.08	0.32	0.36			0.44	3.67	1.63 <0.02	0.20	1.39	0.15	1.16	0.09	
173	L328I/I332E	a									3.49						
174	L328A	a	0.86	0.05	10.48	0.34			0.49	3.67	3.81 0.2	0.30	1.23	0.19	1.32	0.09	

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
175	I332T	a	1.58	0.05	2.82	0.30			0.74	3.66	3.18	0.38	1.15	0.22	1.02	0.09	
176	I332H	a	1.19	0.06	2.12	0.34			0.73	3.71	0.72 1.05	0.14	2.13	0.14	1.24	0.17	
177	I332Y	a	1.88	0.07	4.18	0.29			0.63	3.68	0.46 2.14	0.16	1.53	0.21	1.43	0.17	
178	I332A	a	1.60	0.10	3.01	0.31			0.48	3.67	0.76 1.97	0.20	1.57	0.17	0.96	0.13	
179	S239E/V264I/I332E	a	4.75	0.06	1.73	0.40			2.58	3.66	0.89 142	1.57	1.45	0.18	1.07	0.24	
180	S239Q/V264I/I332E	a	2.44	0.07	0.50	0.41			0.45	3.66	15.5 21.84	0.24	1.07	0.16	0.97	0.16	
181	S239E/V264I/A330Y/I332E	a	7.52	0.12	1.80	0.32			4.69	3.66	2.14 318	0.27	2.05	2309	2.36	0.85	
182	S239E/V264I/S298A/A330Y/I332E	a	6.80	0.11	0.32	0.35			0.73	3.67	8.53 862	0.24	1.98	0.23	1.22	0.10	
183	S239D/N297D/I332E	a	2.82	0.09					0.06	3.67	0.82	0.37	3.14	0.29	0.76	0.07	
184	S239E/N297D/I332E	a	2.27	0.06							0.28 0.28	0.18	2.48	0.25	0.76	0.20	
185	N297D/I332E/S239D/D265V	a									0.06 0.03						
186	S239D/D265I/N297D/I332E	a	0.11	0.11					0.31	4.45	0.44	0.13	7.68	0.24	0.45	0.15	
187	S239D/D265L/N297D/I332E	a	0.10	0.09					0.05	3.74	0.01 0.10	0.24	2.78	0.20	0.47	0.09	
188	S239D/D265F/N297D/I332E	a	0.20	0.09					0.17	3.67	<0.02 0.54	0.35	1.47	0.13	0.62	0.08	
189	S239D/D265Y/N297D/I332E	a	0.19	0.09					0.08	3.69	<0.07 0.39	0.14	2.96	0.24	0.52	0.13	
190	S239D/D265H/N297D/I332E	a	0.09	0.09					0.12	3.68	0.02 0.51	0.23	2.16	0.23	1.26	0.24	
191	S239D/D265T/N297D/I332E	a	0.35	0.07	0.24	0.85			0.11	3.70	0.04 0.51	0.42	8.28	0.25	0.59	0.07	
192	V264E/N297D/I332E	a	0.90	0.08	0.26	0.42			0.04	3.69	<0.02 0.26	0.47	2.41	0.25	0.96	0.07	
193	N297D/I332E/Y296D	a									0.05						
194	N297D/I332E/Y296E	a									<0.02						
195	N297D/I332E/Y296N	a									0.04						
196	N297D/I332E/Y296Q	a									<0.02						
197	N297D/I332E/Y296H	a									<0.02						
198	N297D/I332E/Y296T	a									<0.02						
199	N297D/I332E/T299V	a									<0.02						
200	N297D/I332E/T299I	a									<0.02						
201	N297D/I332E/T299L	a									<0.02						
202	N297D/I332E/T299F	a									<0.02						
203	N297D/I332E/T299H	a									<0.02						
204	N297D/I332E/T299E	a									<0.02						
205	N297D/I332E/A330Y	a									0.43						
206	N297D/I332E/S298A/A330Y	a									0.16						
207	S239D/I332E/A330Y	a p									130						
208	S239N/I332E/A330Y	a									14.2						
209	S239D/A330L/I332E	a t r c p	5.54	0.21	2.52	0.33	7.5	25.98	31.11	5.64	139	6.50					18.48
210	S239N/I332E/A330L	a									13						
211	I332E/V264I/S298A	t									16.5						
212	I332E/S239D/S298A	t p					6.16				295						47.92
213	I332E/S239N/S298A	t					5.15				32.1						6.24
214	S239D/I332E/V264I	t					14.39				36.6						2.54
215	S239D/I332E/V264I/S298A	t															
216	S239D/I332E/V264I/A330L	t															
217	L328N	a									0.59						
218	L328H	a									<0.02						
219	S239D/I332E/A330I	a p									59.1						
220	N297D/I332E/S239D/A330L	a															
221	P230A	t	1.28	0.13	0.99	0.18	1.13	39.94			0.55	0.20	2.53	0.25	0.77	0.19	0.49
222	E233D	t	0.85	0.15	0.81	0.16	1.05	1.12			1.09 0.64	0.18	2.66	0.36	0.76	0.23	0.61
223	P230A/E233D	t	2.03	0.22	0.76	0.13					0.85 0.54	0.17	2.04	0.27	0.84	0.18	
224	P230A/E233D/I332E	t	4.92	0.16	0.97	0.16	2.01	0.90	1.36	75.92	0.92 7.81	0.14	3.64	0.35	0.78	0.16	3.68
											1.87						

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
225	S267T	t	0.93	0.14	0.15	0.32	1.06	1.26	1.01	450	0.86	0.18	3.09	0.28	0.75	0.19	0.81
226	S267H	t	0.34	0.15	0.16	0.23	0.93	14.97			0.34	0.23	3.26	0.28	0.57	0.23	0.36
227	S267D	tp	1.41	0.13	0.75	0.09	5.02	0.89	4.78	75.92	1.45	0.11	2.88	0.18	1.00	0.20	0.29
228	S267N	t	0.72	0.20	0.08	0.71					0.27	0.19	3.18	0.34	0.85	0.16	
229	E269T	t	0.32	0.16	0.20	0.31					0.14	0.60	1.17	0.20	0.92	0.18	
230	E269L	t	0.28	0.15	0.16	0.24					<0.02		1.83	0.29	0.75	0.21	
231	E269N	t	0.19	0.15	0.12	0.38					<0.02		1.36	0.27	0.65	0.22	
232	D270Q	t	0.51	0.22	0.42	0.19					<0.02		2.41	0.24	0.76	0.18	
233	D270T	t	0.33	0.22	0.16	0.23					<0.02		2.50	0.27	0.84	0.17	
234	D270H	t	0.33	0.18	0.24	0.17					<0.02		1.45	0.28	0.85	0.19	
235	E272S	t	1.04	0.20	0.53	0.25	1.15	4.37	1.07	6.40	0.39	0.20	1.28	0.31	0.90	0.23	0.34
236	E272K	t	0.79	0.19	0.55	0.10	1.85	0.30	1.33	0.35	3.41	0.19	1.09	0.30	0.96	0.18	1.84
237	E272I	tp	0.83	0.16	0.72	0.12	1.04	0.40	1.11	2.20	4.96	0.16	1.48	0.31	1.05	0.20	4.79
238	E272Y	t	0.58	0.16	0.80	0.09					0.78	0.17	1.68	0.32	2.08	0.26	
239	V273I	t	0.98	0.17	0.55	0.09	2.20	0.31	1.62	0.34	8.7 0.60	0.17	1.11	0.37	0.95	0.28	0.27
240	K274T	t	1.01	0.24	0.82	0.08			1.10	13.52	0.79 0.90	0.19	1.55	0.33	1.08	0.42	
241	K274E	tp	1.46	0.13	0.86	0.11	1.17	0.29	1.07	0.50	1.41 1.00	0.12	2.73	0.37	1.05	0.27	0.86
242	K274R	tp	0.95	0.16	0.77	0.11			0.85	0.56	6.11 0.71	0.17	2.22	0.35	0.65	0.23	
243	K274L	t	1.17	0.15	0.91	0.11	1.71	0.30	1.41	0.37	1.41 4.35	0.15	1.15	0.30	0.51	0.24	2.54
244	K274Y	tp	1.02	0.16	0.79	0.11	1.09	0.37	1.16	10.90	1.09 0.93	0.13	1.42	0.33	0.63	0.25	0.85
245	F275W	t	1.16	0.17	0.57	0.10	1.15	0.37	1.09	0.48	1.06 1.51	0.14	1.49	0.34	0.90	0.23	1.31
246	N276S	tp	0.84	0.15	0.62	0.09	0.97	0.46	1.24	25.25	1.11 0.71	0.19	2.00	0.32	0.67	0.21	0.74
247	N276E	t	2.07	0.15			1.29	2.40			0.41 0.24	0.19					0.19
248	N276R	t	0.84	0.22	0.64	0.11	0.87	0.50	1.26	21.80	0.87 0.51	0.19	1.43	0.35	1.19	0.31	0.59
249	N276L	tp	0.65	0.29	0.66	0.10	0.94	0.41	1.10	10.72	0.66 0.52	0.22	1.37	0.36	1.21	0.43	0.56
250	N276Y	t	1.23	0.16	1.18	0.09	3.02	0.29	2.97	0.31	1.07 3.47	0.10	1.34	0.31	0.74	0.18	1.15
251	Y278T	t	0.73	0.17	0.35	0.10	0.71	0.55	1.08	2.80	0.56 0.34	0.18	1.55	0.30	0.55	0.18	0.48
252	Y278E	tp	2.11	0.15	0.59	0.14	1.09	0.35	1.04	0.76	1.87 0.54	0.13	1.43	0.33	0.61	0.30	0.49
253	Y278K	t	0.63	0.24	0.45	0.14	1.12	4.55	1.02	5.44	0.9 0.37	0.17	1.18	0.30	0.78	0.20	0.34
254	Y278W	t	0.65	0.15	0.45	0.10	0.83	0.93	1.06	15.47	0.31	0.16	1.40	0.35	0.74	0.22	0.38
255	E283R	t	0.67	0.14	0.62	0.08	0.91	0.70	1.11	3.27	0.41 0.49	0.14	1.36	0.32	1.86	0.18	0.54
256	V302I	t	0.75	0.20	0.66	0.11	1.20	0.41	1.08	0.44	0.67 0.81	0.15	1.13	0.35	2.44	0.24	0.68
257	E318R	t	0.71	0.35	0.57	0.13	1.14	6.22			1.01 0.50	0.19	1.83	0.34	1.17	0.36	0.44
258	K320T	tp	1.37	0.41	1.10	0.16	1.23	0.29	0.91	0.33	1.06 1.53	0.13	1.12	0.34	0.56	0.19	1.25
259	K320D	t	2.29	0.14	0.79	0.19	1.37	0.29	1.06	0.35	0.70	0.21	1.80	0.35	0.58	0.19	0.51
260	K320I	tp	1.87	0.13	0.99	0.15	1.65	0.27	1.21	0.37	1.84	0.20	1.69	0.36	0.72	0.25	1.12
261	K322T	tp	1.64	0.16	0.56	0.16	1.14	0.32	1.08	1.26	0.94	0.18	1.48	0.31	0.83	0.21	0.83
262	K322H	tp	1.20	0.17	0.66	0.14	0.92	0.52	1.20	3.35	0.71	0.13	1.32	0.36	0.77	0.22	0.77
263	V323I	t	0.90	0.13	0.74	0.13	1.64	0.33	1.29	0.35	0.97	0.12	1.81	0.31	0.99	0.22	0.59
264	S324T	tp	2.07	0.28	1.29	0.09	1.15	0.08	1.15	0.06	0.83 2.37	0.36	2.15	0.09			2.07
			1.03	0.23	0.89	0.09	1.00	0.42	1.13	1.80	1.11	0.19	1.60	0.40	1.07	0.26	1.12
265	S324D	tp	3.36	0.25	1.71	0.11	1.25	0.08	1.31	0.07	1.54	0.35	1.71	0.08			1.23
			0.94	0.20	1.03	0.10	0.93	0.67			0.75	0.18	1.46	0.33	1.27	0.44	0.80
266	S324R	t	2.67	0.27	1.18	0.15	1.39	0.10	2.52	0.33	1.07 1.86	0.38	1.23	0.08			1.34
			0.64	0.16	0.73	0.17					0.56 0.71	0.17	2.06	0.19	0.61	0.37	

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
267	S324I	tp	9.07	0.25	1.98	0.15	6.71	0.34	7.80	0.30	1.88	0.30	0.69	0.12			0.28
			1.43	0.17	0.69	0.10					0.54	0.16	2.02	0.21	0.90	0.20	
268	S324V	tp	2.47	0.24	1.96	0.08	1.88	0.09	1.94	0.07	1.15 2.25	0.36	0.90	0.10			1.19
			2.12	0.16	1.32	0.23	1.01	0.98	1.03	76.44	1.06	0.19	1.66	0.19	0.90	0.19	1.05
269	S324L	tp	2.01	0.26	1.95	0.07	1.22	0.08	1.24	0.06	1.17 2.28	0.38	0.62	0.08			1.86
			0.93	0.14	0.96	0.13	0.93	1.00	0.90	79.37	0.74	0.14	1.71	0.19	0.82	0.22	0.79
270	S324Y	t	1.89	0.25	1.53	0.06	1.48	0.07	1.40	0.06	<0.02 1.86	0.44	1.83	0.10			1.26
			1.51	0.13	0.86	0.09	0.97	1.05			0.89	0.14	2.25	0.23	0.76	0.21	0.91
271	K326L	tp	2.19	0.26	1.50	0.09	1.40	0.08	1.37	0.04	0.98 3.20	0.28	1.13	0.08			2.29
			2.66	0.19	0.70	0.18	1.55	0.91	1.79	75.92	1.54	0.17	1.64	0.20	0.70	0.19	1.00
272	K326I	t	2.79	0.25	1.62	0.09	1.39	0.07	1.41	0.05	3.12	0.31	1.06	0.09			2.24
			2.10	0.17	0.67	0.17	1.79	0.92	1.69	75.92	1.68	0.15	2.49	0.21	0.65	0.20	0.94
273	K326T	tp	4.10	0.26	2.07	0.12	1.95	0.07	2.05	0.06	1.43 2.75	0.36	2.25	0.11			1.41
			2.92	0.19	1.26	0.13	1.33	0.91	1.06	75.92	1.79	0.14	2.65	0.21	0.68	0.22	1.34
274	A327D	t	15.80	0.25	2.09	0.19	7.30	0.36	11.30	0.39	1.88 3.34	0.24	0.62	0.17			0.46
			2.55	0.13	0.73	0.16	1.62	0.89	1.11	75.92	0.51	0.14	3.00	0.21	1.01	0.18	0.32
275	A327T	t	1.13	0.25	0.82	0.15	1.06	0.08	1.15	0.06	<0.02 0.65	0.27	2.64	0.08			0.62
			0.19	0.19	0.13	1.18							2.63	0.29	0.67	0.17	
276	A330S	tp	4.00	0.25	1.58	0.13	1.91	0.09	1.84	0.11	<0.02 1.56	0.36	1.88	0.07			0.81
			2.38	0.19	0.80	0.21	0.97	1.11			0.67	0.18	1.64	0.24	0.91	0.21	0.69
277	A330W	t	3.94	0.25	1.33	0.07	1.45	0.08	1.49	0.06	1.37	0.38	1.96	0.08			0.94
			2.14	0.16	0.37	0.17	1.00	8.31			0.76	0.19	2.44	0.23	1.02	0.19	0.76
278	A330M	t	2.30	0.25	1.36	0.09	1.26	0.07	1.09	0.05	1.79	0.38	1.91	0.08			1.42
			2.01	0.15	0.53	0.14	1.15	17.59			1.00	0.15	2.31	0.22	0.77	0.24	0.87
279	P331V	t	2.52	0.24	1.01	0.06	1.30	0.07	1.36	0.05	1.19	0.29	2.12	0.08			0.92
			1.43	0.13	0.34	0.18	0.88	1.06	0.93	76.26	0.26	0.22	3.49	0.18	0.83	0.19	0.29
280	P331H	t	2.28	0.26	1.40	0.09	1.27	0.08	1.34	0.05	1.12	0.29	2.24	0.07			0.88
			2.09	0.46	0.43	0.18	1.24	0.93	0.96	76.55	0.35	0.18	2.86	0.25	0.90	0.22	0.28
281	E333T	t	2.46	0.26	1.43	0.11	1.27	0.08	1.22	0.05	1.77	0.34	1.68	0.75			1.39
			1.21	0.16	0.68	0.12	1.05	1.34	0.98	454	0.72	0.15	3.17	0.21	0.85	0.18	0.68
282	E333H	t	2.91	0.25	1.23	0.09	1.24	0.11	1.30	0.06	0.78 1.77	0.34	2.21	0.12			1.43
			0.40	0.06	0.59	0.33	1.19	0.46	0.73	0.32	0.46	0.17	1.06	0.73	0.84	0.29	0.39
283	E333I	t	2.60	0.26	1.53	0.11	1.78	0.09	2.10	0.07	0.75 1.94	0.34	2.55	0.07			1.09
			0.34	0.13	0.58	0.40	1.72	0.30	0.93	0.23	0.38	0.11	1.52	0.60	0.84	0.26	0.22
284	E333Y	t	7.61	0.25	2.51	0.10	10.60	0.17	11.60	0.21	8.70	0.23	1.10	0.14			0.82
			0.45	0.11	0.64	0.32	1.93	0.31	0.88	0.29	0.90	0.15	0.81	0.94	0.83	0.27	0.47
285	K334I	t	3.99	0.25	1.82	0.07	1.67	0.05	1.60	0.05	10.32	0.28	1.84	0.08			6.18
			0.97	0.15	0.85	0.36	1.89	0.33	1.00	0.28	2.47	0.11	1.16	0.72	0.64	0.27	1.31
286	K334T	tp	3.63	0.26	2.15	0.07	0.93	0.38	0.96	0.06	5.35	0.36	1.03	0.10			5.75
			1.24	0.25	0.98	0.31	2.28	0.30	1.39	0.23	1.69	0.13	1.06	0.80	0.82	0.29	0.74
287	K334F	t	4.03	0.25	1.57	0.10	1.26	0.07	1.15	0.05	5.47	0.42	2.70	0.08			4.33
			1.54	0.11	0.75	0.29	1.77	0.32	0.92	0.23	1.46	0.12	1.01	1.00	0.77	0.26	0.83
288	T335D	tp	3.52	0.28	1.68	0.13	1.21	0.07	1.13	0.07	3.03	0.33	1.93	0.09			2.51
			1.37	0.07	0.82	0.26	1.37	0.30	0.66	0.32	0.96	0.14	1.25	0.67	0.99	0.24	0.70
289	T335R	t	2.72	0.26	1.28	0.09	1.23	0.10	1.22	0.07	2.79 1.47	0.33	2.06	0.15			1.19
			0.38	0.07	0.66	0.26	1.23	0.31	0.66	0.30	0.38	0.12	1.00	0.70	0.74	0.26	0.31
290	T335Y	tp	2.72	0.28	1.48	0.09	1.23	0.06	1.19	0.05	2.58 2.29	0.37	3.22	0.11			1.86
			0.46	0.10	0.70	0.37	0.81	0.62	0.62	0.41	0.52	0.12	1.31	0.69	0.86	0.26	0.64
291	L234I,L235D	t	0.81	0.32	2.20	0.09	0.96	0.10	0.89	0.06	1.56 3.68	0.37	0.60	0.12			3.82
			0.04	0.15	0.25	2.73	1.14	0.34	0.52	0.25	0.57	0.12	2.07	0.60	1.03	0.25	0.50
292	V240I,V266I	t	3.99	0.24	1.86	0.09	1.99	0.11	1.90	0.06	0.07 3.42	0.35	3.08	0.07			1.71
			0.60	0.12	0.46	0.32	1.91	0.37	1.05	0.27	0.52	0.14	1.16	0.73	0.81	0.25	0.27
293	S239D/A330Y/I332E/L234I	t									1.72 22.4						
294	L235D/S239D/A330Y/I332E	t	5.43	0.28	1.62	0.06	1.59	0.06	1.35	0.06	65.84	0.29	1.16	0.09			41.38
			0.15	0.12	0.34	0.35	7.07	0.30	3.66	0.26	80.04	0.11	1.11	0.83	0.78	0.28	11.33
295	S239D/V240I/A330Y/I332E	t	2.64	0.13	2.78	0.25	21.68	0.29	13.70	0.22	7.04 1.15	0.13	0.99	0.90	0.71	0.27	5.33
											28						

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
296	S239D/V264T/A330Y/I332E	i	1.64	0.10	4.85	0.26	22.14	0.30	14.88	0.23	59.09	0.11	0.89	1.07	0.98	0.25	2.67
											17.7						
297	S239D/A330Y/I332E/V266I	i															
298	S239D/K326E/A330Y/I332E	ip	3.21	0.08	3.00	0.26	48.74	0.30	27.56	0.23	298	0.12	1.20	0.66	0.39	0.27	6.12
											64.1						
299	S239D/K326T/A330Y/I332E	i	1.83	0.08	8.89	0.22	41.48	0.29	22.59	0.22	185	0.10	1.27	0.60	0.40	0.28	4.47
											59						
300	S239D/N297D/A330Y/I332E	i	0.10	0.13			0.23	1.70	0.85	11.57	0.08	0.33	1.27	0.62	0.19	0.81	0.32
											<0.02						
301	S239D/F241S/F243H/V262T/V264T/N297D/A330Y/I332E	i	0.08	0.11			0.90	0.87	0.84	9.38	0.03	0.41	1.65	0.59	0.23	0.64	0.03
											<0.02						
302	L235D/S239D/N297D/I332E	i	0.02	0.20							0.08	0.48	1.10	0.78	0.19	0.59	
303	S239D/N297D/K326E/I332E	i	0.23	0.10			0.81	0.68	0.57	0.34	0.36	0.13	1.33	0.66	0.19	0.63	0.45
321	P232E	a	2.97	0.14	0.80	0.14	1.59	0.21	0.99	0.23	1.51	0.36	1.18	0.16	0.76	0.23	0.95
			0.18	0.19	0.06	0.38	0.27	0.20	0.30	0.16	0.32	0.16	0.08	0.59			1.19
322	P232K	a	0.70	0.14	0.87	0.16	0.85	0.17	0.61	0.24	0.77	0.39	0.78	0.18	1.56	0.30	0.91
			0.07	0.25	0.05	0.45	0.27	0.17	0.33	0.20	0.20	0.15	0.07	0.60			0.72
323	P232Y	a	1.91	0.21	1.51	0.12	1.49	0.19	0.96	0.28	0.99	0.34	0.87	0.18	0.68	0.26	0.66
			0.15	0.16	0.22	0.32	0.54	0.14	0.74	0.19	0.21	0.13	0.16	0.61			0.40
324	P232G	a	1.31	0.18	0.49	0.13	0.69	0.18	0.42	0.23	0.51	0.31	0.84	0.15	0.70	0.26	0.74
			0.10	0.19	0.05	0.41	0.11	0.30	0.01	1.67	0.04	0.22	0.14	0.60			0.36
325	S239Q	a	0.98	0.15	1.05	0.12	1.11	0.25	0.59	0.24	1.59	0.31	0.81	0.15	0.57	0.22	1.44
			0.07	0.21	0.09	0.34	0.68	0.16	0.91	0.21	0.92	0.11	0.17	0.59			1.35
326	S239K	a	0.18	0.12	0.94	0.11	0.76	0.22	0.43	0.23	1.20	0.36	0.98	0.15	0.86	0.27	1.58
			0.02	0.16	0.14	0.29	0.78	0.17	0.94	0.17	0.88	0.14	0.49	0.86			1.12
327	S239R	a	0.05	0.14	0.41	0.14	0.51	0.16	0.19	0.37	0.11	0.28	1.29	0.18	1.04	0.20	0.22
			0.01	0.15			0.08	0.63	0.00	2.30			0.12	0.58			
328	S239V	a	0.08	0.19	0.36	0.26	2.49	0.16	1.98	0.15	1.10	0.14	0.36	0.65			0.44
			1.28	0.19	0.29	0.22	1.92	0.49	1.23	0.32	0.05	2.82			1.17	0.36	0.02
329	S239L	ap	0.99	0.16	3.98	0.13	6.06	0.22	3.69	0.22	4.49	0.25	6.30	0.19	4.60	0.25	0.74
			0.00	0.20			0.10	0.35	0.14	0.27			0.06	0.58			
330	S239I	a	0.06	0.18	0.57	0.17	1.47	0.19	0.87	0.26	0.13	0.25	1.28	0.16	0.71	0.29	0.09
			0.14	0.15	0.10	0.35	0.16	0.24	0.07	0.62	0.05	0.14	0.11	0.60			0.34
331	S239M	a	0.90	0.12	0.81	0.16	1.02	0.17	0.91	0.33	0.64	0.29	1.36	0.16	1.03	0.26	0.63
			0.05	0.16	0.05	25.50	0.01	2.15	0.03	5.02	0.03	0.17	0.20	0.61			6.26
332	S239W	a	0.43	0.13	0.52	0.16	0.49	0.17	0.38	0.23	0.45	0.28	1.53	0.15	0.57	0.27	0.92
			0.04	0.16	0.04	13.71	0.11	0.40	0.02	1.84	0.02	0.22	0.15	0.59			0.16
333	S239P	a	0.27	0.16	0.63	0.15	0.91	0.18	0.73	0.23	0.19	0.30	0.96	0.15	0.30	0.30	0.21
			0.15	0.15	0.16	0.30	0.82	0.15	0.55	0.30	0.04	0.19	0.13	0.58			0.05
334	S239G	a	1.20	0.14	0.97	0.14	1.80	0.14	1.31	0.23	0.47	0.30	0.91	0.16	1.16	0.38	0.26
			0.08	0.16	0.05	0.33	0.05	0.50	0.09	0.58	0.03	0.18	0.30	0.81			0.69
335	F241D	a	1.76	0.18	1.37	0.12	1.36	0.14	0.86	0.21	0.60	0.29	0.78	0.16	0.69	0.26	0.45
			0.15	0.16	0.08	0.33	0.09	0.50	0.11	0.63	0.03	0.13	0.13	0.60			0.34
336	F241E	a	0.96	0.15	1.90	0.11	1.18	0.17	1.02	0.23	0.57	0.33	1.10	0.16	1.09	0.19	0.48
			0.14	0.16	0.16	0.28	0.33	0.17	0.29	0.13	0.09	0.15	0.07	0.63			0.29
337	F241Y	a	1.33	0.15	1.15	0.13	2.04	0.17	1.51	0.22	1.04	0.28	1.23	0.23	0.74	0.27	0.51
			0.15	0.17	0.05	152	0.68	0.16	0.55	0.17	0.27	0.13	0.06	0.58			0.40
338	S267E	ap	4.43	0.16	4.76	0.18	337	0.42	248	0.39	1.30	0.33	21.33	0.17	0.20	0.28	0.00
			2.39	0.21	5.92	0.13	97.52	0.21	438	0.49	1.18	0.39	30.15	0.14	1.09	0.19	0.01
			3.50	0.16	11.50	0.20	335	0.37	1321	0.28	0.65	2.82			2.24	0.39	0.00
339	S267Q	ap	1.01	0.12	0.67	0.21	2.03	0.17	1.50	0.23	0.74	0.40	1.14	0.17	0.65	0.27	0.36
			0.02	0.14			0.14	0.24	0.05	0.84		3.25	0.19	0.61			
340	S267K	a	0.32	0.19	1.65	0.14	1.25	0.23	0.69	0.25	0.30	0.24	0.96	0.18	1.70	0.35	0.24
			0.02	0.16			0.01	1.29	0.02	79.64			0.14	0.60			
341	S267R	a	0.15	0.15	0.45	0.19	0.36	0.17	0.17	0.24	0.16	0.24	1.03	0.15	0.75	0.30	0.44
			0.12	0.18	0.05	283	1.18	0.19	1.38	0.22			0.14	0.60			
342	S267V	a	1.21	0.16	0.81	0.13	3.26	0.16	2.35	0.22	0.17	0.25	1.38	0.16	0.50	0.33	0.05
			0.09	0.14			0.35	0.33	0.24	0.45	0.01	0.72	0.15	0.62			0.04
343	S267L	a	0.82	0.15	0.90	0.12	1.29	0.18	1.22	0.22	0.16	0.25	0.90	0.15	0.96	0.27	0.13
			0.10	0.12			0.92	0.17	1.18	0.14	0.02	5.05	0.39	0.84			0.02
344	S267I	a	0.76	0.15	0.55	0.13	2.81	0.18	2.07	0.22	0.13	0.28	1.23	0.16	0.63	0.29	0.04
			0.03	0.13			0.04	0.63	0.03	1.06		6.12	0.12	0.60			
345	S267F	a	0.40	0.17	0.54	0.13	0.71	0.16	0.61	0.25	0.22	0.24	0.87	0.23	0.42	0.34	0.30
			0.18	0.16			0.51	0.17	0.66	0.19	0.02	0.23	0.09	0.65			0.04
346	S267M	a	2.16	0.12	0.91	0.13	2.46	0.23	1.73	0.28	0.44	0.26	1.11	0.18	0.48	0.33	0.18
			0.03	0.14			0.07	0.44	0.09	0.74			0.07	0.63			
347	S267Y	a	0.37	0.13	1.28	0.20	0.95	0.23	0.69	0.30	0.35	0.28	1.10	0.18	0.93	0.33	0.37
			0.05	0.15			0.12	0.33	0.01	1.75			0.10	0.61			
348	S267W	a	0.48	0.16	0.48	0.28	1.09	0.17	0.38	0.27	0.18	0.24	1.36	0.16	0.36	0.33	0.17
			0.02	0.16			0.00	1.59	0.00	5.22	0.02	0.18	0.12	0.62			7.37
349	S267P	a	0.27	0.14	0.58	0.14	0.97	0.15	0.50	0.24	0.49	2.27	1.42	0.16	0.35	0.35	0.50
			0.51	0.16	0.79	0.29	2.99	0.16	3.81	0.15	0.56	0.14	0.11	0.62			0.19

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
350	H268D	a	3.92	0.13	7.02	0.12	12.81	0.17	9.43	0.22	4.97	0.29	1.89	0.17	0.43	0.48	0.39
			0.29	0.13	0.71	0.23	4.42	0.14	5.80	0.20	0.80	0.13	0.29	0.60			0.18
351	H268E	ap	3.25	0.14	5.03	0.14	7.91	0.19	6.42	0.25	4.42	0.27	1.40	0.15	1.71	0.39	0.56
352	H268Q	a	2.13	0.43	1.26	0.12	1.70	0.15	2.05	0.14	1.38	0.49	0.79	0.42	0.98	0.22	0.81
353	H268K	a	0.87	0.40	0.58	0.13	0.38	0.17	0.37	0.11	0.47	0.49	0.50	0.32	0.54	0.25	1.25
354	H268R	a	0.80	0.43	0.55	0.13	0.51	0.12	0.32	0.17	0.41	0.54	0.64	0.39	0.67	0.21	0.79
355	H268T	a	2.20	0.45	0.78	0.09	0.57	0.14	0.39	0.15	0.57	0.68	0.49	1314	0.68	0.29	1.00
356	H268V	a	2.61	0.44	1.03	0.10	0.85	0.15	0.51	0.14	0.58	0.49	0.38	0.49	0.63	0.26	0.68
357	H268L	a	1.33	0.40	0.46	0.13	0.45	0.13	0.31	0.11	0.65	0.49	1.12	0.39	0.39	0.26	1.46
358	H268I	a	3.69	0.43	0.49	0.08	0.61	0.12	0.37	0.13	0.53	0.48	0.52	0.34	0.93	0.23	0.86
			0.43	0.23			1.04	0.85	0.72	15.94	0.07	2.82			0.54	0.42	0.07
359	H268F	a	2.70	0.41	2.13	0.09	0.98	0.12	0.86	0.12	1.44	0.49	2.12	0.42	0.40	0.25	1.48
360	H268M	a	1.15	0.13	0.50	0.24	1.08	0.46	0.73	0.36	0.43	2.82			1.88	0.40	0.40
361	H268W	a	1.41	0.43	0.88	0.11	2.63	0.35	1.29	0.14	0.56	0.66	1.41	0.40	0.35	0.23	0.21
362	H268P	a	1.78	0.40	0.35	0.14	0.91	0.14	0.71	0.12	0.57	0.49	0.67	0.41	0.68	0.16	0.63
363	H268G	ap	2.41	0.42	0.99	0.14	1.38	0.13	1.58	0.08	0.84	0.50	1.11	0.40	0.38	0.19	0.61
364	S298D	a	2.96	0.40	0.20	0.21	0.30	0.12	0.15	0.16	0.66	0.50	1.06	0.42	0.55	0.18	2.24
365	S298E	a	3.36	0.39	0.25	0.19	0.26	0.14	0.17	0.27	0.19	0.50	0.97	0.43	0.31	0.18	0.74
			1.90	0.21	0.09	3.80	0.58	0.44	0.63	0.53	0.04	2.83			1.54	0.37	0.06
366	S298Q	a	1.82	0.40	0.49	0.08	0.87	0.09	0.78	0.10	0.59	0.49	0.66	0.48	0.45	0.19	0.68
367	S298K	a	0.33	0.39	0.21	0.16	0.39	0.15	0.29	0.16	0.14	0.48	0.78	0.28	0.54	0.17	0.36
368	S298R	a	0.86	0.40	0.30	0.12	0.17	0.24	0.13	0.26	0.24	0.48	0.92	0.41	0.48	0.16	1.38
369	S298I	a	3.25	0.40	0.44	0.22	0.69	0.16	0.56	0.16	0.94	0.49	1.54		0.13	0.23	1.36
370	S298F	a	3.35	0.39	1.05	0.15	2.57	0.10	1.48	0.13	1.50	0.48	1.20	0.28	0.25	0.16	0.58
			2.42	0.10	0.16	0.29	0.93	0.42	0.55	0.72	0.08	2.82			1.15	0.38	0.09
371	S298M	a	3.34	0.42	1.76	0.13	2.53	0.12	1.73	0.11	1.24	0.49	1.40	0.62	0.60	0.21	0.49
372	S298Y	a	2.51	0.41	0.54	0.15	0.68	0.11	0.49	0.19	0.98	0.50	0.91	0.49	0.50	0.19	1.43
373	S298W	a	2.46	0.40	0.31	0.16	0.32	0.21	0.22	0.19	0.32	0.48	0.80	0.46	0.23	0.25	0.98
374	T299D	a	0.12	0.41	0.26	0.16	0.26	0.19	0.22	0.12	0.18	0.50	1.50	1.25	0.44	0.34	0.67
375	T299E	a	0.24	0.40	0.39	0.08	0.37	0.14	0.28	0.15	0.28	0.48	1.07	0.29	0.47	0.18	0.76
376	T299N	a	0.22	0.42	0.33	0.21	0.36	0.15	0.27	0.18	0.21	0.48	1.90	0.39	0.61	0.26	0.60
377	T299Q	a	0.15	0.40	0.19	0.39	0.11	0.22	0.16	0.22	0.17	0.48	1.16	0.39	0.25	0.27	1.50
378	T299K	a	0.04	0.54	0.58	0.29	0.30	0.18	0.27	0.16	0.10	0.49	0.50	0.31	0.49	0.15	0.35
379	T299R	a	0.02	0.99	0.23	0.41	0.20	0.36	0.08	0.42	0.00	24.61	0.61	0.41	0.44	0.21	0.00
380	T299L	a	0.26	0.44	0.18	0.30	0.58	0.22	0.43	0.09	0.06	0.59	0.60	12.53	0.34	0.19	0.11
381	T299F	a	0.61	0.43	1.77	0.26	0.95	0.17	0.33	0.20	0.12	0.49	1.31	0.47	1.86	0.20	0.12
382	T299M	a	0.17	0.44	0.21	0.24	0.85	0.13	0.46	0.12	0.06	0.66	0.85	0.33	0.36	0.23	0.08
383	T299Y	a	0.03	0.38	0.77	0.26	0.86	0.27	0.62	0.21	0.11	0.20	1.66	0.38	3.85	0.13	0.13
384	T299W	a	0.09	0.32	0.31	0.20	0.85	0.18	0.59	0.12	0.20	0.13	1.46	0.33	1.09	0.10	0.24
385	T299P	a	0.02	0.36	0.20	0.16	0.34	0.17	0.26	0.17	0.10	0.23	2.60	0.36	0.72	0.11	0.29
386	T299G	a	0.02	0.45	0.15	0.29	0.24	0.21	0.09	0.23	0.03	0.61	1.94	0.52			0.12
387	Y300D	ap	1.58	0.32	0.67	0.08	1.68	0.15	1.37	0.16	1.19	0.15	3.22	0.46	0.97	0.10	0.71
388	Y300E	a	0.12	0.37	0.10	0.33	0.22	0.17	0.11	0.20	0.06	0.24	2.51	0.37	0.82	0.12	0.26
			1.53	0.17	1.00	0.23	3.51	0.40	2.95	0.30	0.14	2.82			1.27	0.41	0.04
389	Y300N	a	1.87	0.44	0.98	0.08	11.42	2509	0.56	0.12	0.63	0.14	0.88	0.38	1.14	0.10	0.06
390	Y300Q	a	0.86	0.31	1.02	0.07	1.71	0.15	1.88	0.12	1.22	0.14	2.29	0.42	1.11	0.12	0.71
391	Y300K	a	0.42	0.29	0.48	0.11	0.54	0.17	0.50	0.13	0.58	0.13	1.14	0.34	1.01	0.18	1.08
392	Y300R	a	0.41	0.38	0.35	0.11	0.57	0.16	0.57	0.14	0.41	0.14	2.12	0.32	0.86	0.13	0.72
393	Y300S	a	0.72	0.31	0.73	0.10	0.48	0.15	0.46	0.14	0.59	0.15	2.79	0.41	0.80	0.14	1.25
394	Y300T	ap	1.16	0.27	0.87	0.11	1.31	0.16	1.18	0.13	2.80	0.15	17.00	0.51			2.14
395	Y300H	a	1.23	0.31	1.23	0.08	3.85	0.13	3.86	0.12	1.31	0.14	3.90	0.45	0.81	0.14	0.34
			1.64	0.13	0.78	0.25	1.47	0.46	0.92	0.36	0.06	2.82			0.80	0.38	0.04
396	Y300A	a	1.16	0.32	0.63	0.08	0.74	0.12	0.55	0.12	0.75	0.13	1.64	0.26	1.04	0.14	1.01
397	Y300V	a	0.80	0.38	1.19	0.10	0.83	0.12	1.07	0.12	0.84	0.14	1.72	0.42	1.09	0.19	1.02
398	Y300M	a	1.32	0.30	1.22	0.11	0.89	0.14	0.84	0.13	1.00	0.19	1.85	0.48	1.10	0.14	1.13
399	Y300W	a	0.68	0.31	0.82	0.10	1.10	0.13	0.99	0.15	1.01	0.14	1.55	0.36	0.96	0.15	0.93
400	Y300P	a	0.11	0.28	0.54	0.13	0.61	0.17	0.47	0.13	0.90	0.12	1.93	0.30	0.61	0.14	1.48
401	Y300G	a	0.83	0.33	0.62	0.16	0.67	0.12	0.64	0.12	0.80	0.13	2.96	0.41	1.07	0.12	1.20
402	A330E	ap	3.27	0.30	0.58	0.08	0.59	0.15	0.51	0.20	1.92	0.18	2.14	0.53			3.25
			2.18	0.14	0.26	0.25	1.35	0.55	0.55	0.71	0.11	2.82			0.86	0.39	0.08
403	A330N	ap	1.44	0.34	0.39	0.11	0.47	0.19	0.22	0.21	0.58	0.17	2.03	0.37	0.80	0.13	1.23
404	A330T	a	0.94	0.32	0.74	0.08	0.71	0.14	0.53	0.15	0.91	0.15	1.06	0.31	0.96	0.12	1.27
405	A330P	a	0.33	0.35	0.40	0.35	1.26	0.23	0.79	0.23	0.12	0.17	0.72	0.31	5.48	0.15	0.09
			0.38	0.21	0.13	22.81	1.86	0.63	1.44	0.31	0.00	2.84			1.37	0.35	0.00
406	A330G	ap	0.91	0.31	1.27	0.11	1.14	0.16	1.34	0.12	1.32	0.19	1.54	0.37	1.01	0.15	1.16
407	I332K	a	0.15	0.29	0.47	0.11	0.59	0.13	0.60	0.15	0.40	0.13	1.52	0.34	0.90	0.17	0.68
408	I332R	a	0.13	0.33	0.39	0.07	0.58	0.16	0.37	0.17	0.27	0.14	1.25	0.33	0.79	0.13	0.47
409	I332S	a	1.63	0.35	1.83	0.12	1.11	0.20	1.00	0.13	1.05	0.13	2.45	0.41	0.98	0.15	0.94
410	I332V	a	1.91	0.37	1.18	0.11	0.78	0.20	0.51	0.21	1.05	0.21	5.94	0.50	59.27	0.70	1.35
411	I332L	a	1.76	0.31	0.86	0.07	0.99	0.18	0.76	0.17	0.97	0.14	3.98	0.56	0.73	0.19	0.98
412	I332F	a	1.56	0.32	1.66	0.09	1.55	0.16	1.26	0.16	1.13	0.14	3.32	0.34	0.78	0.18	0.73
413	I332M	a															
414	I332W	a															
415	I332P	a								20.57							

Figure 41 (continued)

			FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
Variant	Substitution(s)	Context	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
417	L234K	a	0.43	0.34	0.65	0.50	1.42	0.32	1.09	0.12	0.53	0.75	2.02	0.07	0.62	0.14	0.38
418	L234R	a	0.38	0.36	0.87	0.57	1.49	0.37	1.52	0.19	0.73	0.59	1.72	0.10	1.19	0.12	0.49
419	L234S	a	0.49	0.20	1.01	0.41	1.40	0.26	1.30	0.14	0.69	0.32	1.10	9.38	0.93	0.10	0.49
420	L234A	a	0.44	0.09	0.80	0.30	0.85	0.19	0.62	0.09	0.35	0.24	0.88	0.04	0.58	0.10	0.41
421	L234M	a	0.64	0.08	0.89	0.24	0.90	0.17	0.65	0.10	0.49	0.16	0.88	0.26	0.55	0.10	0.54
422	L234W	a															
423	L234P	a															
424	L234G	a	0.70	0.47	3.26	0.53	3.62	0.34	3.48	0.26	2.17	0.61	1.91	0.08	2.54	0.11	0.60
			0.08	0.20			0.62	0.68	0.69	26.67	0.01	2.83			1.75	0.37	0.02
425	L235E	a	0.34	0.28	0.63	0.31	0.83	0.19	0.80	0.08	1.06	0.18	0.93	0.04	0.78	0.14	1.28
426	L235K	a	0.42	0.64	0.56	0.55	1.28	0.35	1.34	0.13	0.63	0.71	1.55	0.13	0.96	0.17	0.49
427	L235R	a	0.35	0.69	0.71	0.52	1.93	0.29	1.15	0.11	0.62	0.68	1.73	0.07	0.53	0.17	0.32
428	L235A	a	0.34	0.22	0.62	0.35	0.84	0.21	0.78	0.10	0.41	0.30	1.00	0.04	0.97	0.15	0.49
429	L235M	a	0.38	0.09	0.79	0.26	0.89	0.19	0.64	0.09	0.46	0.23	1.05	0.05	0.69	0.11	0.51
430	L235W	a	0.11	0.34	0.90	0.19	0.77	0.17	0.50	0.08	0.32	0.24	0.83	0.04	0.46	0.11	0.42
431	L235P	a	0.13	0.62	1.16	0.27	1.16	0.18	0.89	0.10	0.78	0.23	1.31	0.05	0.86	0.12	0.67
432	L235G	a		5.79	0.99	0.31	1.02	0.19	0.74	0.11	0.43	0.34	1.12	0.06	0.68	0.11	0.42
433	V264D	a	0.56	0.20	0.19	0.22	0.24	0.49	0.54	0.38	0.93	0.69	0.54	0.67	7.67	0.51	3.92
434	V264E	a	0.67	0.06	0.37	0.44	0.74	0.26	0.94	0.09	0.44	0.67	0.60	0.07	0.93	0.17	0.60
435	V264N	a	0.93	0.15	1.04	0.17	1.63	0.28	1.60	0.25	0.34	0.69			3.39	0.56	0.21
436	V264Q	a	0.62	0.08	0.48	0.25	0.68	0.20	0.61	0.09	0.38	0.20	0.73	0.13	0.72	0.14	0.55
437	V264K	a	0.48	0.13	0.46	0.39	0.77	0.24	0.67	0.09	0.36	0.45	0.97	0.05	0.50	0.11	0.47
438	V264R	a	0.31	1.12	1.21	0.66	2.37	0.30	2.01	0.13	7.42	11.18	3.05	0.04	0.67	0.10	3.13
439	V264S	a	1.15	0.23	0.69	0.17	1.37	0.51	0.81	0.37	0.35	0.69	0.83	0.72	5.13	0.52	0.26
440	V264H	a	0.34	0.09	0.27	0.25	0.30	0.20	0.22	0.13	0.16	0.22	0.58	0.05	0.55	0.18	0.52
441	V264W	a	0.59	0.06	0.81	0.27	0.81	0.18	0.67	0.09	0.39	0.27	0.86	0.03	0.87	0.15	0.48
442	V264P	a															
443	V264G	a	0.41	0.19	0.26	0.19	1.11	0.26	1.14	0.33	0.21	0.70	1.13	0.53	0.93	0.57	0.19
444	D265Q	a	0.33	0.23	0.94	0.30	0.89	0.19	0.71	0.11	0.51	0.45	1.04	0.13	0.76	0.14	0.57
445	D265K	a	0.20	1.32	1.72	0.42	2.15	0.23	1.46	0.13	1.00	1.01	2.12	0.05	0.87	0.19	0.47
446	D265R	a	0.71	1.23	0.77	0.79	2.55	0.45	2.18	0.14	1.50	1.54	2.98	0.04	1.16	0.13	0.59
447	D265S	a	0.29	0.47	0.50	0.44	1.07	0.27	0.89	0.10	0.49	0.65	1.47	0.07	0.53	0.11	0.46
448	D265T	a	0.41	0.39	0.64	0.46	1.41	0.26	1.04	0.12	0.61	0.67	1.66	0.07	0.74	0.13	0.43
449	D265H	a	0.33	0.23	0.48	0.53	0.86	0.23	0.74	0.09	0.40	0.52	1.24	0.04	0.72	0.10	0.47
450	D265V	a	0.11	0.76	0.72	0.38	0.93	0.22	0.92	0.11	0.47	0.60	1.39	0.06	0.44	0.11	0.50
451	D265L	a	0.14	0.58	0.86	0.34	0.90	0.19	0.78	0.10	0.53	0.52	0.92	0.04	0.55	0.11	0.59
452	D265I	a	0.24	1.08	1.70	0.36	1.63	0.20	1.44	0.11	0.90	0.65	1.60	0.06	0.49	0.12	0.55
453	D265F	a	0.12	0.67	1.00	0.32	0.98	0.19	0.88	0.11	0.67	0.75	0.97	0.04	0.55	0.09	0.68
454	D265M	a	0.49	0.28	0.56	0.34	0.80	0.18	0.74	0.09	0.59	0.32	0.63	0.08	0.61	0.13	0.74
455	D265Y	a	0.01	1.21		13.21	0.58	0.40	0.30	1.04	0.02	1.09			0.43	0.46	0.03
456	D265W	a	0.52	0.43	0.72	0.34	0.99	0.17	0.98	0.09	0.84	0.42	1.02	0.09	0.67	0.13	0.85
457	D265P	a	0.74	0.43	1.13	0.41	1.94	0.20	1.56	0.10	1.19	0.56	1.92	0.10	1.18	0.12	0.61
458	K326P	a															
459	A327E	a	0.99	0.11	0.71	0.17	0.54	0.12	0.45	0.07	0.64	0.20	0.59	0.08	0.91	0.15	1.18
460	A327K	a	0.93	0.17	1.19	0.29	1.25	0.15	0.96	0.09	1.01	0.46	1.21	0.10	1.01	0.14	0.81
461	A327R	ap	0.91	0.17	1.20	0.27	1.36	0.15	0.95	0.10	0.98	0.51	1.29	0.10	0.80	0.12	0.72
462	A327H	ap	1.36	0.14	0.52	0.47	1.01	0.23	0.97	0.13	0.75	0.54	1.39	0.11	1.29	0.15	0.74
463	A327V	a															
464	A327I	a	0.65	0.07	0.26	0.26	0.44	0.21	0.33	0.11	0.27	0.25	0.56	0.09			0.60
465	A327F	a	0.69	0.07	0.45	0.27	0.64	0.17	0.51	0.09	0.37	0.27	0.60	0.08	0.71	0.20	0.58
466	A327M	a	0.82	0.07	0.64	0.26	0.78	0.16	0.67	0.09	0.51	0.24	0.75	0.08	1.08	0.14	0.66
467	A327Y	a	1.04	0.09	0.70	0.31	0.86	0.18	0.76	0.10	0.61	0.30	0.86	0.08	1.23	0.13	0.71
468	A327W	a	0.76	0.09	0.66	0.25	0.70	0.14	0.59	0.08	0.47	0.28	0.68	0.08	0.90	0.12	0.67
469	A327P	a	1.06	0.09	0.78	0.23	0.76	0.13	0.63	0.08	0.47	0.22	0.80	0.07	0.86	0.14	0.61
470	L328D	a	0.95	0.15	0.64	0.19	0.54	0.12	0.51	0.09	0.51	0.31	0.43	0.09	0.89	0.15	0.95
471	L328Q	ap	1.15	0.07	0.70	0.22	0.86	0.14	0.77	0.07	0.67	0.22	0.79	0.10	0.89	0.16	0.78
472	L328K	a	0.77	0.22	0.51	0.38	0.99	0.20	0.91	0.09	0.87	0.32	1.13	0.09	0.95	0.19	0.88
473	L328R	a	0.07	0.27	0.10	0.82	0.88	0.58	0.37	1.05	0.11	0.93	1.21	0.52	1.82	0.46	0.12
474	L328S	a	0.96	0.08	1.14	0.17	0.90	0.13	0.70	0.07	0.59	0.19	0.76	0.08	0.66	0.20	0.65
475	L328T	a	0.60	0.07	0.62	0.23	0.61	0.12	0.44	0.07	0.46	0.24	0.59	0.08	0.74	0.14	0.76
476	L328V	a	0.70	0.06	0.54	0.18	0.60	0.13	0.43	0.08	0.49	0.22	0.57	0.09	0.52	0.12	0.82
477	L328I	a	0.79	0.08	0.69	0.19	0.67	0.12	0.55	0.07	0.58	0.20	0.60	0.08	0.77	0.14	0.86
478	L328Y	a	1.05	0.09	0.88	0.19	0.75	0.12	0.63	0.08	0.47	0.30	0.71	0.07	0.92	0.13	0.63
479	L328W	a	1.01	0.06	1.16	0.19	0.90	0.13	0.82	0.09	0.73	0.30	0.83	0.09	1.35	0.13	0.81
480	L328P	a	0.72	0.07	0.38	0.29	0.61	0.17	0.52	0.08	0.42	0.33	0.56	0.09	0.76	0.19	0.68
481	L328G	a	1.18	0.10	0.71	0.34	0.90	0.16	0.93	0.08	0.64	0.41	0.80	0.08	1.16	0.24	0.70
482	P329D	a	0.72	0.12	0.55	0.32	0.82	0.17	0.80	0.09	0.62	0.29	0.80	0.09	0.79	0.26	0.76
483	P329E	a															
484	P329N	a	0.76	0.08	0.65	0.54	0.98	0.15	0.86	0.08	0.97	0.21	0.97	0.08	1.00	0.13	0.99
485	P329Q	a	0.72	0.15	0.70	0.33	0.84	0.17	0.81	0.09	0.68	0.41	0.91	0.08			0.80
486	P329K	a	0.20	2.88			0.16	0.47	0.57	0.42	0.02	0.90	1.17	0.53	0.72	0.12	0.10
487	P329R	a	1.83	0.18	2.06	0.33	2.38	0.17	2.03	0.10	1.52	0.43	2.23	0.07	1.64	0.16	0.64
488	P329S	a	0.60	0.13	0.77	0.25	0.76	0.14	0.75	0.52	0.62	0.36	0.87	0.07	0.77	0.13	0.82

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
489	P329T	a	0.34	0.11	0.49	0.21	0.47	0.14	0.33	0.10	0.41	0.32	0.52	0.09	0.70	0.13	0.88
490	P329H	a	0.09	0.21	0.24	0.57	0.24	0.15	0.30	0.23	0.03	0.25	1.05	0.12	0.64	0.41	0.12
491	P329V	a	0.51	0.19	0.33	0.49	0.31	0.21	0.28	0.26	0.04	0.27	1.62	0.12	0.64	0.39	0.12
492	P329L	a	0.17	0.21	0.24	0.58	0.22	0.13	0.22	0.17	0.04	0.19	2.78	0.16	0.56	0.42	0.18
493	P329I	a	0.40	0.15	0.31	0.54	0.27	0.21	0.27	0.21	0.03	0.18	2.57	0.14	0.48	0.36	0.12
494	P329M	a	0.21	0.16	0.23	0.57	0.21	0.21	0.16	0.18	0.03	0.21	4.36	0.15	0.62	0.43	0.13
495	P329Y	a															
496	P329W	a	0.54	0.55			0.09	1.39	0.61	0.76	0.02	1.47	1.04	0.49	3.16	0.72	0.25
497	P329G	a	1.03	0.14	0.30	0.47	0.25	0.16	0.29	0.14	0.06	0.19	4.72	0.13	0.45	0.40	0.23
498	P331D	ap	3.14	0.18	0.92	0.49	1.18	0.12	1.23	0.19	0.74	0.18	5.89	0.12	0.79	0.40	0.63
			1.65	0.12	0.32	0.19	1.00	0.50	0.86	4.39	0.05	2.82			0.80	0.42	0.05
499	P331Q	a	1.71	0.14	0.60	0.40	0.63	0.13	0.77	0.17	0.64	0.12	2.46	0.12	0.60	0.46	1.01
500	P331R	a	2.29	0.19	0.39	0.42	0.54	0.22	0.32	0.22	0.29	0.09	0.98	0.15	0.89	0.37	0.54
501	P331T	a	1.67	0.13	0.53	0.41	0.71	0.17	0.88	0.23	0.57	0.10	3.25	0.14	0.57	0.37	0.81
502	P331L	ap	1.95	0.33	0.53	0.45	0.92	0.12	0.99	0.24	0.50	0.12	6.07	0.15	0.54	0.40	0.54
			0.64	0.16	0.68	0.14	1.14	0.11	1.37	0.36	0.35	0.36	5.28	0.12	1.77	0.13	0.31
503	P331I	a	1.63	0.15	0.41	0.41	0.71	0.18	0.78	0.19	0.22	0.19	3.81	0.16	0.56	0.41	0.32
504	P331F	a	1.02	0.13	0.51	0.18	0.67	0.41	0.97	0.26	0.29	0.69	0.96	0.48	3.91	0.90	0.44
505	P331M	a	1.74	0.12	0.60	0.47	1.13	0.18	0.94	0.16	0.77	0.12	2.50	0.12	0.53	0.37	0.68
506	P331Y	a	1.20	0.13	1.24	0.16	0.47	0.47	0.82	0.35	0.69	0.69	0.95	0.55	6.06	0.75	1.47
507	P331W	a	1.95	0.13	0.79	0.41	1.46	0.14	1.32	0.18	0.76	0.12	2.41	0.13	0.87	0.46	0.52
508	E333L	a	1.03	0.14	0.56	0.44	0.93	0.15	0.94	0.23	0.90	0.10	3.06	0.16	1.03	0.49	0.97
509	E333F	ap	2.22	0.14	0.69	0.45	0.93	0.18	1.55	0.30	1.69	0.15	6.96	0.16	0.82	0.42	1.82
			0.91	0.17	0.86	0.14	1.58	0.18	1.66	0.39	1.22	0.40	5.83	0.20	1.86	0.15	0.77
510	E333M	a	1.17	0.18	0.86	0.15	1.20	1.87	0.21	0.76	0.74	0.70	0.96	0.53	5.46	0.78	0.82
511	E333P	a															
512	K334P	a															
513	K222E	a	1.77	0.13	1.26	0.41	1.04	0.16	1.22	0.20	1.51	0.14	1.23	0.15	0.64	0.38	1.44
514	K222Y	a	0.77	0.14	0.48	0.51	0.50	0.15	0.34	0.26	0.34	0.10	1.06	0.12	0.66	0.41	0.68
			1.92	0.22	1.28	0.28	1.69	0.42	1.33	0.44	0.11	2.86			1.31	0.39	0.07
515	E243E	a	0.93	0.13	0.18	0.33	1.24	0.49	0.63	0.52	0.14	2.84			1.14	0.40	0.11
516	D270R	a	0.60	0.32	0.37	0.56	0.94	0.12	0.36	0.19	0.14	0.13	0.47	0.16	0.82	0.43	0.14
517	D270S	a	0.81	0.16	0.69	0.44	1.80	0.14	0.61	0.18	0.19	0.13	0.81	0.19	1.03	0.49	0.10
518	D270L	a	1.03	0.18	0.59	0.47	0.35	0.19	0.31	0.16	0.40	0.11	0.72	0.12	0.54	0.43	1.15
519	D270I	a	0.58	0.15	0.15	0.30	0.76	0.60			0.02	2.83			1.23	0.38	0.03
520	D270F	a	0.66	0.18	0.64	0.40	0.39	0.17	0.21	0.15	0.19	0.14	0.70	0.13	0.70	0.40	0.49
521	D270M	a	0.74	0.19	0.43	0.49	0.21	0.18	0.37	0.19	0.36	0.09	1.11	0.12	0.99	0.44	1.72
522	D270Y	a	0.51	0.22	0.54	0.48	0.34	0.14	0.37	0.16	0.28	0.11	0.62	0.18	0.93	0.37	0.83
523	D270W	a	0.84	0.20	0.49	0.44	0.25	0.20	0.38	0.21	0.17	0.10	0.62	0.21	0.92	0.43	0.68
524	D270P	a	0.37	0.21	0.32	0.60	0.25	0.19	0.32	0.22	0.04	0.23	0.91	0.27	0.55	0.34	0.15
525	D270G	a	0.52	0.24	0.42	0.50	0.38	0.12	0.22	0.23	0.08	0.18	0.63	0.30	0.97	0.46	0.21
526	P271D	ap	1.48	0.15	0.77	0.43	1.20	0.13	1.02	0.14	1.12	0.13	1.80	0.14	0.52	0.42	0.93
527	P271E	a	1.87	0.14	0.65	0.46	0.95	0.15	0.72	0.17	0.75	0.17	0.72	0.14	0.41	0.50	0.79
528	P271N	a	1.61	0.13	0.78	0.41	0.98	0.11	0.79	0.12	0.83	0.14	1.17	0.13	0.54	0.41	0.64
529	P271Q	a	0.55	0.24	0.71	0.09	1.07	0.79	0.66	0.30	0.60	0.23	0.86	0.18	0.56	0.12	0.56
530	P271K	a	0.63	0.27	0.67	0.09	0.90	0.87	0.36	0.29	0.71	0.17	0.71	0.20	0.87	0.16	0.79
531	P271R	a	0.60	0.30	0.67	0.08	1.68	1.14	0.28	0.31	0.51	0.19	0.52	0.20	0.78	0.14	0.31
532	P271S	a	0.55	0.24	0.73	0.08	1.71	1.10	0.61	0.27	0.70	0.21	0.71	0.16	1.14	0.14	0.41
533	P271T	a	0.77	0.22	0.97	0.07	2.73	0.90	0.83	0.30	0.53	0.19	0.95	0.17	3.88	0.12	0.19
534	P271H	a	0.56	0.30	0.63	0.13	0.37	0.66	0.45	0.31	0.67	0.20	0.88	0.18	0.74	0.13	1.80
535	P271A	ap	0.85	0.24	0.70	0.07	1.05	0.87	0.93	0.27	0.73	0.23	1.02	0.17	1.01	0.21	0.70
536	P271V	a	0.33	0.30	0.43	0.14	1.73	0.95	0.15	0.33	0.17	0.18	0.50	0.18	0.54	0.16	0.10
			1.52	0.15	0.35	0.27	0.84	0.43	0.75	0.42	0.06	2.82			1.06	0.38	0.07
537	P271L	a	1.77	0.27	0.73	0.09	1.09	0.79	1.17	0.30	0.46	0.22	1.56	0.16	0.43	0.23	0.42
538	P271I	ap	0.99	0.22	2.13	0.08	1.42	0.71	1.09	0.27	1.28	0.19	1.51	0.16	1.99	0.20	0.90
539	P271F	a	0.64	0.25	0.54	0.12	1.66	0.92	0.45	0.29	0.44	0.20	0.89	0.19	0.68	0.12	0.26
540	P271M	a	0.91	0.30	0.62	0.08	2.37	1.38	0.67	0.28	0.52	0.20	0.91	0.20	0.54	0.14	0.22
541	P271Y	a	0.71	0.31	0.70	0.12	3.65	1.10	0.21	0.36	0.37	0.21	0.64	0.17	1.48	0.14	0.10
542	P271W	a	0.60	0.24	0.63	0.47	0.52	0.73	0.25	0.32	0.72	0.22	1.06	0.18	0.98	0.15	1.37
543	P271G	a	0.88	0.21	2.33	0.04	1.79	0.86	5.03	0.27	1.09	0.27	0.96	0.17	0.57	0.22	0.61
			2.07	0.14	1.50	0.25	4.50	0.37	4.02	0.34	0.07	2.82			0.79	0.37	0.02
544	D280K	a	1.99	0.32	0.68	0.08	1.54	0.83	0.51	0.32	0.59	0.17	0.68	0.20	0.38	0.17	0.38
545	D280L	a	0.62	0.25	0.84	0.06	1.33	0.78	0.39	0.29	0.65	0.29	0.86	0.19	0.45	0.16	0.49
546	D280W	a	0.47	0.26	0.83	0.07	1.30	0.78	0.33	0.30	0.57	0.24	0.76	0.18	0.38	0.16	0.44
547	D280P	a	0.81	0.12			0.91	0.34			0.28	0.17					0.31
548	D280G	a	1.75	0.15	0.92	0.25	2.12	0.63	1.71	0.31	0.15	2.82			0.98	0.38	0.07
549	K290D	a	0.91	0.31	1.42	0.07	1.36	1.07	1.87	0.28	1.81	0.23	2.20	0.20	0.33	0.15	1.33
550	K290N	a	0.85	0.30	1.26	0.07	0.76	0.90	1.31	0.28	1.48	0.21	1.97	0.17	0.39	0.14	1.93
551	K290H	a	1.14	0.34	1.13	0.06	1.65	0.86	0.83	0.30	1.50	0.23	1.88	0.19	0.41	0.16	0.90
552	K290L	a	1.07	0.10			0.86	0.29			0.30	0.18					0.35
553	K290W	a	0.76	0.19	1.00	0.15	0.38	0.66	1.44	0.29	1.37	0.28	1.53	0.19	0.68	0.13	3.63
554	E293N	a	1.24	0.25	0.83	0.08	1.43	0.91	0.62	0.30	0.67	0.18	1.06	0.21	0.71	0.24	0.47

Figure 41 (continued)

			FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
Variant	Substitution(s)	Context	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
555	E293R	ap	172	0.64	0.66	0.20	1.75	0.82	0.40	0.46	68.81	2.94	3.16	0.48	0.67	0.15	39.28
			18.03	0.43	0.93	0.16	2.22	0.28	0.88	0.31	2.90	1.26	1.77	0.36	0.38	0.31	1.31
556	E293S	a	2.69	0.25	0.91	0.17	1.61	0.76	0.57	0.34	0.86	0.22	1.01	0.21	0.53	0.20	0.53
557	E293T	a	1.50	0.38	0.73	0.09	2.11	0.91	0.55	0.27	0.69	0.21	0.91	0.24	0.58	0.15	0.33
558	E293H	a	2.26	0.21	0.59	0.09	1.85	1.06	0.29	0.26	0.61	0.18	1.05	0.28	0.48	0.13	0.33
559	E293V	a	2.23	0.30	0.77	0.13	4.03	0.97	0.55	0.28	0.90	0.19	1.08	0.22	0.63	0.14	0.22
560	E293L	a	1.66	0.28	0.85	0.14	2.79	0.83	0.56	0.30	0.51	0.18	1.02	0.26	0.77	0.15	0.18
561	E293I	a	1.28	0.22	0.79	0.16	0.47	0.68	0.33	0.29	0.61	0.19	0.77	0.23	0.60	0.13	1.29
562	E293F	a	0.74	0.13	0.51	0.09	1.27	0.95	0.31	0.31	0.23	0.25	0.64	0.12	0.61	0.20	0.18
563	E293M	a	1.30	0.21	1.05	0.09	0.60	0.95	1.01	0.29	0.39	0.26	0.53	0.14	0.90	0.21	0.65
564	E293Y	a	0.84	0.14	0.59	0.13	0.91	1.15	0.28	0.33	0.24	0.24	0.61	0.13	0.66	0.20	0.26
565	E293W	a	0.92	0.21	0.68	0.12	4.93	1.73	0.21	0.56	0.24	0.23	0.45	0.14	0.65	0.23	0.05
566	E293P	a	0.34	0.28	0.26	0.14	9.25	1.72	0.10	0.31	0.10	0.23	0.66	0.14	0.44	0.17	0.01
567	E293G	a	1.25	0.26	0.68	0.09	1.00	1.38	0.24	0.31	0.31	0.25	0.77	0.13	0.59	0.18	0.31
568	E294K	a	0.70	0.29	0.57	0.13	1.44	1.19	0.45	0.34	1.02	0.25	0.50	0.14	0.74	0.23	0.71
			0.68	0.19	0.36	0.27	1.57	0.64	0.61	0.81	0.07	2.82			1.16	0.40	0.04
569	E294R	a	0.71	0.10	0.60	0.14	0.98	0.98	0.65	0.22	0.86	0.25	0.58	0.13	0.92	0.28	0.89
570	E294S	a	0.87	0.11			0.84	0.72			0.30	0.18					0.36
571	E294T	a	1.28	0.11	1.37	0.10	0.68	0.98	1.16	0.26	0.45	0.25	1.07	0.15	0.71	0.33	0.66
572	E294H	a	1.50	0.27	1.11	0.13	0.58	0.92	0.55	0.22	0.45	0.27	0.81	0.12	0.76	0.20	0.77
573	E294V	a	0.86	0.21	0.74	0.10	0.39	1.28	0.87	0.22	0.43	0.49	0.87	0.13	0.70	0.17	1.11
574	E294L	a	0.43	0.26	0.35	0.15	0.42	1.14	0.45	0.24	0.35	0.58	0.93	0.12	0.45	0.19	0.83
			1.23	0.26	0.70	0.32	1.30	0.20	1.26	0.30	1.65	0.16			0.98	0.47	1.26
575	E294I	a	1.70	0.25	0.95	0.14	3.65	1.09	0.83	0.26	0.71	0.23	1.05	0.13	1.09	0.22	0.19
576	E294F	a	1.08	0.35	0.89	0.16	0.56	0.95	0.58	0.22	0.43	0.31	0.72	0.16	0.90	0.18	0.78
577	E294M	a	0.96	0.15	0.84	0.09	1.70	1.26	0.65	0.27	0.67	0.28	1.17	0.14	0.78	0.21	0.39
578	E294Y	a	0.70	0.12			0.68	0.49			1.32	0.17					1.95
579	E294W	a	0.74	0.18	0.93	0.10	0.99	1.08	0.77	0.22	1.70	0.38	1.37	0.15	0.80	0.20	1.73
580	E294P	a	1.00	0.20	1.09	0.12	1.34	0.97	0.50	0.23	0.67	0.24	0.50	0.12	0.77	0.26	0.50
581	E294G	a	1.55	0.20	1.18	0.09	0.55	0.97	1.45	0.21	0.61	0.25	0.94	0.14	1.25	0.27	1.10
582	Q295D	a	1.73	0.24	0.57	0.10	3.31	1.54	0.67	0.30	0.54	0.26	2.41	0.27	0.55	0.17	0.16
583	Q295E	a	4.42	0.12	1.49	0.14	1.91	1.40	0.88	0.22	1.03	0.24	0.84	0.17	0.96	0.23	0.54
			1.36	0.26	1.37	0.26	0.80	0.27	0.72	0.20	0.89	0.15			0.81	0.49	1.10
584	Q295N	a	2.09	0.18	0.81	0.12	5.76	1.58	0.50	0.34	0.45	0.25	0.69	0.15	0.93	0.17	0.08
585	Q295R	a	1.30	0.19	0.78	0.11	0.51	0.87	0.45	0.30	0.35	0.28	1.43	0.22	0.67	0.16	0.69
586	Q295S	a	1.27	0.12	0.74	0.13	0.95	1.07	0.77	0.31	0.55	0.24	1.89	0.13	0.72	0.23	0.57
587	Q295T	a	1.46	0.12	1.84	0.11	1.09	1.04	1.54	0.23	1.36	0.24	1.48	0.21	3.82	0.20	1.25
588	Q295H	a	1.14	0.20	1.01	0.11	4.39	1.62	0.79	0.31	0.43	0.25	1.39	0.20	0.76	0.32	0.10
589	Q295V	a	2.12	0.19	1.63	0.10	0.99	1.15	1.56	0.24	0.61	0.25	1.35	0.18	1.19	0.20	0.62
590	Q295I	a	1.42	0.17	1.99	0.12	1.94	1.00	1.04	0.21	0.53	0.27	1.28	0.15	0.68	0.37	0.27
591	Q295F	a	1.38	0.27	0.87	0.13	1.79	1.17	0.28	0.28	0.33	0.26	1.73	0.12	0.83	0.24	0.19
592	Q295M	a	2.88	0.26	1.69	0.11	1.50	1.00	0.66	0.40	0.81	0.27	2.93	0.17	0.70	0.25	0.54
593	Q295Y	a	0.94	0.22	0.61	0.11	0.18	0.86	0.56	0.22	0.27	0.29	2.30	0.14	0.62	0.34	1.47
594	Q295W	a	0.12	0.24	0.43	0.48	0.38	0.42	0.50	0.33	0.27	0.24	3.15	0.16	0.32	0.38	0.71
595	Q295P	a	0.38	0.30	0.94	0.28	0.57	0.37	0.71	0.20	0.48	0.32	3.14	0.14	0.49	0.36	0.83
596	Q295G	a	0.19	0.23	0.62	0.35	0.35	0.51	0.47	0.25	0.54	0.25	4.08	0.12	0.35	0.37	1.54
597	Y296K	a	0.21	0.26	0.40	0.36	0.33	0.53	0.54	0.30	0.35	0.16	2.67	0.14	0.58	0.34	1.07
598	Y296R	a	0.26	0.41	0.58	0.28	0.41	0.48	0.74	0.20	0.54	0.15	2.51	0.13	0.49	0.34	1.33
599	Y296A	a	0.56	0.35	0.44	0.27	0.48	0.39	0.68	0.33	1.06	0.23	4.09	0.14	0.42	0.40	2.20
600	Y296V	a	0.41	0.29	1.08	0.51	0.58	0.31	0.88	0.14	0.72	0.26	6.49	0.13	0.48	0.41	1.25
601	Y296M	a	0.21	0.33	0.94	0.36	0.64	0.34	0.90	0.17	0.65	0.28	3.02	0.13	0.53	0.36	1.01
602	Y296G	a	0.63	0.82	1.65	0.42	0.58	0.32	1.01	0.21	0.33	0.27	5.51	0.19	0.59	0.38	0.56
603	S324H	ap	0.99	0.33	0.84	0.25	0.74	0.29	0.57	0.17	0.73	0.36	3.54	0.13	0.57	0.34	0.98
604	S324F	a	1.17	0.40	0.94	0.29	0.65	0.33	0.74	0.23	0.92	0.30	4.10	0.15	0.50	0.33	1.43
605	S324M	a	0.76	0.80	1.13	0.28	0.88	0.23	1.07	0.12	1.46	0.24	2.02	0.13	0.61	0.33	1.66
606	S324W	a															
607	S324P	a	0.28	0.30	0.42	0.29	1.23	0.26	1.01	0.15	1.38	0.29	1.68	0.14	0.63	0.34	1.12
608	S324G	a	1.61	0.33	2.07	0.27	1.92	0.27	1.89	0.34	6.18	0.22	3.22	0.16	1.70	0.36	3.22
			0.60	0.15	3.06	0.11	2.56	0.18	2.18	0.30	3.93	0.30	2.14	0.13	2.74	0.18	1.53
			1.46	0.20	1.55	0.23	1.07	0.20	0.89	0.27	1.88	0.10			1.25	0.50	1.77
609	P230E	a	2.07	0.52	1.25	0.31	2.34	0.45	1.47	0.15	1.40	0.24	2.70	0.13	1.01	0.34	0.60
610	P230Y	a	0.44	0.52	0.40	0.30	0.85	0.34	1.22	0.20	0.56	0.33	2.00	0.12	0.65	0.33	0.66
611	P230G	a	1.04	0.45	0.99	0.38	1.13	0.36	0.75	0.21	0.48	0.22	1.27	0.16	1.16	0.34	0.42
612	A231E	a															
613	A231K	a	0.50	0.36	0.62	0.34	0.41	0.61	0.58	0.24	0.58	0.49	1.40	0.16	0.52	0.33	1.39
614	A231Y	a															
615	A231P	a	1.17	0.15			0.81	0.43			0.31	0.17					0.38
616	A231G	a															
617	E233N	a	0.16	0.28	0.50	0.44	0.34	0.79	0.46	0.22	0.48	0.17	1.28	0.15	0.74	0.33	1.42
618	E233Q	a	0.19	0.22	0.52	0.42	0.27	0.62	0.39	0.25	0.51	0.17	1.17	0.16	0.61	0.34	1.88
619	E233K	a															
620	E233R	a	0.14	0.26	0.75	0.27	0.36	0.68	0.60	0.19	0.35	0.16	1.13	0.18	1.05	0.33	0.97
621	E233S	a	0.17	0.18	0.62	0.35	0.31	0.59	0.37	0.35	0.36	0.19	1.18	0.16	1.10	0.33	1.14

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
622	E233T	a	0.15	0.35	1.28	0.39	0.78	0.40	0.83	0.13	0.42	0.19	0.99	0.17	1.19	0.35	0.54
623	E233H	a	0.17	0.32	0.74	0.27	0.58	0.40	0.78	0.14	0.32	0.27	1.05	0.15	0.99	0.33	0.55
624	E233A	a	0.10	0.31	1.23	0.33	0.60	0.44	0.71	0.20	0.46	0.21	1.02	0.13	0.93	0.38	0.75
625	E233V	a	0.25	0.48	0.71	0.31	0.37	0.61	0.61	0.17	0.50	0.21	0.70	0.15	0.91	0.33	1.34
626	E233L	a	0.53	0.40	0.55	0.29	0.26	0.53	0.54	0.27	0.52	0.19	2.24	0.17	0.60	0.34	1.99
627	E233I	a p	0.30	0.28	1.09	0.29	1.69	0.27	1.80	0.14	0.88	0.27	2.30	0.14	0.95	0.34	0.52
628	E233F	a	0.23	0.34	0.64	0.31	0.73	0.38	0.84	0.27	0.58	0.20	1.27	0.15	0.90	0.35	0.79
629	E233M	a	0.29	0.27	0.67	0.27	0.49	0.48	0.85	0.15	0.70	0.18	1.56	0.14	1.13	0.43	1.42
630	E233Y	a	0.31	0.14	0.96	0.10	0.97	0.16	0.55	0.14	0.37	0.09	0.70	410	1.86	0.27	0.38
631	E233W	a	0.28	0.17	0.86	0.12	0.82	0.14	0.70	0.15	0.35	0.13	0.91	0.34	1.64	0.24	0.43
632	E233G	a	0.36	0.14	1.21	0.11	0.94	0.22	0.74	0.13	1.21	0.10	1.03	0.29	2.09	0.25	1.29
633	E272D	a	1.26	0.24	1.25	0.10	1.12	0.13	1.41	0.12	1.49	0.16	1.48	0.18	1.37	0.22	1.33
634	E272R	a p	66.62	0.43	0.84	0.11	0.80	0.17	1.91	0.27	41.60	2.06		26.26	1.83	0.22	51.94
			98.41	0.98	0.94	0.21	1.26	0.31	0.47	0.30	0.67	0.35		2.58	1.62	0.25	0.53
635	E272T	a	3.32	0.22	1.24	0.11	1.74	0.31	1.34	0.18	3.04	0.25	0.69	0.23	2.46	0.21	1.75
			0.96	0.23	0.44	0.26	0.75	0.23	0.74	0.17	0.31	0.17			0.79	0.48	0.41
636	E272H	a p	7.21	0.20	0.84	0.09	1.92	0.10	0.83	0.13	28.57	0.15	0.55	0.20	1.45	0.27	14.86
			4.09	0.51	0.88	0.15	1.70	0.15	1.18	0.26	9.83	0.37	1.42	0.25	0.90	0.23	5.77
			1.02	0.26	0.49	0.29	0.43	0.39	0.26	0.47	0.35	0.10			0.92	0.43	0.80
637	E272V	a	2.80	0.28	0.96	0.10	0.72	0.13	0.50	0.17	1.19	0.23	0.67	0.20	1.77	0.25	1.64
638	E272L	a	2.07	0.22	1.10	0.10	0.83	0.13	0.62	0.13	1.07	0.19	0.75	0.21	1.81	0.21	1.29
639	E272F	a															
640	E272M	a															
641	E272W	a	1.61	0.32	1.06	0.11	1.09	0.12	0.68	0.15	2.59	0.15	0.62	0.23	1.82	0.23	2.38
642	E272P	a	5.27	0.21	1.14	0.14	2.99	0.14	3.36	0.22	0.67	0.11	0.55	0.30	2.17	0.21	0.23
			1.73	0.23	0.37	0.30	3.46	0.17	4.31	0.13	0.32	0.11			0.67	0.62	0.09
643	E272G	a	1.25	0.11			0.46	0.45			0.24	0.18					0.52
644	K274D	a															
645	K274N	a	1.25	0.17	1.37	0.10	1.17	0.13	1.42	0.13	1.18	0.09	1.55	0.21	1.26	0.25	1.01
647	K274H	a	1.02	0.22			1.21	0.30			0.27	0.24					0.22
648	K274V	a															
649	K274I	a	1.83	0.16	1.42	0.08	1.51	0.14	2.20	0.13	1.47	0.16	2.03	0.19	1.08	0.28	0.98
650	K274F	a	1.98	0.15	1.22	0.09	1.04	0.14	1.89	0.16	1.25	0.09	3.52	0.18	1.02	0.22	1.20
651	K274M	a	1.42	0.14	1.65	0.09	1.28	0.10	1.18	0.12	1.42	0.08	1.89	0.21	1.01	0.22	1.11
652	K274W	a															
653	K274P	a															
654	K274G	a	1.57	0.14	1.70	0.11	1.06	0.11	0.92	0.14	1.44	0.08	1.20	0.25	1.04	0.22	1.36
655	N276D	a p	1.54	0.13	1.34	0.13	1.21	0.11	1.04	0.11	0.88	0.05	1.10	0.26	1.18	0.21	0.72
656	N276T	a															
657	N276H	a	2.78	0.18	0.98	0.09	1.10	0.10	0.72	0.14	0.71	0.15	0.79	2.83	1.19	0.21	0.64
658	N276V	a	1.25	0.15	1.06	0.12	1.03	0.13	1.12	0.15	1.04	0.07	0.91	0.21	1.27	0.24	1.01
659	N276I	a															
660	N276F	a	1.34	0.30	1.18	0.10	1.30	0.15	1.57	0.14	1.53	0.15	2.20	0.17	1.18	0.21	1.17
661	N276M	a	1.20	0.26			0.99	0.36			0.26	0.24					0.26
662	N276W	a	2.53	0.26	1.24	0.11	1.32	0.16	2.06	0.14	1.21	0.09	1.57	0.26	2.00	0.21	0.92
663	N276P	a															
664	N276G	a															
665	Y278D	a	2.17	0.12	1.25	0.09	1.38	0.10	1.19	0.14	1.25	0.12	2.00	0.17	1.79	0.22	0.91
666	Y278N	a	1.54	0.18	0.88	0.10	0.78	0.12	0.66	0.12	0.82	0.08	0.74	9.38	1.33	0.22	1.05
667	Y278Q	a p															
668	Y278R	a p	1.98	0.25	0.92	0.12	0.62	0.11	0.58	0.15	0.54	0.10	0.82	0.25	1.23	0.22	0.87
669	Y278S	a	2.19	0.18	0.97	0.10	1.10	0.13	0.99	0.12	0.79	0.07	2.24	0.18	1.23	0.22	0.72
670	Y278H	a p															
671	Y278V	a	1.64	0.15	1.37	0.09	1.82	0.11	1.73	0.14	0.97	0.10	2.21	0.18	1.27	0.23	0.53
672	Y278L	a	2.57	0.20	1.05	0.13	1.32	0.12	0.94	0.12	2.92	0.09	0.44	0.21	1.74	0.21	2.21
673	Y278I	a	1.25	0.34	1.09	0.10	0.94	0.13	1.03	0.11	0.97	0.12	1.18	0.19	1.52	0.22	1.04
674	Y278M	a	1.49	0.16	0.94	0.09	0.71	0.10	1.02	0.15	0.55	0.15	1.22	0.20	1.28	0.21	0.77
675	Y278P	a															
676	Y278G	a															
677	K320N	a	2.63	0.13	1.33	0.10	1.45	0.11	1.42	0.12	1.64	0.11	1.89	0.18	2.01	0.22	1.13
678	K320S	a															
679	K320H	a	0.80	0.18	1.12	0.14	1.32	0.13	2.45	0.31	1.21	0.35	2.24	0.12	1.13	0.21	0.92
680	K320V	a	0.66	0.15	1.18	0.12	1.13	0.11	1.83	0.30	1.83	0.37	2.45	0.13	0.83	0.18	1.61
681	K320L	a	0.97	0.13	0.95	0.11	1.20	0.14	1.19	0.36	1.84	0.38	4.14	0.10	1.07	0.16	1.53
682	K320F	a	0.79	0.15	1.18	0.11	1.16	0.15	1.18	0.32	1.23	0.37	1.64	0.13	0.76	0.21	1.06
683	K320Y	a p	0.87	0.14	0.95	0.11	1.00	0.20	1.01	0.32	1.11	0.37	1.88	0.14	0.80	0.20	1.11
684	K320W	a	0.98	0.18	1.19	0.13	1.10	0.15	1.39	0.30	1.31	0.33	1.70	0.29	1.11	0.19	1.20
685	K320P	a															
686	K320G	a	0.73	0.20	1.11	0.12	1.06	0.14	1.19	0.37	1.21	0.36	1.53	0.12	0.69	0.22	1.13
687	K322D	a	1.11	0.15	0.80	0.12	0.78	0.10	1.43	0.31	0.80	0.36	1.69	0.11	0.48	0.25	1.03
688	K322S	a	0.93	0.43	0.94	0.11	0.97	0.11	1.99	0.31	1.14	0.36	1.86	0.11	0.87	0.20	1.17
689	K322V	a	0.69	0.14	1.07	0.11	1.25	0.14	2.00	0.31	1.16	0.39	1.51	0.11	0.72	0.18	0.92
690	K322I	a	0.69	0.28	0.90	0.11	1.33	0.15	1.54	0.32	0.92	0.36	1.61	0.11	0.75	0.24	0.69

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI Fold	FcγRI Conf	FcγRIIa Fold	FcγRIIa Conf	FcγRIIb Fold	FcγRIIb Conf	FcγRIIc Fold	FcγRIIc Conf	FcγRIIIa Fold	FcγRIIIa Conf	C1q Fold	C1q Conf	FcRn Fold	FcRn Conf	IIIa:IIb
691	K322F	a	0.79	0.15	0.95	0.11	1.33	0.13	1.30	0.29	0.86	0.38	1.15	0.15	0.75	0.19	0.65
692	K322Y	ap	0.77	0.14	0.95	0.11	1.11	0.17	1.18	0.37	1.03	0.34	2.10	0.11	0.87	0.22	0.93
693	K322W	a	0.65	0.17	0.87	0.13	0.73	0.18	0.77	0.35	0.95	0.32	1.48	0.11	0.66	0.18	1.31
694	K322P	a															
695	K322G	a	0.86	0.18	0.64	0.14	0.73	0.11	0.69	0.40	0.57	0.39	1.86	0.11	0.62	0.18	0.78
696	N325K	a	0.06	0.14	0.59	0.14	0.76	0.13	0.43	0.45	0.67	0.29	1.09	0.15	0.77	0.13	0.88
697	N325R	a	2.02	0.36	0.47	0.15	0.81	0.16	0.58	0.38	0.43	0.35	1.15	0.42	0.72	0.22	0.53
698	N325S	a	0.43	0.17	0.60	0.15	1.05	0.12	1.21	0.30	0.84	0.33	0.49	0.14	0.79	0.16	0.80
699	N325F	a	0.32	0.17	0.71	0.13	2.87	0.17	3.26	0.27	0.62	0.27	0.60	0.13	1.22	0.21	0.21
700	N325M	a	0.39	0.15	0.82	0.11	1.54	0.14	1.92	0.29	1.03	0.28	1.61	0.13	1.43	0.19	0.67
701	N325Y	a	0.27	0.14	0.54	0.13	0.73	0.23	0.65	0.35	0.57	0.30	1.72	0.13	0.91	0.24	0.77
702	N325W	a	0.23	0.19	0.45	0.17	0.57	0.25	0.40	0.49	0.51	0.30	1.35	0.12	0.86	0.23	0.89
703	N325P	a	0.06	0.21			0.37	2.05			0.03	0.53					0.07
704	N325G	a	0.18	0.21	0.46	0.16	0.76	0.16	0.70	0.34	0.75	0.27	0.69	0.66	0.53	0.15	0.99
705	P227E	a	1.47	0.23	1.55	0.32	1.55	0.19	1.67	0.12	2.10	0.10			1.49	0.49	1.36
706	P227K	a	0.44	0.37	0.64	0.17	0.84	0.27	3.04	0.28	0.38	0.24	0.92	0.46			0.46
			0.97	0.10	1.00	0.42	0.79	0.53	0.94	0.56	0.26	0.25	2.21	0.28	1.45	0.39	0.33
			0.92	0.20	0.85	0.29	0.89	0.22	0.77	0.22	1.03	0.13			1.16	0.51	1.16
707	P227Y	a	1.06	0.27	0.89	0.33	0.79	0.21	0.73	0.27	0.44	0.15			0.80	0.49	0.56
708	P227G	a	0.70	0.38	1.39	0.16	1.93	0.22	6.56	0.26	15.77	0.20	0.59	0.37			8.18
			1.67	0.15	0.91	0.37	1.98	0.24	3.47	0.32	12.61	0.37	1.16	0.32	1.67	0.40	6.36
709	P228E	a															
710	P228K	a	0.78	0.37	1.42	0.17	0.72	0.38	1.23	0.33	1.86	0.18	0.73	0.36			2.56
			1.91	0.28	1.31	0.58	1.14	0.25	1.13	0.54	1.28	0.25	1.62	0.29	1.55	0.39	1.12
			0.48	0.29	2.65	0.26	1.67	0.20	1.94	0.18	1.73	0.14			1.29	0.53	1.04
711	P228Y	a	0.62	0.39	1.10	0.17	0.60	0.31	2.04	0.29	0.71	0.21	1.11	0.34			1.18
			1.15	0.11	1.68	0.64	1.59	0.29	1.61	0.43	0.75	0.19	2.25	0.31	1.45	0.35	0.47
712	P228G	a	1.69	0.49	0.70	0.17	0.66	0.25	1.14	0.30	0.98	0.45	0.99	0.41			1.49
			1.00	0.19	2.60	0.68	0.96	0.24	0.54	0.54	0.98	0.18	1.89	0.42	1.77	0.37	1.01
713	G236D	a	0.42	0.57	1.31	0.16	3.39	0.21	7.15	0.54	0.19	9.45	1.08	0.38			0.05
			0.15	0.16	5.01	0.70	3.77	0.19	4.74	0.34	0.11	0.23	1.64	0.32	1.53	0.37	0.03
714	G236E	a	0.06	0.42	4.88	0.20	1.53	0.22	3.39	0.30	1.41	0.19	0.48	0.39			0.92
			0.22	0.10	3.04	0.39	1.68	0.22	2.15	0.29	1.05	0.19	1.58	0.25	1.46	0.39	0.62
			0.07	0.34	1.65	0.24	0.98	0.18	0.67	0.21	0.47	0.13			0.56	0.52	0.48
715	G236N	a	0.07	0.34	0.26	0.29	0.69	0.21	0.79	0.26	0.07	0.44			1.89	0.47	0.10
716	G236Q	a	0.03	0.44	0.83	0.14	0.49	0.72	1.28	0.34	0.21	0.39	0.99	0.35			0.43
			0.12	0.15	0.60	0.34	0.89	7.57	0.26	0.53	0.17	0.20	1.89	0.33	1.46	0.40	0.18
717	G236K	a	0.01	0.40	0.27	11.52	45.05	8.94	1.38	0.29	0.48	0.28	1.15	0.35			0.01
			0.11	0.29	3.21	4.73	0.90	3.50	0.55	0.69	0.46	0.25	2.18	0.37	1.38	0.35	0.51
			0.02	0.40					0.08	0.70	0.01	1.89			0.73	0.46	
718	G236R	a	0.01	0.38	0.29	0.23	0.63	0.33	0.62	0.69	0.20	0.72	1.04	0.34			0.32
			0.10	0.09	0.31	0.56	0.98	16.50	0.19	0.55	0.10	0.27	2.03	0.35	1.99	0.36	0.10
719	G236S	a	0.12	0.38	28.92	0.14	2.23	0.29	7.98	0.26	6.10	0.21	0.68	0.36			2.73
			0.55	0.12	22.71	0.37	2.77	0.21	3.68	0.45	5.77	0.26	1.82	0.29	1.77	0.38	2.08
720	G236T	a	0.02	0.42	1.58	0.16	0.36	0.55	1.35	0.28	0.21	0.91	0.99	0.33			0.59
			0.11	0.13	1.89	0.39	0.95	0.32	0.48	0.57	0.11	0.22	3.25	0.34	1.56	0.35	0.12
			0.06	0.36	0.58	0.26	0.34	0.47	0.15	0.35	0.04	0.85			0.43	0.58	0.10
721	G236H	a	0.05	0.47	0.69	0.20	0.36	1.36	0.46	0.39			0.87	0.36			
			0.19	0.16	2.02	0.51	0.87	15.81	0.28	0.97	0.07	0.33	2.32	0.47	1.48	0.37	0.07
			0.03	0.40	0.37	0.31	0.31	0.49	0.21	0.45	0.08	0.13			0.52	0.51	0.26
722	G236A	a	0.37	0.43	45.05	0.19	1.20	0.22	1.58	0.32	0.73	0.22	1.05	0.36			0.61
			0.48	0.16	44.99	0.28	1.05	0.24	1.45	0.50	0.65	0.18	1.64	0.27	1.75	0.35	0.62
723	G236V	a	0.03	0.52	2.06	0.15	0.23	0.88	0.96	0.36	0.24	0.37	0.99	0.37			1.02
			0.14	0.15	1.52	0.36	0.82	0.46	0.47	0.38	0.27	0.19	1.59	0.28	1.35	0.39	0.33
724	G236L	a	0.04	0.28			1.07	0.48			0.18	0.25					0.17
725	G236I	a	0.02	0.40	1.95	0.15	0.11	2.97	1.10	0.38			1.04	0.34			
			0.11	0.18	1.33	0.30	0.75	2.41	0.12	0.69	0.02	0.87	1.96	0.26	1.33	0.37	0.02
726	G236F	a	0.06	0.41	0.43	0.17	0.55	0.43	0.88	0.34	0.18	0.64	1.19	0.34			0.33
			0.21	0.23	0.44	0.54	0.92	46.70	0.08	1.29	0.05	0.76	2.56	0.48	1.75	0.36	0.06
727	G236M	a	0.03	0.38	0.29	0.19	0.43	0.37	1.22	0.42	0.21	0.44	0.67	0.34			0.49
			0.14	0.12	0.34	0.44	0.79	0.83	0.40	0.67	0.19	0.20	1.40	0.55	1.60	0.35	0.24
728	G236Y	a	0.04	0.39	0.83	0.16	0.44	1.15	0.91	0.44	0.22	1.31	0.77	0.36			0.50
			0.17	0.13	0.78	0.58	0.85	1.07	0.44	1.38	0.14	0.26	1.34	0.33	1.52	0.35	0.16
			0.10	0.38	0.37	0.31	0.41	1.22	0.00	2.84	0.04	0.88			0.56	0.52	0.09
729	G236W	a	0.32	0.39	1.71	0.18	0.52	0.55	0.67	0.30	0.33	0.33	0.98	0.34			0.63
			0.78	0.17	2.13	0.40	0.70	0.51	0.29	0.69	0.29	0.20	1.40	0.26	1.52	0.36	0.41
			0.68	0.27	1.23	0.27	0.83	0.21	1.56	0.15	0.34	0.13			0.56	0.51	0.40
730	G236P	a	0.04	0.48	0.25	0.30	0.27	1.53	0.42	0.41	0.19	28.37	1.25	0.35			0.70
			0.15	0.16		7.93	0.90	10.17	0.15	0.68	0.10	0.23	1.38	0.86	1.41	0.37	0.11
			0.04	0.47	0.11	0.72	0.24	0.76	0.10	1.03	0.07	0.21			0.66	0.52	0.30
731	G237D	a	0.18	0.55	0.21	2.59	54.08	9.16	2.51	0.27			1.50	0.37			
			0.10	0.25		8.65	1.00	0.27	1.13	0.52	0.13	0.19	2.86	0.27	1.84	0.36	0.13
			0.08	0.33			1.04	0.19	0.74	0.17					0.80	0.50	

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
732	G237E	a	0.01	0.48	0.26	9.34	0.88	0.24	1.03	0.32	0.21	12.54	0.89	0.36			0.24
			0.09	0.13	0.70	0.95	0.88	0.45	0.42	0.48	0.02	0.60	1.16	0.24	1.36	0.42	0.02
733	G237N	a	0.02	0.40	0.27	13.28	0.65	0.38	2.79	0.26	0.18	5.37	0.71	0.36			0.27
			0.08	0.24	0.10	0.62	0.98	0.26	0.73	0.43	0.02	1.05	1.29	0.24	1.39	0.36	0.02
734	G237Q	a	0.01	0.39	0.26	14.91	0.85	8.46	1.20	0.30			0.84	0.34			
			0.07	0.32	0.46	4.47	0.78	17.18	1.80	5.62	0.00	3.01	1.33	0.31	1.39	0.37	0.00
735	G237K	a	0.01	0.39	0.22	0.34	0.32	0.81	1.29	0.38	0.17	0.73	0.81	0.35			0.54
			0.09	0.18	0.32	0.63	0.74	0.73	0.32	0.56	0.10	0.28	1.52	0.29	1.47	0.36	0.13
			0.02	0.56			0.46	0.27	0.11	0.85	0.07	2.82			1.28	0.48	0.15
736	G237R	a	0.01	0.38	0.21	0.32	0.48	0.83			0.21	0.66	0.73	0.35			0.43
			0.08	0.20		41.28			0.39	1.04	0.16	0.28	1.01	0.34	1.36	0.36	
737	G237S	a	0.03	0.42	0.17	1.31	0.75	0.34	1.94	0.26			1.04	0.33			
			0.12	0.15		6.61	1.02	0.24	0.78	0.53	0.07	0.49	1.86	0.34	1.29	0.36	0.06
738	G237T	a	0.05	0.54			0.50	0.68	0.77	0.29			0.69	0.35			
			0.13	0.18		5.66			0.21	0.72	0.09	0.21	1.08	0.35	1.32	0.38	
739	G237H	a	0.06	0.25	0.24	0.38	0.59	0.29	1.76	1.61	0.09	0.24	0.97	0.36	1.48	0.36	0.15
740	G237V	a	0.03	0.26			1.07	0.83	1.81	0.40	0.06	0.41	2.03	0.24	1.00	0.19	0.06
741	G237L	a	0.01	0.35			0.54	0.81	1.19	0.46	0.03	0.56	1.88	0.29	1.21	0.25	0.06
742	G237I	a					0.29	0.84	0.43	0.56	0.35	0.21	1.51	0.28	0.60	0.70	1.18
			0.02	0.22							0.40	0.15			1.01	0.27	
743	G237F	a	0.07	0.36			0.41	0.73	1.08	0.45	0.04	0.56	1.65	0.29	0.81	0.28	0.11
744	G237M	a	0.04	0.32			0.30	0.58	1.06	0.49	0.06	0.65	1.80	0.27	0.94	0.25	0.18
			0.07	0.37	0.14	0.35	0.57	0.26	0.66	0.27	0.10	0.15			1.74	0.45	0.17
745	G237Y	a	0.21	0.44			0.37	0.58	0.67	0.71	0.08	0.22	2.06	0.32	1.00	0.21	0.21
746	G237W	a	0.04	1.92			2.62	0.83	1.92	0.38			0.85	0.24	1.20	0.21	
747	G237P	a	0.02	0.18			0.52	0.90	0.52	0.51	0.01	0.69	1.17	0.25	1.21	0.21	0.02
748	P238D	a	0.26	0.32			13.02	1.16	5.89	0.39	0.72	0.25	1.03	0.24	0.63	0.89	0.06
			0.07	0.24							0.58	0.13			1.03	0.21	
749	P238E	a	0.95	0.29			1.18	0.86	1.46	0.41		3.53	1.20	0.25	3.71	1.18	
			0.30	0.14							0.04	0.32			0.68	0.28	
			0.19	0.34			0.42	0.33	0.36	0.19	0.05	0.61			1.43	0.62	0.12
750	P238N	a	0.21	0.31			0.53	0.91	1.11	0.49			0.99	0.22	1.15	0.99	
			0.09	0.16							0.01	1.23			1.01	0.28	
751	P238Q	a															
752	P238K	a		1.05			0.24	0.59	0.20	0.85			1.00	0.25	5.01	0.83	
			0.04	8.30							0.00	3.28			0.77	0.29	
753	P238R	a	0.17	0.32			0.35	0.58	0.54	0.67	0.62	0.20	1.18	0.24	0.83	0.66	1.78
			0.25	0.21	0.31	3.96					0.50	0.16			0.92	0.26	
754	P238S	a	0.29	0.31			0.31	0.55	0.75	0.77		3.07	0.97	0.27	0.42	0.60	
			0.44	0.12							0.08	0.17			0.93	0.22	
			0.57	0.26	0.15	0.38	0.63	0.40	1.08	0.22	0.23	0.13			1.12	0.51	0.37
755	P238T	a	0.21	0.35			0.60	0.66	0.78	0.54		3.34	1.51	0.30	0.91	0.61	
			0.11	0.22	0.26	277					0.02	0.64			1.12	0.19	
756	P238H	a	0.44	0.35			1.89	0.85	1.35	0.41	1.51	0.18	1.32	0.24	0.90	0.53	0.80
			0.26	0.09	0.32	2638					1.12	0.13			1.46	0.22	
757	P238V	a	1.09	0.28			2.24	0.91	1.99	0.38		2.80	1.55	0.28	1.43	0.57	
			1.22	0.18	0.38	0.37					0.06	0.43			1.09	0.19	
758	P238L	a	1.78	0.31			2.54	0.95	3.64	0.41	0.79	0.22	2.34	0.29	1.71	0.54	0.31
			1.17	0.14	0.31	12.20					0.69	0.15			1.40	0.30	
759	P238I	a	1.32	0.29			0.40	0.82	0.38	0.73			1.79	0.29	1.06	0.52	
			0.62	0.21							0.02	0.77			1.44	0.26	
760	P238F	a	1.70	0.31					3.72	0.38		2.56	2.32	0.32	2.41	0.55	
			2.60	0.12							0.02	0.84			1.09	0.26	
761	P238M	a	1.38	0.27			0.44	0.66	1.27	0.44		2.89	3.23	0.35	2.33	1.22	
			1.39	0.09							0.03	0.55			0.91	0.24	
762	P238Y	a	0.66	0.26			0.43	0.62	0.99	0.56		6.35	1.16	0.29	0.80	0.54	
			3.05	0.20											0.92	0.21	
763	P238W	a	1.27	0.27			0.73	0.69	1.12	0.53		2.95	1.92	0.31	0.10	0.54	
			0.73	0.21											1.30	0.20	
764	P238G	a	0.33	0.35			1.30	0.86	0.84	0.41	0.39	0.21	1.41	0.26	0.12	0.53	0.30
			0.11	0.16	0.34	0.27					0.36	0.20			1.53	0.22	
765	E269K	a	0.14	0.36			1.00	0.79	0.95	0.44			1.46	0.26	0.13	0.53	
			0.08	0.17							0.14	0.12			1.23	0.20	
766	E269S	a	0.31	0.30			0.74	0.77	1.19	0.44	0.30	0.20	0.93	0.28	0.13	0.55	0.41
			0.21	0.15	0.29	8.99					0.21	0.20			1.31	0.33	
767	E269V	a	0.30	0.29			0.35	0.80	0.32	0.68		4.69	1.48	0.28	0.13	0.52	
			0.24	0.17	0.26	34.19					0.19	0.54			1.38	0.28	
768	E269I	a	0.35	0.29			0.29	0.63	0.40	0.42			2.10	0.40	0.13	0.52	
			0.41	0.22	0.28	1.372					0.12	0.24			1.26	0.30	
769	E269M	a	0.38	0.25			0.37	0.58	0.66	0.58		14.73	2.66	0.34	0.14	0.52	
			0.51	0.14							0.12	0.16			1.11	0.24	
770	E269W	a	0.20	0.29			0.34	0.55	0.92	0.62		1.83	1.43	0.32	0.08	0.52	
			0.37	0.19							0.06	0.38			1.19	0.22	

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
771	E269P	a	0.36	0.16	0.13	0.41	0.73	0.25	1.33	0.66	0.02	0.70	0.00	12605	1.23	0.21	0.02
772	E269G	a			0.58	0.54	0.51	0.28	1.11	0.66	0.03	0.63	0.00	7.64	1.34	0.18	0.05
			0.39	0.29	0.23	0.37	0.58	0.28	0.44	0.51	0.23	0.16			1.18	0.50	0.39
773	H285D	a	1.81	0.16	1.57	0.54	1.18	0.33	2.56	0.72	1.22	0.64	0.00	7.64	2.40	0.27	1.03
774	H285E	a	1.67	0.25	1.39	0.37	0.98	0.29	1.53	0.35	1.46	0.19			1.93	0.50	1.50
775	H285Q	a	2.42	0.16	1.68	0.55	0.66	0.45	1.45	0.67	0.33	0.60	0.00	7.64	1.25	0.27	0.50
			1.28	0.22	1.41	0.29	1.81	0.22	2.15	0.17	1.59	0.16			1.38	0.49	0.88
776	H285K	a	1.80	0.20	2.04	0.50	1.37	0.37	2.89	0.80	2.46	0.66	0.00	7.64	1.76	0.30	1.79
777	H285Y	a p	2.68	0.31	1.95	0.56	0.95	0.49	4.24	1.43	1.77	0.97			1.25	0.24	1.87
778	H285W	a	1.32	0.14	0.84	0.41	1.31	0.23	2.37	0.66	0.69	0.48	0.00	7.65	1.33	0.17	0.53
779	N286E	a		3.40	0.07	0.40	0.38	0.25	0.37	0.94	0.01	1.71	0.00	7.65	2.12	0.18	0.03
780	N286Y	a		2.92	0.07	0.44	0.42	0.22	1.16	0.66	0.02	0.62	0.00	7.66	1.45	0.17	0.05
781	N286P	a	2.62	0.15	1.80	0.40	2.35	0.23	5.43	0.62	1.18	0.51	0.17	8.96	2.31	0.18	0.50
			1.16	0.28	1.05	0.32	2.50	0.21	3.86	0.13	0.71	0.11			2.90	0.49	0.29
782	N286G	a															
783	K288D	a	2.19	0.10			1.85	0.21			1.78	0.18					0.96
784	K288E	a	2.76	0.14	1.72	0.41	3.27	0.26	8.05	0.63	2.77	0.52	0.00	7.64	0.89	0.19	0.85
785	K288Y	a	2.17	0.13	1.80	0.53	1.14	0.27	2.71	0.64	0.69	0.54	0.00	7.64	1.10	0.19	0.61
786	R292D	a	2.38	0.17	5.10	0.39	1.12	0.25	2.81	0.68	0.51	0.50	0.00	7.64	1.67	0.22	0.46
787	R292E	a	1.56	0.13	1.00	0.44	0.73	0.41	4.46	4.23	0.34	0.50	0.00	7.64	1.45	0.22	0.47
788	R292T	a	1.30	0.15	1.11	0.40	0.95	0.24	1.11	0.75	0.41	0.51	0.25	8.57	0.85	0.18	0.43
789	R292Y	a	1.59	0.13	0.35	0.40	0.86	0.27	2.24	0.60	0.40	0.50	0.00	7.65	1.36	0.16	0.47
790	T335N	a	1.89	0.12	1.21	0.40	1.27	0.22	2.14	0.64	0.85	0.51	0.00	7.65	1.23	0.16	0.67
791	T335S	a	2.02	0.14	6.31	0.38	1.27	0.22	2.70	0.68	1.43	0.58			1.42	0.16	1.12
792	T335H	a	2.26	0.19	1.31	0.45	1.07	0.24	1.67	0.67	1.25	0.61	0.00	7.65	1.16	0.21	1.17
793	T335V	a	2.33	0.13	1.80	0.53	0.97	0.27	2.53	0.72	1.41	0.63	0.00	7.64	1.25	0.17	1.46
794	T335I	a	2.48	0.18	1.96	0.51	2.62	0.32	14.39	0.70	2.22	0.50	0.00	2101	1.50	0.26	0.85
795	T335I	a	2.25	0.15	2.47	0.50	1.16	0.36	1.76	1.04	1.51	0.70	0.00	7.64	1.41	0.22	1.30
796	T335F	a	1.21	0.11	0.71	0.41	1.21	0.24	1.70	0.76	0.49	0.54	0.25	9.47	1.19	0.17	0.40
797	T335M	a	2.06	0.12	0.60	0.41	1.13	0.26	1.98	0.64	0.52	0.51	0.00	7.65	0.79	0.19	0.46
			1.31	0.24	1.14	0.26	1.13	0.24	1.46	0.13	1.18	0.10			1.35	0.48	1.04
798	T335W	a	2.11	0.13	0.68	0.40	1.16	0.22	2.08	0.66	0.59	0.51			1.35	0.17	0.51
799	T335P	a	2.80	0.12	2.42	0.46	0.93	0.26	1.75	0.65	1.35	0.60			1.45	0.17	1.45
800	T335G	a	1.99	0.16	0.93	0.46	0.77	0.25	1.47	0.66	0.32	0.51			0.90	0.24	0.42
801	D221K	a	4.53	0.19	4.32	0.39	3.50	0.28	17.75	0.61	65.60	0.48	0.00	7.64	5.66	0.18	18.72
			0.97	0.25	1.01	0.30	0.68	0.40	1.04	0.17	2.82	0.09			1.84	0.46	4.17
802	D221Y	a	2.43	0.19	2.62	0.44	2.41	0.28	10.01	0.67	0.56	0.48			2.74	0.21	0.23
803	T223E	a	2.12	0.14	2.37	0.42	1.74	0.23	3.70	0.69	0.75	0.49	0.00	7.64	2.04	0.22	0.43
804	T223K	a	1.61	0.17	2.18	0.29	1.81	0.25		11.88	9.37	0.36	1.31	0.30	2.97	0.36	5.19
			1.15	0.27	0.55	0.27	0.60	0.23	0.41	0.26	0.67	0.12			0.78	0.60	1.11
805	H224E	a	1.91	0.13	3.67	0.31	2.18	0.25		11.88	14.28	0.36	2.80	0.32	5.11	0.38	6.54
			0.54	0.09	0.27	0.21	0.21	0.36	0.66	0.71	0.58	1.31			0.43	0.23	2.73
806	H224Y	a	1.74	0.20	1.17	0.30	1.29	0.31		11.88	0.86	0.37	2.01	0.31	1.68	0.44	0.66
807	T225E	a	2.28	0.16	2.75	0.30	2.38	0.25	97.09	11.88	9.84	0.36	1.96	0.31	4.89	0.47	4.14
			0.46	0.14	0.35	0.19	0.44	0.44	1.21	0.66	0.76	1.31			0.41	0.16	1.71
808	T225K	a	0.30	0.17	0.37	0.32	0.45	0.34	95.70	11.88	0.22	0.44	1.12	0.28	5.68	0.68	0.48
			0.53	0.27	0.31	0.23	0.45	0.26	1.01	0.65	0.68	1.31			0.50	0.20	1.51
809	T225W	a	2.30	0.29	1.04	0.42	1.44	0.24	93.33	11.88	0.59	0.37	1.92	0.29	6.89	0.75	0.41
810	K246D	a	1.78	0.13	0.92	0.30	1.36	0.24	67.73	11.90	0.56	0.39	1.22	0.33	0.93	0.41	0.41
811	K246E	a	1.58	0.15	1.25	0.28	0.98	0.32	35.41	11.89	2.86	0.40	1.86	0.33	0.51	0.38	2.91
812	K246H	a	1.67	0.15	1.66	0.29	1.24	0.26		11.88	14.37	0.36	1.49	0.29	4.02	0.36	11.56
			0.35	0.17	0.26	0.21	0.16	0.76	0.24	0.83	0.36	1.31			0.38	0.14	2.22
813	K246Y	a	1.53	0.13	1.16	0.28	1.18	0.28	49.45	11.89	5.25	0.36	1.87	0.32	2.47	0.40	4.46
814	D249Q	a	0.30	0.20	0.22	0.33	0.61	0.82	74.56	11.89	0.36	0.36	2.13	0.33	2.06	0.37	0.59
			0.46	0.17	0.52	0.22	0.46	0.32	1.07	0.74	1.06	1.31			0.49	0.15	2.30
815	D249H	a	0.39	0.14	0.37	0.23	0.28	0.46	0.64	0.78	0.86	1.32			0.41	0.19	3.04
816	D249Y	a	1.80	0.14	1.87	0.29	1.13	0.28		11.88	3.92	0.37	2.09	0.30	2.57	0.45	3.47
			0.47	0.17	0.37	0.39	0.55	0.34	0.79	1.42	749	42.72			0.41	0.22	
817	R255E	a	1.80	0.13	1.38	0.31	0.95	0.28	89.36	11.89	0.72	0.36	1.50	0.30	1.16	0.41	0.76
818	R255Y	a	3.21	0.28	5.87	0.31	2.30	0.23		11.88	34.11	0.39	2.07	0.34	12.88	0.52	14.80
			0.38	0.23	0.35	0.33	0.33	0.46	0.79	0.75	0.43	1.32			0.36	0.21	1.33
819	E258S	a	2.79	0.30	1.13	0.34	1.39	0.27	40.92	11.92	0.65	0.56	1.36	0.32	0.54	0.52	0.47
820	E258H	a	2.62	0.23	2.92	0.40	1.77	0.29	48.21	11.89	11.08	0.58	1.69	0.28	0.89	0.39	6.25
821	E258Y	a	2.62	0.18	1.28	0.36	2.12	0.27		11.88	10.52	0.43	1.66	0.29	1.07	0.49	4.96
			0.56	0.27	0.30	0.24	0.39	0.30	0.95	0.66	0.36	1.31			0.31	0.28	0.91
822	T260D	a	1.79	0.16	0.58	0.32	0.65	0.29			0.31	0.37	4.06	0.32	1.71	0.53	0.47
823	T260E	a	2.21	0.14	1.00	0.31	1.21	0.44	94.92	11.88	1.70	0.41	2.89	0.34	5.49	0.61	1.41
824	T260H	a	2.03	0.20	1.85	0.34	1.70	0.29		11.88	11.25	0.43	1.63	0.28	7.30	0.53	6.61
			0.52	0.16	0.27	0.19	0.16	0.93	0.50	0.77	0.53	1.32			0.50	0.16	3.40
825	T260Y	a	1.59	0.16	0.84	0.37	1.03	0.27		11.88	0.48	0.38	1.62	0.27	7.51	0.93	0.47
			0.38	0.32	0.59	0.29	0.51	0.26	1.08	0.65	1.40	1.31			0.69	0.18	2.73
826	V262E	a	1.03	0.34	0.16	0.43	0.92	0.24	36.47	11.91			2.85	0.29	9.27	0.52	
827	V262F	a	1.04	0.15	0.43	0.28	1.23	0.26					5.20	0.39	0.50	0.38	

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		IIa:IIb
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	
828	F275L	a	1.85	0.15	0.83	0.31	1.43	0.31	97.71	11.88	1.17	0.38	3.58	0.37	0.89	0.35	0.82
829	G281D	ap	2.19	0.17	1.81	0.29	2.15	0.23		11.88	4.55	0.38	6.23	0.38	1.33	0.36	2.11
830	G281K	a	1.25	0.15	1.01	0.26	1.20	0.29		11.88	0.79	0.39	1.92	0.30	0.95	0.35	0.66
831	G281Y	a	1.89	0.14	2.08	0.52	2.47	0.34		11.88	0.89	0.39	2.87	0.35	1.46	0.35	0.36
			0.42	0.18	0.80	0.21	0.73	0.27	1.17	0.64	1.31	1.31			0.69	0.14	1.79
832	G281P	a															
833	V282E	a	1.89	0.23	1.10	0.33	1.43	0.28	85.43	11.88	0.49	0.36	5.37	0.30	1.91	0.40	0.34
834	V282K	a	1.50	0.23	0.58	0.31	0.65	0.28	82.37	11.89	0.54	0.39	2.23	0.37	1.44	0.44	0.83
			0.40	0.20	0.85	0.19	1.26	0.23	1.76	0.64	2.97	1.31			1.11	0.17	2.37
835	V282Y	a	2.34	0.26	1.43	0.29	1.41	0.24		11.88	1.10	0.37	2.38	0.36	1.92	0.37	0.78
			0.37	0.16	0.53	0.22	0.49	0.40	0.86	0.72	0.89	1.32			0.65	0.18	1.83
836	V282P	a															
837	V282G	ap	1.41	0.19	1.58	0.18	1.12	0.39	1.08	0.70	0.98	0.26	8.93	0.45	1.16	0.18	0.87
838	E283K	a	2.47	0.14	1.20	0.16	2.81	0.28	3.63	0.64	3.26	0.22	1.25	0.35	2.74	0.94	1.16
839	E283H	a	4.36	0.41	3.56	0.24	3.85	0.36	2.13	0.71	27.06	0.35	3.62	0.40	6.25	1.29	7.04
			0.78	0.16	0.50	0.41	0.32	0.39	0.66	1.13		28.71			1.18	0.16	
840	E283L	a	1.44	0.15	4.67	0.12	6.05	0.28	9.30	0.65	22.32	0.26	3.95	0.40	9.25	0.69	3.69
			0.42	0.24	0.34	0.34	0.67	0.46	1.06	0.79	0.52	1.32			0.82	0.20	0.78
841	E283Y	a	1.68	0.16	1.19	0.15	1.51	0.30	0.85	0.71	1.43	0.23	2.35	0.49	1.42	0.68	0.94
842	E283P	a	1.56	0.18	0.95	0.23	2.51	0.32	1.14	0.71	1.65	0.26	3.62	0.50	1.33	0.41	0.66
843	E283G	a	0.47	0.11	0.33	0.24	0.45	0.27	0.89	0.68	0.43	1.31			0.77	0.20	0.97
844	V284E	a	1.45	0.17	5.92	0.13	4.86	0.30	2.89	0.66	18.48	0.28	2.72	0.57	25.76	0.15	3.80
			0.59	0.10	0.41	0.22	0.57	0.61	0.97	0.67	0.89	1.32			1.11	0.14	1.55
845	V284N	a	0.45	0.29	0.43	0.27	0.60	0.28	1.13	0.66	0.73	1.32			0.77	0.17	1.21
846	V284T	ap	0.25	0.18	0.41	0.17	1.26	0.47	1.08	0.67	1.16	0.23	4.49	0.57	1.15	0.16	0.92
			0.37	0.11	0.45	0.19	0.53	0.34	0.95	0.68	0.78	1.31			0.79	0.16	1.47
847	V284L	a	1.56	0.16	1.90	0.16	3.13	0.32	1.32	0.70	2.71	0.23	2.56	0.48	1.51	0.20	0.87
848	V284Y	a															
849	P291D	a	1.11	0.18	1.19	0.14	1.07	0.32	1.89	0.65	0.72	0.22	1.06	0.37	0.89	0.86	0.67
850	P291E	a	1.82	0.28	1.00	0.30	1.24	0.44	0.68	0.98	0.92	0.28	1.08	0.44	0.76	0.94	0.74
851	P291Q	a	1.06	0.17	1.40	0.16	1.81	0.32	1.33	0.65	0.80	0.31	1.26	0.40	1.24	0.51	0.44
852	P291T	a	0.55	0.18	0.49	0.14	1.00	0.34	0.67	0.73	0.53	0.25	1.44	0.40	0.94	0.44	0.53
853	P291H	a	1.85	0.18	2.66	0.23	1.47	0.29	1.35	0.73	2.40	0.28	0.75	0.39	2.56	0.57	1.63
854	P291I	a	1.24	0.25	1.20	0.13	1.19	0.34	2.15	0.67	0.52	0.25	1.30	0.41	1.15	0.17	0.44
855	P291G	a	0.08	0.29	0.35	0.22	1.26	0.37	0.68	0.75	0.31	0.24	2.19	0.41	0.81	0.18	0.24
			0.46	0.17	0.64	0.20	0.98	0.26	1.66	0.65	1.14	1.31			0.78	0.14	1.17
856	N297Q	a															
857	N297K	a															
858	N297R	a	0.01	0.20	0.01	0.80	0.01	2.77	0.06	1.66	0.01	3.89			0.45	0.17	1.03
859	N297T	a															
860	N297H	a															
861	N297V	a															
862	N297L	a															
863	N297I	a															
864	N297F	a															
865	N297M	a															
866	N297Y	a															
867	N297W	a															
868	N297P	a															
869	N297G	a															
870	R301D	a	0.87	0.16	0.11	0.60	0.06	2.49	0.04	2.89	0.03	1.45	1.58	0.43	0.50	0.24	0.47
871	R301E	a	0.62	0.23	0.36	0.15	0.84	0.43	0.44	0.73	0.69	0.24	2.71	0.49	2.92	0.99	0.82
872	R301H	a	1.65	0.25	0.37	0.24	0.97	0.64	0.74	0.93	0.41	0.30	1.58	0.48	0.76	0.98	0.42
873	R301Y	a	0.72	0.15	0.64	0.17	1.27	0.35	0.95	0.68	0.17	0.31	1.49	0.44	0.78	0.51	0.13
874	V303D	a	0.69	0.18	0.67	0.15	0.55	0.64	0.53	0.75	0.29	0.30	1.45	0.45	0.91	0.33	0.52
875	V303E	a	2.29	0.23	1.02	0.19	1.41	0.28	1.31	0.68	1.43	0.25	1.43	0.40	1.63	0.35	1.02
876	V303Y	a	0.78	0.18	2.56	0.21	1.43	0.33	1.26	0.73	0.44	0.25	1.02	0.42	1.15	0.16	0.31
877	S304D	a	1.12	0.19	0.53	0.29	1.17	0.57			0.14	0.28	2.17	0.52	0.61	0.20	0.12
878	S304N	a	0.95	0.18	0.69	0.19	0.81	0.42	0.90	0.90	1.08	0.25	1.32	0.41	1.19	0.19	1.34
879	S304T	a	1.00	0.15	2.86	0.18	1.61	0.31	0.73	0.80	6.13	0.21	3.30	0.48	2.86	1.08	3.80
880	S304H	a	1.11	0.29	0.32	0.31	0.79	0.97	1.65	15.76	0.18	0.28	1.59	0.50	0.38	0.97	0.23
881	S304L	a															
882	V305E	a	0.89	0.16	0.90	0.16	1.45	0.31	1.14	0.76	0.65	0.24	1.99	0.49	0.67	0.51	0.45
883	V305T	a	1.17	0.22	0.91	0.16	1.23	0.33	0.07	1.74	0.68	0.25					0.55
884	V305Y	a	1.59	0.22	0.98	0.24	0.95	0.31	0.22	1.23	0.66	0.30	1.12	0.49	0.74	0.30	0.70
885	K317E	a	0.85	0.18	0.79	0.22	0.48	0.55	0.29	0.95	0.39	0.72			0.45	0.56	0.81
886	K317Q	a	1.22	0.10			0.98	0.42			1.25	0.17					1.27
887	E318Q	a	0.62	0.14	0.80	0.18	0.35	0.37	0.72	0.33	0.40	0.70	0.99	0.55	0.56	0.66	1.17
888	E318H	a	0.49	0.15	0.46	0.35	0.38	0.45			0.26	1.71			0.61	0.21	0.69
889	E318L	a	1.05	0.37	0.67	0.23	0.18	1.28	0.87	0.45	0.38	0.71			3.61	1.60	2.12
890	E318Y	a	0.67	0.16	0.63	0.14	0.22	0.83	0.51	0.80	0.25	0.69			6.14	1.63	1.13
891	I336E	a	0.36	0.27	0.08	0.77	0.05	0.95	0.17	1.59	0.06	0.82	1.07	0.52	8.11	1.03	1.10
			0.70	0.44	0.38	0.29	0.34	0.59	1.02	0.86	1.79	1.33			0.64	0.21	5.20

Figure 41 (continued)

Variant	Substitution(s)	Context	FcγRI		FcγRIIa		FcγRIIb		FcγRIIc		FcγRIIIa		C1q		FcRn		
			Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	Fold	Conf	IIIa:IIb
892	I336K	a	1.11	0.21	0.94	0.20	1.05	1.26	0.47	1.27	0.73	0.71	1.13	0.40	12.12	0.94	0.69
893	I336Y	a	0.45	0.15	0.28	0.19	0.59	0.50	0.64	0.68	0.21	0.71			0.49	0.50	0.36
894	S337E	a	0.71	0.17	1.15	0.18	1.13	0.27	0.95	0.24	0.74	0.69			0.39	0.47	0.65
895	S337N	a	0.77	0.20	1.45	0.24	1.50	0.37	0.93	0.50	0.58	0.75			0.52	0.48	0.39
896	S337H	a	0.66	0.14	0.78	0.14	0.64	0.29	0.85	0.25	0.35	0.69			0.56	0.51	0.55
912	S239D/E272Y/I332E	tr	1.98	0.18	3.33	0.30	12.09	0.30	9.89	0.23	43.67	0.12	0.88	0.96	1.31	0.27	3.61
913	S239D/E272S/I332E	tr	1.23	0.09	3.11	0.24	14.47	0.29	12.02	0.23	18.57	0.11	0.87	1.07	1.49	0.25	1.28
914	S239D/E272K/I332E	tr															
915	S239D/E272M/I332E	tr	3.23	0.07	7.99	0.24	22.11	0.30	18.91	0.23	64.80	0.10	1.07	0.75	1.81	0.23	2.93
916	S239D/E272Y/A330L/I332E	tr	1.83	0.12	0.89	0.28	2.92	0.34	3.04	0.23	46.36	0.12			1.00	0.25	15.90
917	S239D/E272S/A330L/I332E	tr															
918	S239D/E272K/A330L/I332E	tr															
919	S239D/E272M/A330L/I332E	tr	1.83	0.09	2.34	0.30	11.04	0.32	9.15	0.23	70.29	0.10	0.88	0.75	0.98	0.27	6.37
920	S239D/K274E/I332E	tr	3.20	0.09	3.66	0.31	26.79	0.34	14.88	0.23	86.88	0.10	1.23	0.70	0.60	0.27	3.24
921	S239D/Y278T/I332E	tr	0.04	0.15	0.26	16.94	1.36	1.57	0.75	0.38	0.60	0.14	1.12	0.74	0.21	0.51	0.44
922	S239D/K326T/I332E	trp	5.76	0.13	20.99	0.23	122	0.31	78.15	0.22	332	0.11	0.70	1.34	2.22	0.26	2.71
923	S239D/K326E/I332E	trp	2.87	0.18	4.08	0.29	59.31	0.29	35.60	0.22	184	0.11	0.89	1.20	0.64	0.27	3.10
924	S239D/K274E/A330L/I332E	tr	1.94	0.10	1.26	0.29	10.27	0.29	7.71	0.22	84.23	0.10	0.92	2.08	0.72	0.30	8.20
925	S239D/Y278T/A330L/I332E	tr															
926	S239D/K326E/A330L/I332E	tr															
927	S267E	r															
928	S239D/S267E/I332E	r															
929	S239D/S267E/A330L/I332E	r															
930	Y278W	r															
931	E283R/V302I/Y278W/E283R	r															
934	Y278W/V302I	r															
935	Y278W/E283R/V302I	r															
1145	S239D/I332E/G236S	l															
1146	S239D/I332E/G236A	l															
1147	S239D/I332E/K246H	l															
1148	S239D/I332E/R255Y	l															
1149	S239D/I332E/S267E	l															
1150	S239D/I332E/E272R	l															
1151	S239D/I332E/E272H	l															
1152	I332E/G281D	l															
1153	S239D/I332E/E283H	l															
1154	S239D/I332E/E283L	l															
1155	I332E/V284E	l															
1156	S239D/I332E/V284E	l															
1157	S267E/S324I	l															
1158	S267E/A327D	l															
1159	S324I/A327D	l															
1160	S267E/P331D	l															
1161	S267E/V282G	l															
1162	G281D/V282G	l															
1163	V282G/P331D	l															
1164	G281E	l															
1165	G281N	l															
1166	G281Q	l															
1167	V284D	l															
1168	V284Q	l															
1169	S298A/K326E	l															
1170	S298A/K334L	l															
1171	S298A/K326E/K334L	l															
1608	S239D/S298A/K326E/I332E	lp															
1609	S239D/S298A/K326T/I332E	l															
1877	I332E/H268E	p															
1878	I332E/H268D	p															
1879	S239D/H268E	p															
1880	S239D/H268D	p															
1881	S239D/I332E/H268E	p															
1882	S239D/I332E/H268D	p															
1883	S239D/I332E/A327D	p															
1884	S239D/I332E/V284D	p															
1885	S239D/I332E/V284E	p															

Figure 42

SEQ ID NO:5

```
Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
221                 225                 230                 235

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Lys Xaa Thr Leu Met
            240                 245                 250

Ile Ser Xaa Thr Pro Xaa Val Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        255                 260                 265

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Val Xaa Xaa Xaa Xaa Xaa
    270                 275                 280

Xaa Xaa Ala Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
285                 290                 295                 300

Xaa Xaa Xaa Xaa Xaa Leu Thr Val Leu His Gln Asp Xaa Leu Asn Gly
                305                 310                 315

Xaa Xaa Tyr Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            320                 325                 330

Xaa Xaa Xaa Xaa Xaa
        335
```

Figure 43A

Allotype	Allotype	Position		
		214	356 358	431
G1m(1,17)	G1m(a,z)	K	D L	A
G1m(1,2,17)	G1m(a,x,z)	K	D L	G
G1m(3)	G1m(f)	R	E M	A
G1m(1,3)	G1m(a,f)	R	D L	A

Figure 43B

Allotype	Allotype	Position
		282
G2m(23)	G2m(n+)	V
	G2m(n-)	M

Figure 44

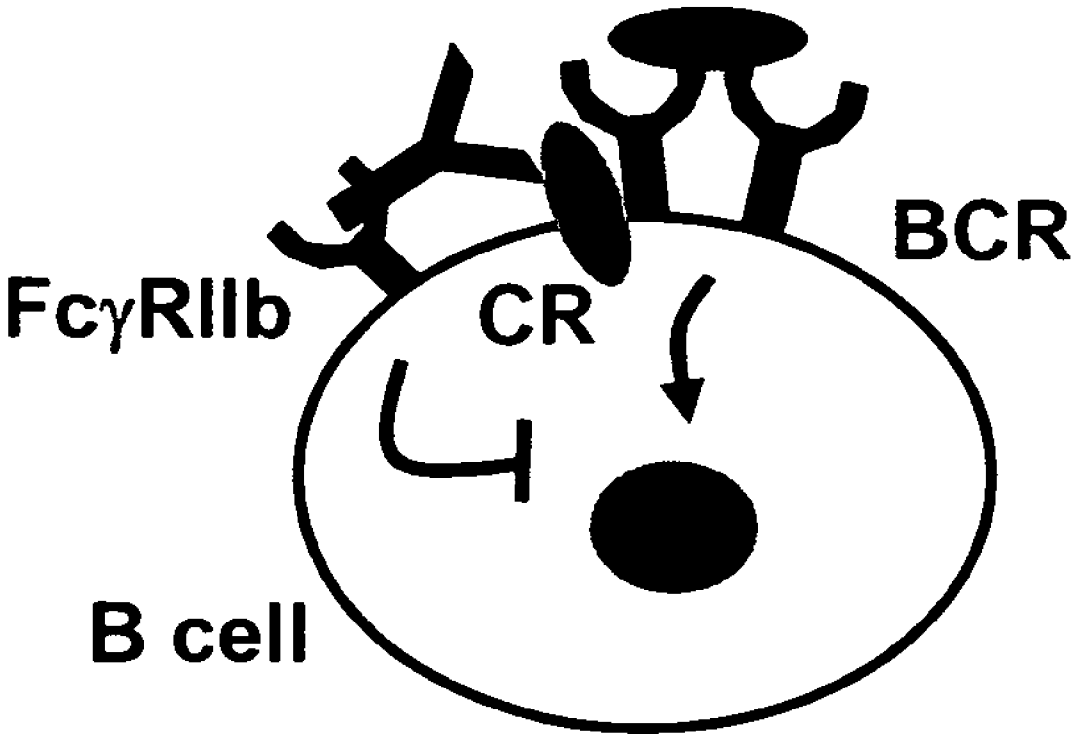


Figure 45

FcγR positions contributing to FcγRIIb:FcγRIIIa binding selectivity					
Position	human FcγRIIb	human FcγRIIIa(V)	Position	human FcγRIIb	human FcγRIIIa(V)
116	V	H	113	K	T
154	N	L	152	T	R
159	L	N	158	T	K
86	E	G	112	D	N
157	Y	S	126	S	G
132	S	H	19	E	K
130	S	F	129	F	Y
114	P	A	127	K	R
131	R	H	18	Q	E
134	P	S	60	N	V
160	Y	V	150	H	F
85	S	I	59	N	T

Figure 46

IgG positions contributing to FcγRIIb:FcγRIIIa binding selectivity									
Position	IgG1	IgG2	IgG3	IgG4	Position	IgG1	IgG2	IgG3	IgG4
236	G	_	G	G	269	E	E	E	E
237	G	G	G	G	266	V	V	V	V
235	L	A	L	L	332	I	I	I	I
329	P	P	P	P	325	N	N	N	N
298	S	S	S	S	270	D	D	D	D
239	S	S	S	S	268	H	H	H	Q
265	D	D	D	D	326	K	K	K	K
327	A	G	A	G	331	P	P	P	S
330	A	A	A	S	264	V	V	V	V
297	N	N	N	N	233	E	P	E	E
267	S	S	S	S	240	V	V	V	V
234	L	V	L	F	241	F	F	F	F
238	P	P	P	P	263	V	V	V	V
299	T	T	T	T	300	Y	F	F	Y
328	L	L	L	L					

Figure 47

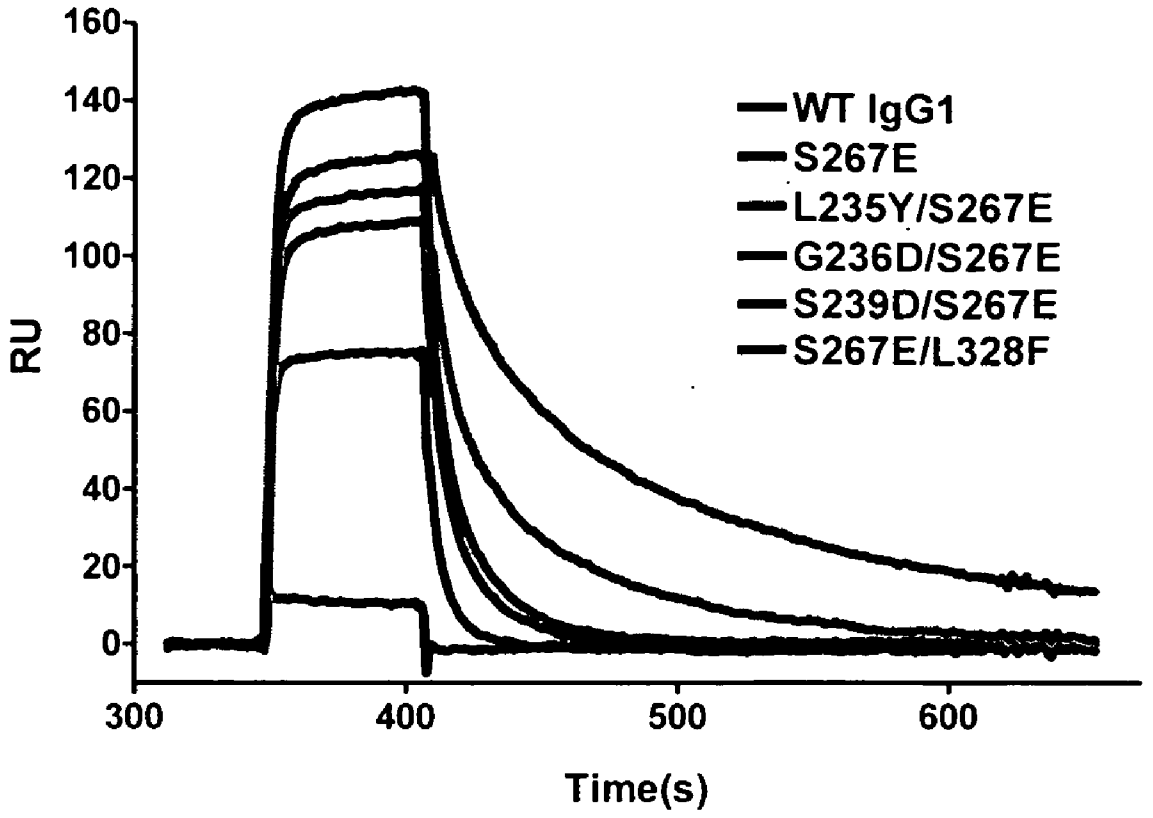

160
140
120
100
80
60
40
20
0
RU
300
400
500
600
Time(s)
WT IgG1
S267E
L235Y/S267E
G236D/S267E
S239D/S267E
S267E/L328F

Figure 48

Substitution(s)	FcγRI Kd (pM)	FcγRIIaH Kd (nM)	FcγRIIaR Kd (nM)	FcγRIIb Kd (nM)	FcγRIIIaV Kd (nM)	FcγRIIIaF Kd (nM)
IgG1 WT	329	646	859	1467	191	1352
L234D/G236N/S267E			1180	287		
L234D/S267E	11500		67.7	67.8	1370	
L234E/H268D				249		
L234E/S267E	2510	n.d.	80.4	97	n.d.	
L234E/S267E/L328F	7750	8920	4.93	7.53	n.d.	
L234F	9110	n.d.	3760	3590	n.d.	
L234F/G236N			n.d.	n.d.		
L234F/S236D			n.d.	n.d.		
L234F/S267E	498	1270	41.6	55.7	2040	
L234G			10000	10000		
L234I			15500	13600		
L234K			100000	100000		
L234N			n.d.	n.d.		
L234P			60700	22800		
L234Q			23100	10000		
L234S			1240	7640		
L234V			6425	3221		
L234W	10500	1160	1897	1771	6590	
L234W/G236D/S239E/S267E			151	129		
L234W/H268D/L328Y				248		
L234W/L328Y/I332E				232		
L234W/S239D/L328Y				44.8		
L234W/S239E/S267E			8.72	34.7		
L234Y			16800	61900		
L235A	18400	13300	5178	4183	609	
L235D/S239D				357		
L235D/S267E	854000	n.d.	66.1	88.1	n.d.	
L235D/S267E/L328F	573000	2350	6.45	18.2	n.d.	
L235E			2580	2668		
L235F/H268D/L328Y				370		
L235F/L328Y/I332E				443		
L235F/S239D/L328Y				215		
L235F/S267E	18700	1610	26.4	51.7	n.d.	
L235H			1136	1998		
L235I	16700	3580	1289	1615	212	
L235N			24100	10000		
L235P			7013	251022		
L235Q			420	n.d.		
L235R			838	263		
L235S			100000	100000		
L235S/S267E			1200	37800		
L235T/S267E			281	619		

Substitution(s)	FcγRI Kd (pM)	FcγRIIaH Kd (nM)	FcγRIIaR Kd (nM)	FcγRIIb Kd (nM)	FcγRIIIaV Kd (nM)	FcγRIIIaF Kd (nM)
L235W			n.d.	n.d.		
L235Y	142000	479	669	1400	380	
L235Y/G236D/S267E	n.d.	n.d.	88.8	58.7	n.d.	
L235Y/S239D/S267E	307	617	8.68	12.6	73.5	
L235Y/S267D				92.2		
L235Y/S267E	95000	687	22.9	39.4	n.d.	
L235Y/S267E/H268E	32100	4130	17.8	21	447	
L235Y/S267E/L328F	75539	853	5.02	7.83	n.d.	
G236A/G237A				25400		
G236D	15631	3871	1133	953	n.d.	n.d.
G236D/H268D				126		
G236D/S239D/S267E	4810	2980	32.2	17.3	n.d.	
G236D/S267E	3705	2728	34.0	26.6	579	n.d.
G236D/S267E/H268E	3650	6300	28.7	13.4	n.d.	
G236D/S267E/L328F	4478	21500	14.3	9.87	n.d.	
G236E/S267E			23.5	129		
G236F			100000	100000		
G236H			6350	n.d.		
G236I			n.d.	n.d.		
G236K			100000	100000		
G236L			n.d.	n.d.		
G236M			10000	10000		
G236N/S267E	9270	n.d.	263	74.2	n.d.	
G236P			10000	10000		
G236Q			10000	10000		
G236R			100000	100000		
G236S	12300	172	369	1441	52200	
G236S/G237A				18400		
G236T	21000	1330	2456	651920	n.d.	
G236V			8080	100000		
G236W			10000	10000		
G236Y			n.d.	n.d.		
G237A	30500	n.d.	1220	7676	n.d.	
G237D/S267E	3770	n.d.	63.1	86.1	n.d.	
G237E			100000	100000		
G237H			n.d.	n.d.		
G237K			100000	100000		
G237L			n.d.	n.d.		
G237N/S267E	3250		14	36.2	n.d.	
G237P			100000	100000		
G237Q			10000	10000		
G237S			10600	10000		
G237V			25100	10000		
G237Y			952	4450		
S239D	93.4	590	230	408	23.5	214

Substitution(s)	FcγRI Kd (pM)	FcγRIIaH Kd (nM)	FcγRIIaR Kd (nM)	FcγRIIb Kd (nM)	FcγRIIIaV Kd (nM)	FcγRIIIaF Kd (nM)
S239D/A327D/L328Y				123		
S239D/H268D				102		
S239D/H268D/L328F				167		
S239D/H268D/L328F/I332E				27.6		
S239D/H268D/L328W				28.7		
S239D/H268D/L328W/I332E				52.7		
S239D/H268D/L328Y				60.1		
S239D/H268D/L328Y/I332E				27.1		
S239D/H268E/L328Y				67.7		
S239D/I332E	37.4	163	68.6	101	7.07	28.2
S239D/K326D/L328Y				113		
S239D/L328F/I332E				176		
S239D/L328Y				264		
S239D/L328Y/I332E				198		
S239D/S267A/L328Y				74.1		
S239D/S267D				65.9		
S239D/S267E	14.2	510	7.16	13.3	51.2	516
S239D/S267E/H268E	326	817	7.52	6.91	18.6	
S239D/S267E/I332E				11.8		
S239D/S267E/L328F	227	378	2.06	3.43	887	
S239E	200	1320	1249	1828	54.8	
S239N			990	1013		
S239Q			1007	2012		
D265E			2794	3517		
V266D			1220	10000		
V266I			n.d.	n.d.		
V266M	264	553	274	770	350	
V266M/S267E	166	59.2	28	50.2	4270	
S267A	287	530	200	408	201	
S267A/H268D/L328Y				137		
S267A/L328Y/I332E				109		
S267D	156	695	95.5	330	127	
S267D/A327D				213		
S267D/A327E				121		
S267D/H268D				103		
S267D/H268E				82.6		
S267E	117	859	29.1	71.9	503	n.d.
S267E/A327D	198		51.3	69.1	96300	
S267E/A327E	143	243	29.3	47.5	21400	
S267E/H268D				44		
S267E/H268E	93.5	845	20.6	36.1	60.8	
S267E/H268E/L328F	333	783	3.4	4.26	2080	
S267E/L328F	220	923	3.12	6.06	5040	n.d.
S267E/L328H			185	284		
S267E/L328I			11.6	27.5		

Substitution(s)	FcγRI Kd (pM)	FcγRIIaH Kd (nM)	FcγRIIaR Kd (nM)	FcγRIIb Kd (nM)	FcγRIIIaV Kd (nM)	FcγRIIIaF Kd (nM)
S267E/L328Q				121		
S267E/L328Y	1470	481	7.06	34.1	n.d.	
S267E/N325L			20.7	46.6		
S267G	626	2120	517	1450	2120	
H268D	140	342	205	480	62.2	
H268D/A327D				191		
H268D/A327D/L328Y				420		
H268D/K326D/L328Y				78.9		
H268D/L328F/I332E				119		
H268D/L328W/I332E				36.9		
H268D/L328Y				767		
H268D/L328Y/I332E				300		
H268E	120	453	269	560	87.5	
H268E/L328Y/I332E				172		
H268N			481	1250		
H268Q			544	n.d.		
S298D			592	1840		
S298E			n.d.	n.d.		
S298L				n.d.		
S298M				n.d.		
S298Q			n.d.	n.d.		
K326A				n.d.		
K326D/L328Y/I332E				553		
K326E				241		
K326W				483		
A327D	160	882	536	1100	481	
A327D/L328Y/I332E				636		
A327G			2692	4159		
A327L				n.d.		
A327N	11800	n.d.	1410	1740	n.d.	
A327Q			1354	133661		
L328E				n.d.		
L328F	452	2360	166	541	58408	5109
L328Y/I332E				705		
P329E			10000	10000		
A330D				n.d.		
A330H				n.d.		
A330K				947		
A330S				23100		
P331S				39400		
IgG1/2ELLGG	161	428	481	563	667	
IgG1/2ELLGG_S267E/L328F	140	651	3.19	6.63	n.d.	
G236R/L328R	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
^236R/L328R	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

Figure 49

Substitution(s)	Fold FcγRI	Fold FcγRIIaH	Fold FcγRIIaR	Fold FcγRIIb	Fold FcγRIIIaV	Fold FcγRIIIaF
IgG1 WT	1	1	1	1	1	1
L234D/G236N/S267E			0.728	5.11		
L234D/S267E	0.0286		12.7	21.7	0.14	
L234E/H268D				5.89		
L234E/S267E	0.131	n.d.	10.7	15.1	n.d.	
L234E/S267E/L328F	0.0425	0.0725	174	195	n.d.	
L234F	0.0362	n.d.	0.228	0.409	n.d.	
L234F/G236N			n.d.	n.d.		
L234F/S236D			n.d.	n.d.		
L234F/S267E	0.661	0.509	20.7	26.4	0.0938	
L234G			0.0859	0.147		
L234I			0.0554	0.108		
L234K			0.00859	0.0147		
L234N			n.d.	n.d.		
L234P			0.0141	0.0644		
L234Q			0.0372	0.147		
L234S			0.693	0.192		
L234V			0.134	0.456		
L234W	0.0314	0.557	0.453	0.829	0.029	
L234W/G236D/S239E/S267E			5.69	11.4		
L234W/H268D/L328Y				5.92		
L234W/L328Y/I332E				6.32		
L234W/S239D/L328Y				32.8		
L234W/S239E/S267E			98.5	42.3		
L234Y			0.0511	0.0237		
L235A	0.0179	0.0486	0.166	0.351	0.314	
L235D/S239D				4.11		
L235D/S267E	0.00039	n.d.	13	16.7	n.d.	
L235D/S267E/L328F	0.00057	0.275	133	80.4	n.d.	
L235E			0.333	0.55		
L235F/H268D/L328Y				3.97		
L235F/L328Y/I332E				3.31		
L235F/S239D/L328Y				6.82		
L235F/S267E	0.0176	0.402	32.5	28.4	n.d.	
L235H			0.756	0.734		
L235I	0.0197	0.181	0.666	0.908	0.903	
L235N			0.0356	0.147		
L235P			0.122	0.00585		
L235Q			2.04	n.d.		
L235R			1.02	5.58		
L235S			0.00859	0.0147		
L235S/S267E			0.716	0.0388		
L235T/S267E			3.06	2.37		
L235W			n.d.	n.d.		

Substitution(s)	Fold FcγRI	Fold FcγRIIaH	Fold FcγRIIaR	Fold FcγRIIb	Fold FcγRIIIaV	Fold FcγRIIIaF
L235Y	0.00232	1.35	1.28	1.05	0.504	
L235Y/G236D/S267E	n.d.	n.d.	9.67	25	n.d.	
L235Y/S239D/S267E	1.07	1.05	98.9	116	2.6	
L235Y/S267D				15.9		
L235Y/S267E	0.00347	0.941	37.5	37.2	n.d.	
L235Y/S267E/H268E	0.0103	0.157	48.2	69.9	0.428	
L235Y/S267E/L328F	0.00436	0.758	171	187	n.d.	
G236A/G237A				0.0578		
G236D	0.0211	0.167	0.758	1.54	n.d.	n.d.
G236D/H268D				11.6		
G236D/S239D/S267E	0.0685	0.217	26.7	84.8	n.d.	
G236D/S267E	0.0889	0.237	25.2	55.1	0.331	n.d.
G236D/S267E/H268E	0.0902	0.103	29.9	110	n.d.	
G236D/S267E/L328F	0.0736	0.0301	59.9	149	n.d.	
G236E/S267E			36.5	11.4		
G236F			0.00859	0.0147		
G236H			0.135	n.d.		
G236I			n.d.	n.d.		
G236K			0.00859	0.0147		
G236L			n.d.	n.d.		
G236M			0.0859	0.147		
G236N/S267E	0.0355	n.d.	3.27	19.8	n.d.	
G236P			0.0859	0.147		
G236Q			0.0859	0.147		
G236R			0.00859	0.0147		
G236S	0.0268	3.76	2.33	1.02	0.00367	
G236S/G237A				0.0797		
G236T	0.0157	0.486	0.35	0.00225	n.d.	
G236V			0.106	0.0147		
G236W			0.0859	0.147		
G236Y			n.d.	n.d.		
G237A	0.0108	n.d.	0.704	0.191	n.d.	
G237D/S267E	0.0874	n.d.	13.6	17	n.d.	
G237E			0.00859	0.0147		
G237H			n.d.	n.d.		
G237K			0.00859	0.0147		
G237L			n.d.	n.d.		
G237N/S267E	0.101		61.5	40.5	n.d.	
G237P			0.00859	0.0147		
G237Q			0.0859	0.147		
G237S			0.081	0.147		
G237V			0.0342	0.147		
G237Y			0.902	0.33		
S239D	3.53	1.1	3.73	3.6	8.14	6.32
S239D/A327D/L328Y				11.9		
S239D/H268D				14.4		

Substitution(s)	Fold FcγRI	Fold FcγRIIaH	Fold FcγRIIaR	Fold FcγRIIb	Fold FcγRIIIaV	Fold FcγRIIIaF
S239D/H268D/L328F				8.79		
S239D/H268D/L328F/I332E				53.2		
S239D/H268D/L328W				51.1		
S239D/H268D/L328W/I332E				27.8		
S239D/H268D/L328Y				24.4		
S239D/H268D/L328Y/I332E				54.1		
S239D/H268E/L328Y				21.7		
S239D/I332E	8.81	3.98	12.5	14.6	27.1	48
S239D/K326D/L328Y				13		
S239D/L328F/I332E				8.34		
S239D/L328Y				5.56		
S239D/L328Y/I332E				7.41		
S239D/S267A/L328Y				19.8		
S239D/S267D				22.3		
S239D/S267E	23.2	1.27	120	111	3.74	2.62
S239D/S267E/H268E	1.01	0.791	114	212	10.3	
S239D/S267E/I332E				124		
S239D/S267E/L328F	1.45	1.71	416	428	0.216	
S239E	1.65	0.49	0.688	0.803	3.49	
S239N			0.867	1.45		
S239Q			0.853	0.729		
D265E			0.307	0.417		
V266D			0.704	0.147		
V266I			n.d.	n.d.		
V266M	1.25	1.17	3.13	1.91	0.547	
V266M/S267E	1.98	10.9	30.7	29.2	0.0448	
S267A	1.15	1.22	4.29	3.6	0.952	
S267A/H268D/L328Y				10.7		
S267A/L328Y/I332E				13.5		
S267D	2.11	0.93	8.99	4.45	1.51	
S267D/A327D				6.89		
S267D/A327E				12.1		
S267D/H268D				14.2		
S267D/H268E				17.8		
S267E	2.81	0.753	29.5	20.4	0.381	n.d.
S267E/A327D	1.66		16.7	21.2	0.00199	
S267E/A327E	2.3	2.66	29.3	30.9	0.00894	
S267E/H268D				33.3		
S267E/H268E	3.52	0.765	41.7	40.6	3.15	
S267E/H268E/L328F	0.991	0.826	253	344	0.092	
S267E/L328F	1.5	0.7	275	242	0.038	n.d.
S267E/L328H			4.64	5.17		
S267E/L328I			74	53.4		
S267E/L328Q				12.1		
S267E/L328Y	0.224	1.34	122	43.1	n.d.	
S267E/N325L			41.5	31.5		

Substitution(s)	Fold FcγRI	Fold FcγRIIaH	Fold FcγRIIaR	Fold FcγRIIb	Fold FcγRIIIaV	Fold FcγRIIIaF
S267G	0.526	0.305	1.66	1.01	0.0903	
H268D	2.35	1.89	4.19	3.06	3.08	
H268D/A327D				7.68		
H268D/A327D/L328Y				3.49		
H268D/K326D/L328Y				18.6		
H268D/L328F/I332E				12.3		
H268D/L328W/I332E				39.8		
H268D/L328Y				1.91		
H268D/L328Y/I332E				4.89		
H268E	2.74	1.43	3.19	2.62	2.19	
H268E/L328Y/I332E				8.53		
H268N			1.79	1.17		
H268Q			1.58	n.d.		
S298D			1.45	0.797		
S298E			n.d.	n.d.		
S298L				n.d.		
S298M				n.d.		
S298Q			n.d.	n.d.		
K326A				n.d.		
K326D/L328Y/I332E				2.65		
K326E				6.09		
K326W				3.04		
A327D	2.06	0.733	1.6	1.33	0.398	
A327D/L328Y/I332E				2.31		
A327G			0.319	0.353		
A327L				n.d.		
A327N	0.0279	n.d.	0.609	0.843	n.d.	
A327Q			0.634	0.011		
L328E				n.d.		
L328F	0.728	0.274	5.16	2.71	0.00328	0.265
L328Y/I332E				2.08		
P329E			0.0859	0.147		
A330D				n.d.		
A330H				n.d.		
A330K				1.55		
A330S				0.0635		
P331S				0.0372		
IgG1/2ELLGG	2.05	1.51	1.79	2.61	0.287	
IgG1/2ELLGG_S267E/L328F	2.35	0.993	269	221	n.d.	
G236R/L328R	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
^236R/L328R	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.

Figure 50

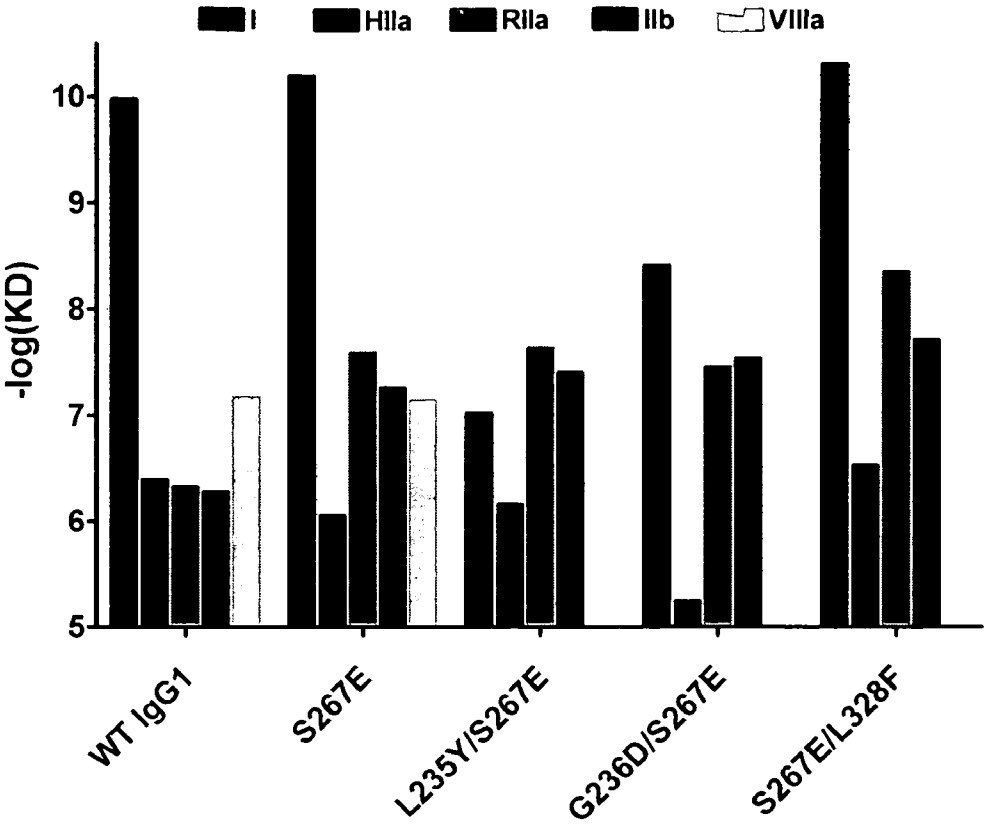


Figure 51

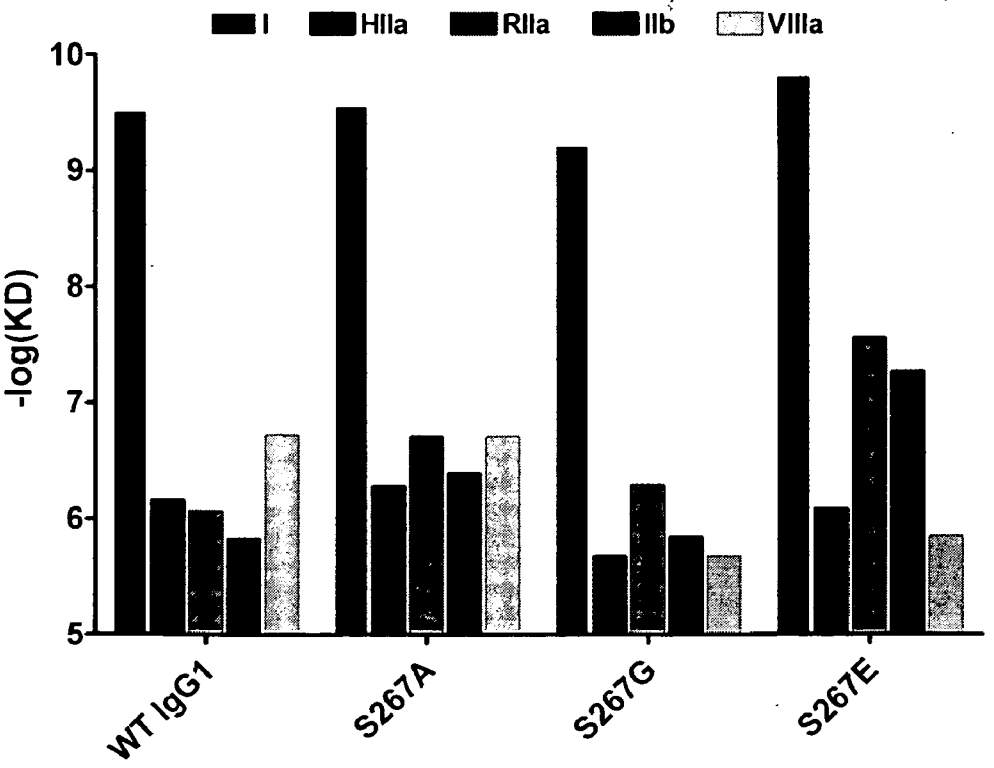


Figure 52A

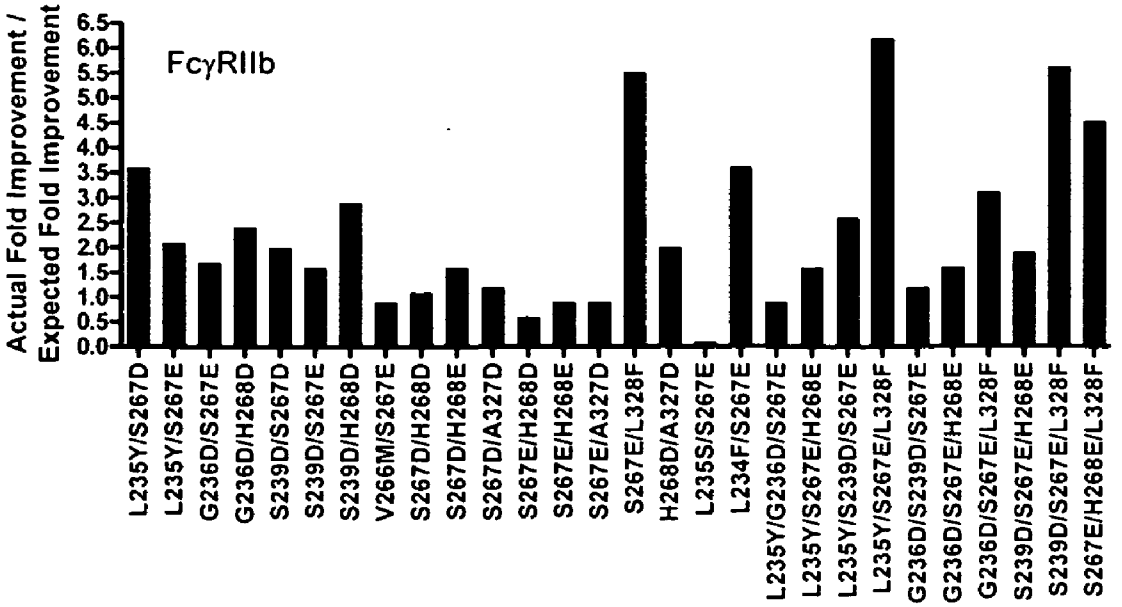


Figure 52B

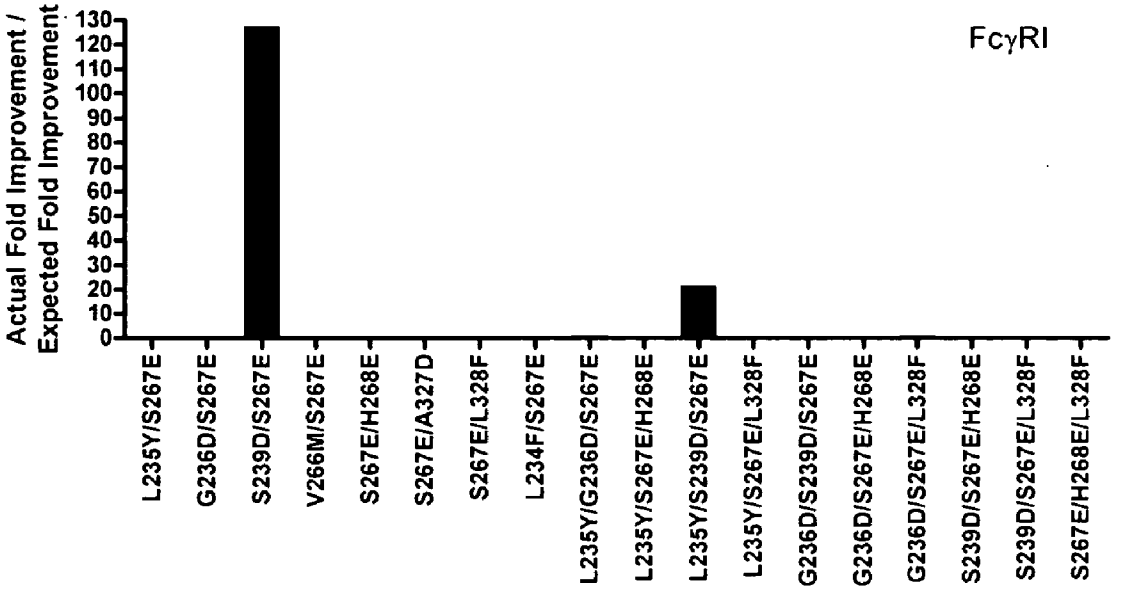


Figure 52 C

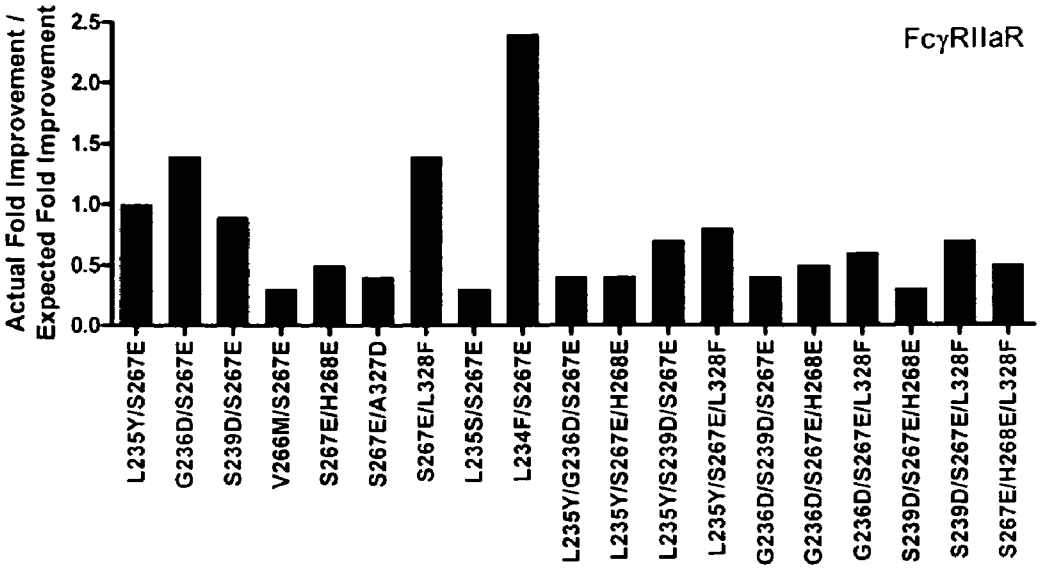


Figure 52 D

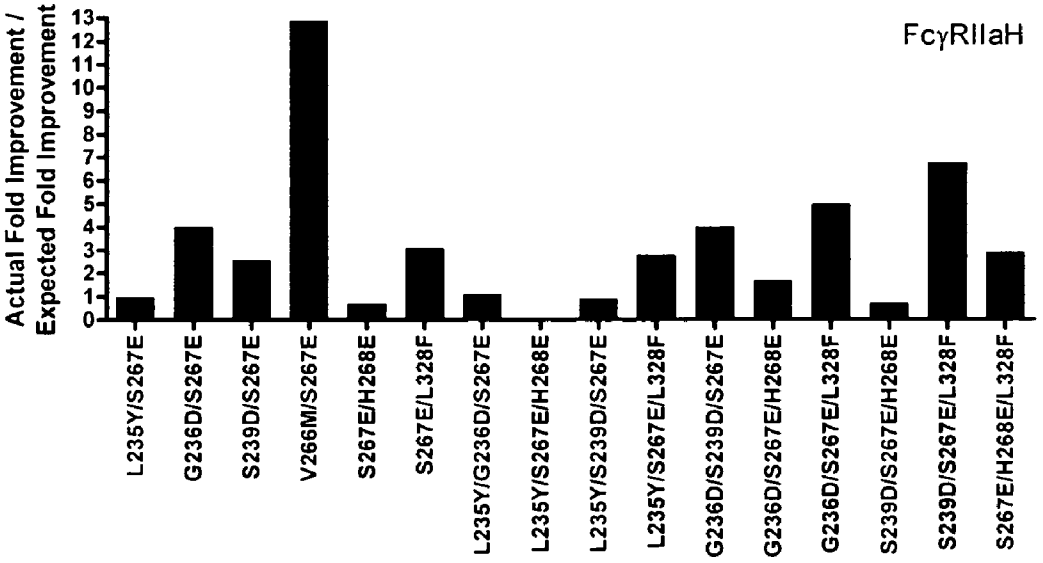


Figure 52E

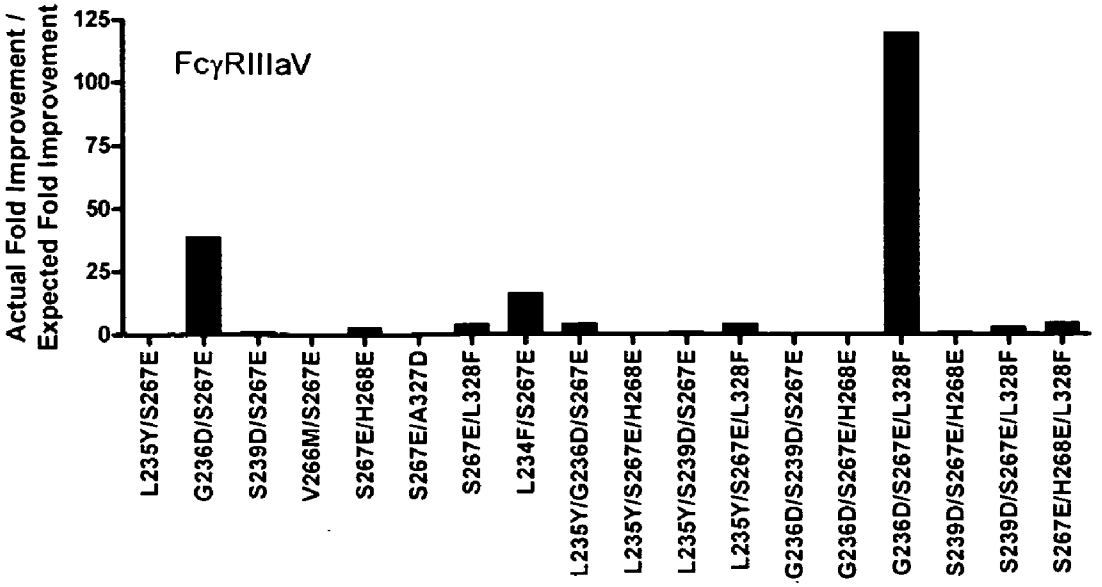

Actual Fold Improvement / Expected Fold Improvement
FcγRIIIaV
125
100
75
50
25
0
L235Y/S267E
G236D/S267E
S239D/S267E
V266M/S267E
S267E/H268E
S267E/A327D
S267E/L328F
L234F/S267E
L235Y/G236D/S267E
L235Y/S267E/H268E
L235Y/S239D/S267E
L235Y/S267E/L328F
G236D/S239D/S267E
G236D/S267E/H268E
G236D/S267E/L328F
S239D/S267E/H268E
S239D/S267E/L328F
S267E/H268E/L328F

Figure 53

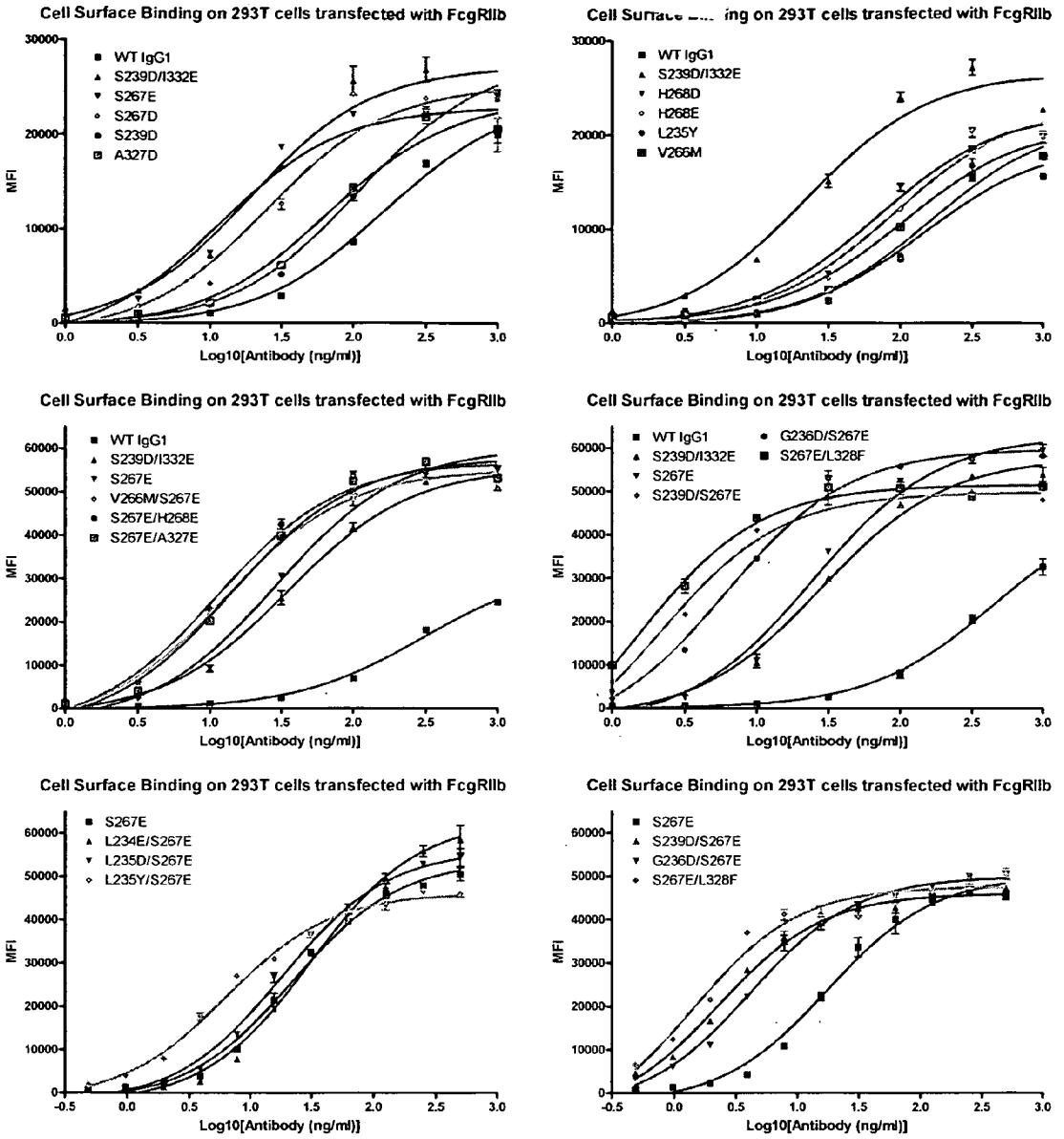

Cell Surface Binding on 293T cells transfected with FcgRIIb
WT IgG1
S239D/I332E
S267E
S267D
S239D
A327D
MFI
Log10[Antibody (ng/ml)]
Cell Surface Binding on 293T cells transfected with FcgRIIb
WT IgG1
S239D/I332E
H268D
H268E
L235Y
V266M
MFI
Log10[Antibody (ng/ml)]
Cell Surface Binding on 293T cells transfected with FcgRIIb
WT IgG1
S239D/I332E
S267E
V266M/S267E
S267E/H268E
S267E/A327E
MFI
Log10[Antibody (ng/ml)]
Cell Surface Binding on 293T cells transfected with FcgRIIb
WT IgG1
S239D/I332E
S267E
S239D/S267E
G236D/S267E
S267E/L328F
MFI
Log10[Antibody (ng/ml)]
Cell Surface Binding on 293T cells transfected with FcgRIIb
S267E
L234E/S267E
L235D/S267E
L235Y/S267E
MFI
Log10[Antibody (ng/ml)]
Cell Surface Binding on 293T cells transfected with FcgRIIb
S267E
S239D/S267E
G236D/S267E
S267E/L328F
MFI
Log10[Antibody (ng/ml)]

Figure 54

Substitution(s)	Method	mFcγRIIb Fold	mFcγRIV Fold	cynoFcγRIIb Fold	cynoFcγRIIIa Fold
L234D/G236N/S267E	Kd	NB		NB	
L234D/S267E	off-	1.041	NB		
L234D/S267E	off-			0.495	0.116
L234F	off-	NB	0.144		
L234F	off-			0.936	0.561
L234G	off-	NB	NB		
L234G	off-			NB	0.113
L234K	off-	NB	NB		
L234K	off-			NB	NB
L234N	off-	NB	0.200		
L234N	off-			NB	0.371
L234Q	off-	NB	NB		
L234Q	off-			NB	0.379
L234W	Kd			1.896	
L234W/G236D/S239E/S267E	Kd	0.029		NB	
L234W/H268D/L328Y	Kd	5.923		4.629	
L234W/L328Y/I332E	Kd	0.617		2.038	
L234W/S239D/L328Y	Kd	44.110		5.922	
L234W/S239E/S267E	Kd	0.761		2.246	
L234Y	Kd			1.013	
L235A	off-	NB	0.496		
L235A	off-			NB	0.530
L235D/S239D	off-		1.571		1.407
L235E	off-	NB	0.857		
L235E	off-			NB	0.367
L235F/H268D/L328Y	Kd	6.822		3.169	
L235F/L328Y/I332E	Kd	0.843		4.109	
L235F/S239D/L328Y	Kd	31.204		5.196	
L235F/S267E	off-	NB	0.515		
L235F/S267E	off-			1.392	0.255
L235H	Kd			0.832	
L235N	off-	NB	0.241		
L235N	off-			NB	0.351
L235R	off-	NB	0.347		
L235R	off-			NB	NB
L235W	Kd			1.443	
L235Y	off-	1.022	0.507		
L235Y	off-			0.920	0.535
G236A/G237A	Kd	NB		NB	
G236D	off-	NB	NB		
G236D	off-			NB	NB
G236D/S267E	off-	NB	NB		
G236D/S267E	off-			NB	NB
G236E/S267E	off-	NB	NB		
G236E/S267E	off-			NB	0.327
G236F	off-	NB	NB		
G236F	off-			NB	0.138
G236N/S267E	off-	NB	NB		
G236N/S267E	off-			0.587	NB

G236P	off-	NB	NB		
G236P	off-			NB	NB
G236R	off-	NB	NB		
G236R	off-			NB	NB
G236S	Kd			3.549	1.453
G236S/G237A	Kd	NB		NB	
G236V	off-	NB	NB		
G236V	off-			0.703	NB
G237A	off-	NB	NB		
G237A	off-			NB	NB
G237E	off-	NB	NB		
G237E	off-			NB	NB
G237H	off-	NB	NB		
G237H	off-			NB	NB
G237K	off-	NB	NB		
G237K	off-			NB	NB
G237S	off-	NB	NB		
G237S	off-			NB	NB
S239D	Kd	2.006	2.525	1.638	7.579
S239D	off-	2.912	1.907		
S239D	off-			1.986	2.325
S239D/A327D/L328Y	Kd	45.296		1.309	
S239D/H268D	Kd	1.857	1.063	5.683	8.675
S239D/H268D	Kd	1.518		16.693	
S239D/H268D	off-		2.209		3.618
S239D/H268D/L328F	Kd	6.007		3.169	
S239D/H268D/L328F/I332E	Kd	2.592		27.604	
S239D/H268D/L328W	Kd	47.801		23.740	
S239D/H268D/L328W/I332E	Kd	4.814		4.549	
S239D/H268D/L328Y	Kd	48.629		22.246	
S239D/H268D/L328Y/I332E	Kd	3.036		9.099	
S239D/H268E/L328Y	Kd	26.535		5.873	
S239D/I332E	Kd	5.442	7.473	10.196	11.520
S239D/I332E	Kd	1.150		17.815	
S239D/K326D/L328Y	Kd	131.128		10.192	
S239D/L328F/I332E	Kd	2.093		3.086	
S239D/L328Y	Kd	11.463		2.135	
S239D/L328Y/I332E	Kd	1.702		5.121	
S239D/S267A/L328Y	Kd	46.483		6.463	
S239D/S267D	Kd	1.983	1.005	1.793	7.660
S239D/S267D	off-		1.875		2.734
S239D/S267E	Kd	1.746	0.726	1.588	3.881
S239D/S267E	off-	7.871	1.545		
S239D/S267E	off-			2.526	1.677
S239D/S267E/I332E	Kd	1.003		10.047	
S239D/S267E/L328F	Kd			4.581	1.171
S239E	off-	3.105	1.925		
S239E	off-			1.249	2.261
S239N	off-	0.610	1.074		
S239N	off-			0.660	1.146
S239Q	off-	1.740	0.711		
S239Q	off-			0.401	0.622
D265E	off-	0.833	0.526		
D265E	off-			0.648	0.636
V266D	off-	NB	NB		
V266D	off-			NB	NB
V266I	off-	1.416	1.193		
V266I	off-			0.826	0.979
V266M	off-	2.036	1.229		

V266M	off-			NB	0.433
S267A	off-	3.022	1.534		
S267A	off-			1.048	1.274
S267A/H268D/L328Y	Kd	32.404		3.262	
S267A/L328Y/I332E	Kd	2.633		3.655	
S267D	off-	1.945	1.267		
S267D	off-			1.031	1.271
S267D/A327D	off-	0.000		0.000	
S267D/H268D	Kd	0.902	0.598	1.860	5.333
S267D/H268D	off-	0.968		1.956	
S267E	off-	1.437	0.770		
S267E	off-			1.093	0.515
S267E/A327D	off-	0.971		0.697	
S267E/A327E	off-	2.796	1.036		
S267E/A327E	off-			1.033	0.465
S267E/H268E/L328F	Kd			3.514	1.043
S267E/L328F	Kd	1.060	0.020	0.881	NB
S267E/L328F	off-	4.887	0.198		
S267E/L328F	off-			1.263	NB
S267E/L328H	off-	1.111	NB		
S267E/L328H	off-			0.420	NB
S267E/L328I	off-	2.105	0.588		
S267E/L328I	off-			0.831	0.437
S267E/L328Q	off-	0.881	0.454		
S267E/L328Q	off-			0.367	0.124
S267E/L328Y	Kd	1.513	0.026	1.313	NB
S267E/L328Y	Kd	1.037		0.404	
S267E/L328Y	off-	7.915	NB		
S267E/L328Y	off-			1.934	NB
S267E/N325L	off-	NB	0.240		
S267E/N325L	off-			NB	NB
S267G	off-	NB	0.586		
S267G	off-			NB	0.343
H268D	Kd	1.111	0.470	1.475	4.235
H268D	off-	2.626	1.447		
H268D	off-			3.937	1.653
H268D/A327D	Kd	3.220	0.443	1.467	1.733
H268D/A327D	off-	5.095		1.797	
H268D/A327D/L328Y	Kd	18.722		3.581	
H268D/K326D/L328Y	Kd	19.368		9.381	
H268D/L328F/I332E	Kd	1.478		4.885	
H268D/L328W/I332E	Kd	4.260		7.465	
H268D/L328Y	Kd	2.785		2.924	
H268D/L328Y/I332E	Kd	1.281		4.085	
H268E	off-	2.443	1.417		
H268E	off-			2.230	1.509
H268E/L328Y/I332E	Kd	1.498		4.157	
H268N	off-	1.597	1.025		
H268N	off-			1.345	0.990
H268Q	off-	0.877	1.085		
H268Q	off-			0.864	0.983
S298D	off-	NB	0.618		
S298D	off-			NB	0.309
S298E	off-	NB	0.136		
S298E	off-			NB	0.046
S298L	Kd	0.208		0.040	
S298M	Kd	0.549		2.846	
S298Q	off-	1.412	0.291		
S298Q	off-			0.714	0.271

K326A	Kd	0.164		1.359	
K326D/L328Y/I332E	Kd	1.872		4.775	
K326E	Kd	0.605		1.029	
K326W	Kd	0.429		0.078	
A327D	Kd	1.857	0.315	1.156	0.783
A327D	off-	4.102	0.876		
A327D	off-			1.147	0.515
A327D/L328Y/I332E	Kd	1.239		1.019	
A327G	off-	1.452	1.229		
A327G	off-			0.903	0.443
A327L	Kd	NB		NB	
A327N	off-	0.643	1.159		
A327N	off-			NB	0.313
A327Q	off-	NB	0.361		
A327Q	off-			NB	0.223
L328E	Kd	0.016		NB	
L328F	off-	3.122	0.261		
L328F	off-			0.380	0.144
L328Y/I332E	Kd	0.434		4.599	
P329E	off-	NB	NB		
P329E	off-			NB	NB
A330D	Kd	2.633		NB	
A330H	Kd	0.013		NB	
A330K	Kd	0.296		2.019	
A330S	Kd	0.054		0.255	
P331S	Kd	0.085		0.250	

Figure 55

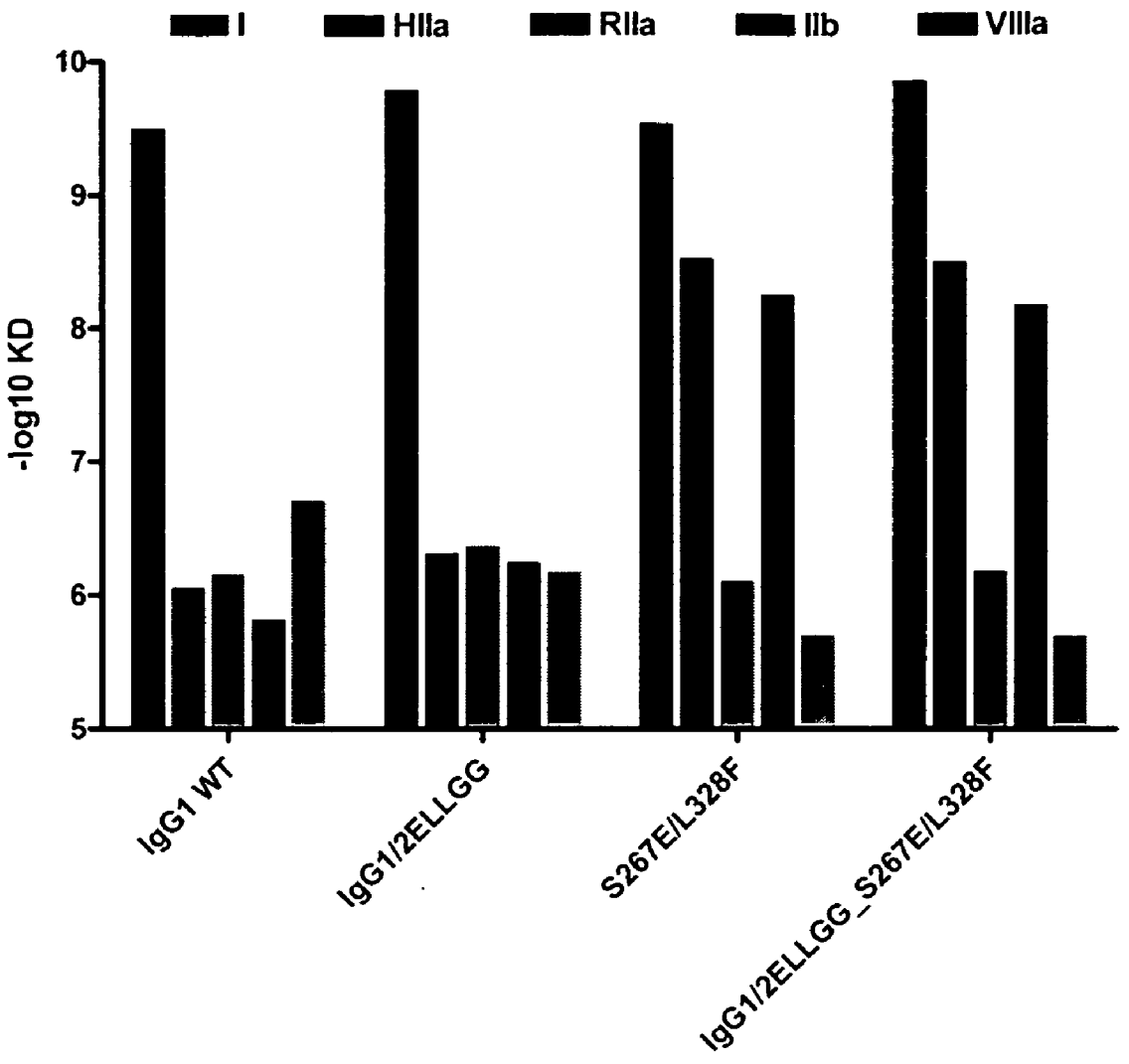

I
IIIa
IIIa
IIb
VIIIa
10
9
8
7
6
5
-log10 KD
IgG1 WT
IgG1/2ELLGG
S267E/L328F
IgG1/2ELLGG_S267E/L328F

Figure 56A

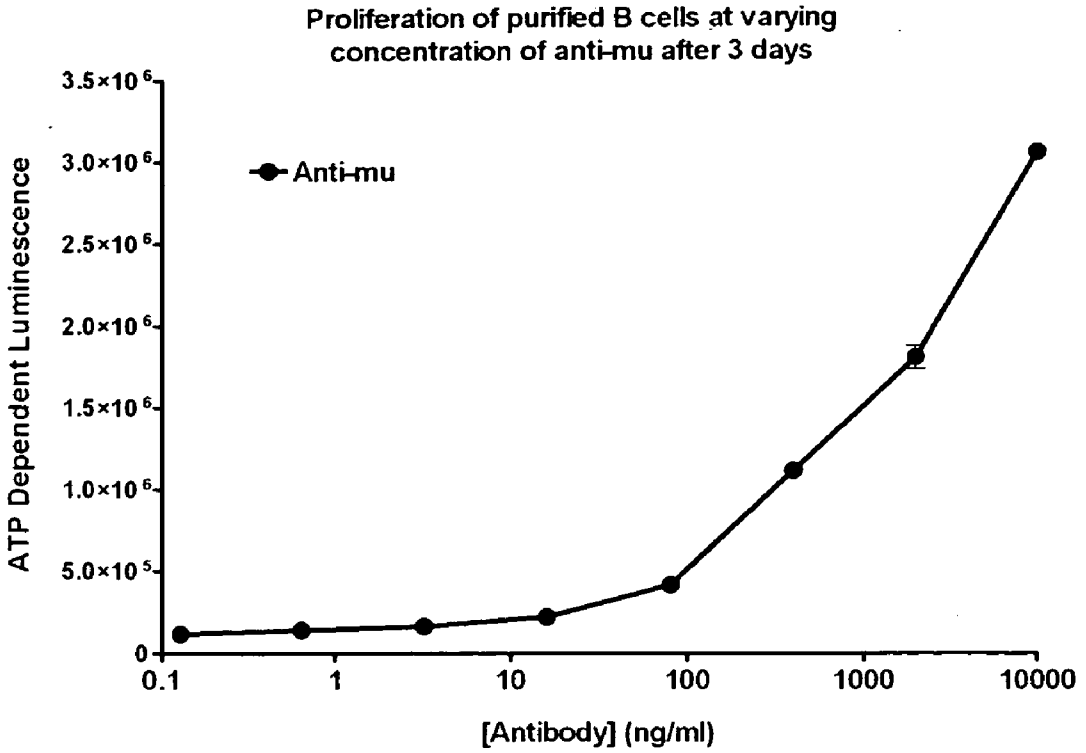


Figure 56B

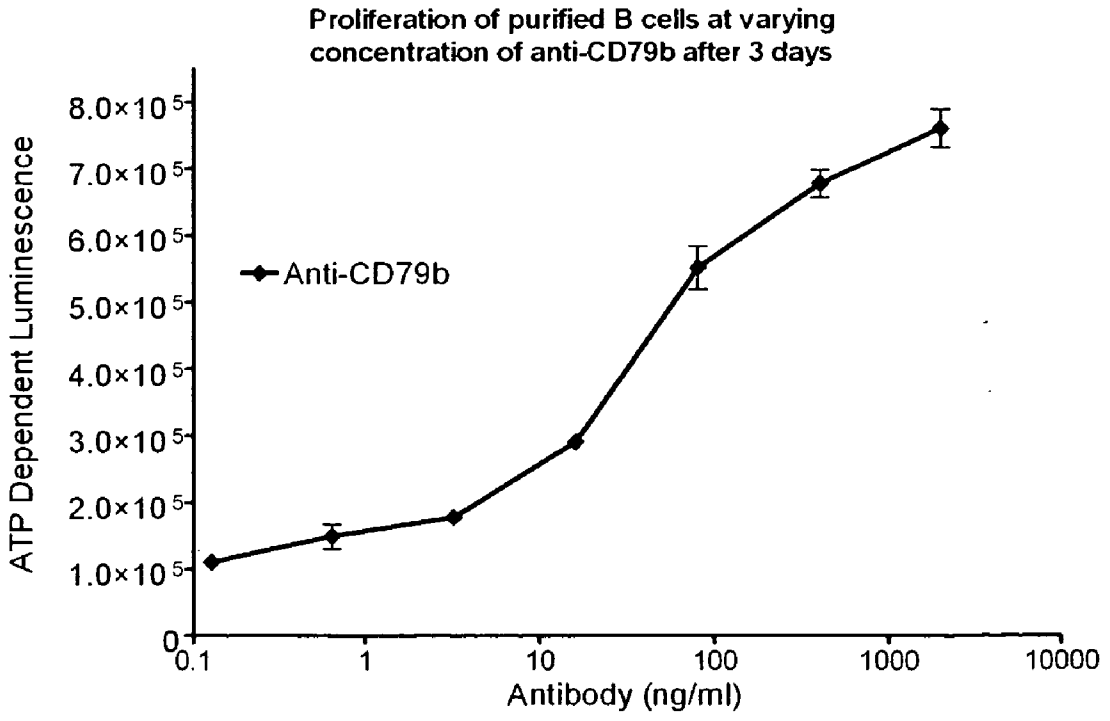


Figure 57

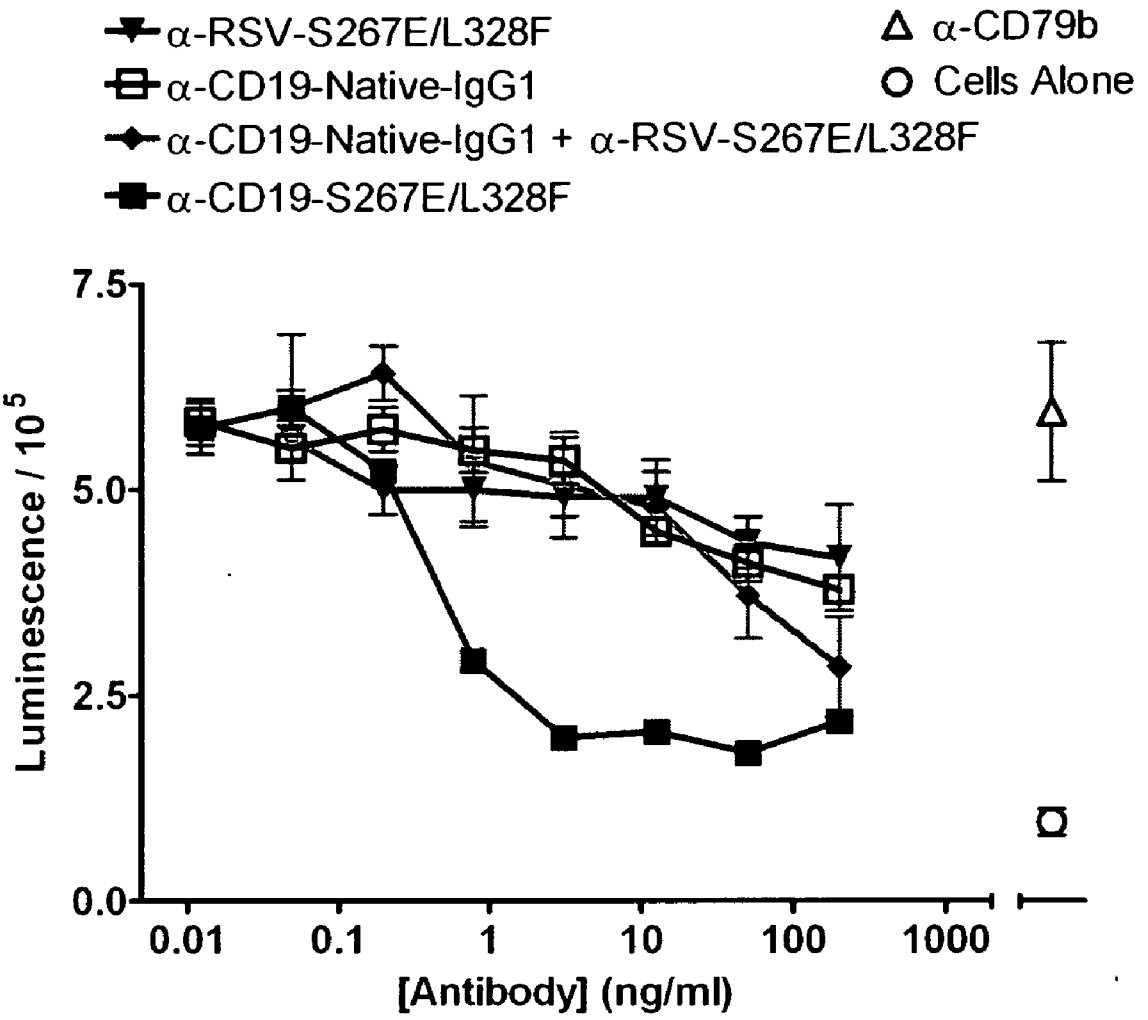

α-RSV-S267E/L328F
α-CD19-Native-IgG1
α-CD19-Native-IgG1 + α-RSV-S267E/L328F
α-CD19-S267E/L328F
α-CD79b
Cells Alone
Luminescence / 10^5
7.5
5.0
2.5
0.0
0.01
0.1
1
10
100
1000
[Antibody] (ng/ml)

Figure 58

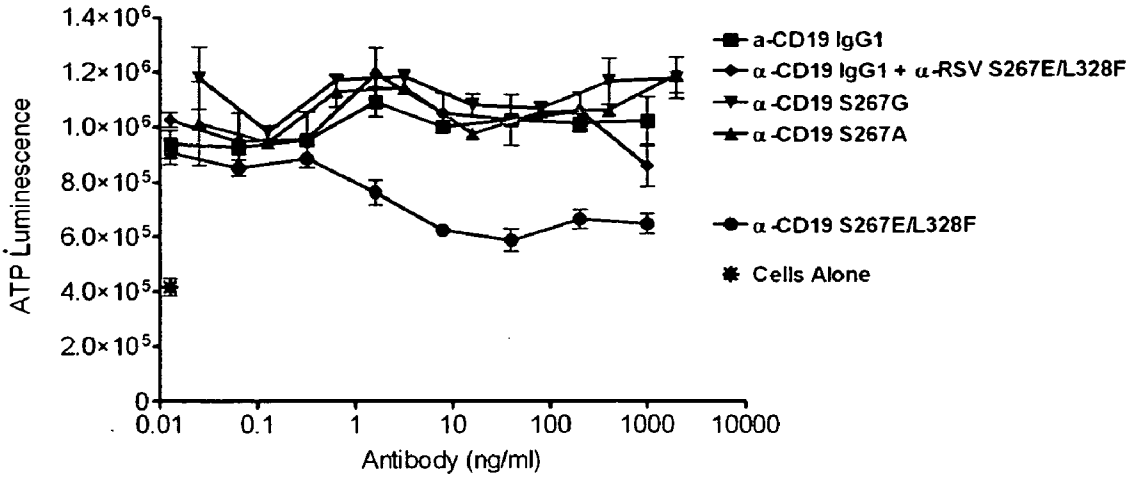


Figure 59

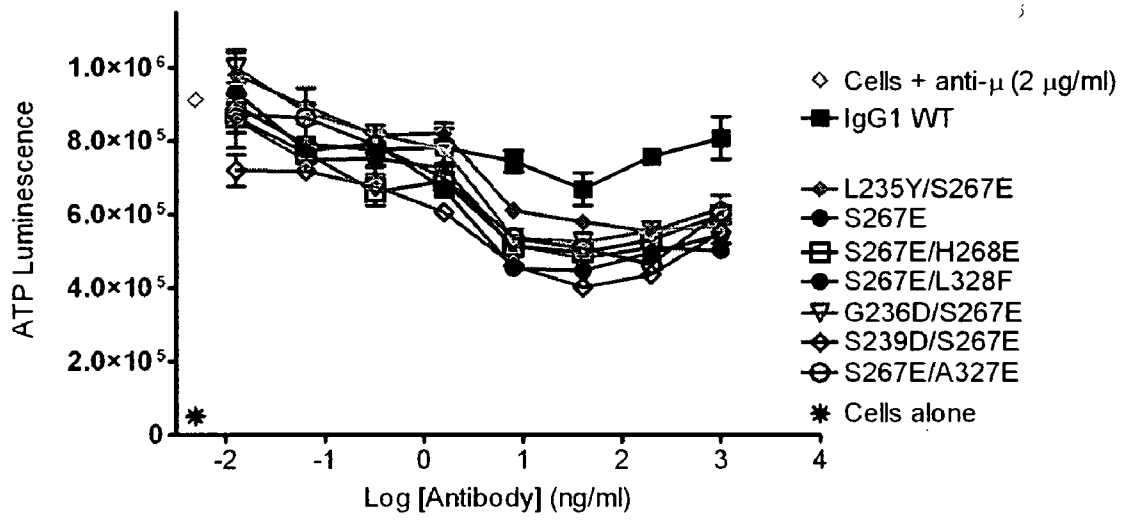


Figure 19 60

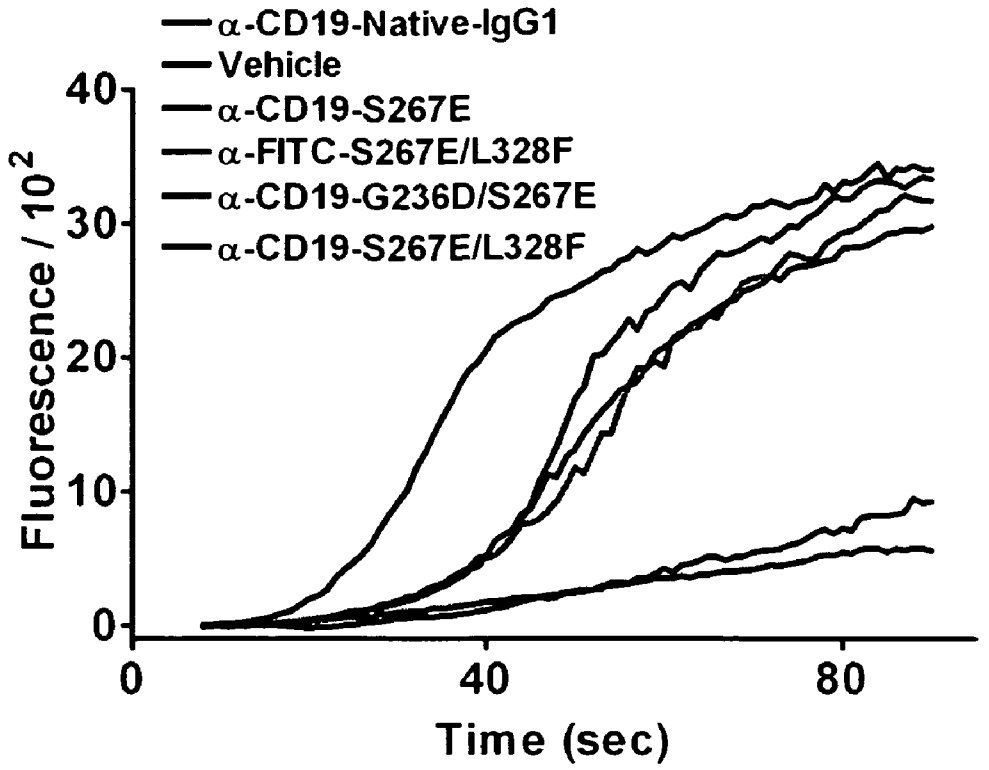


Figure 61

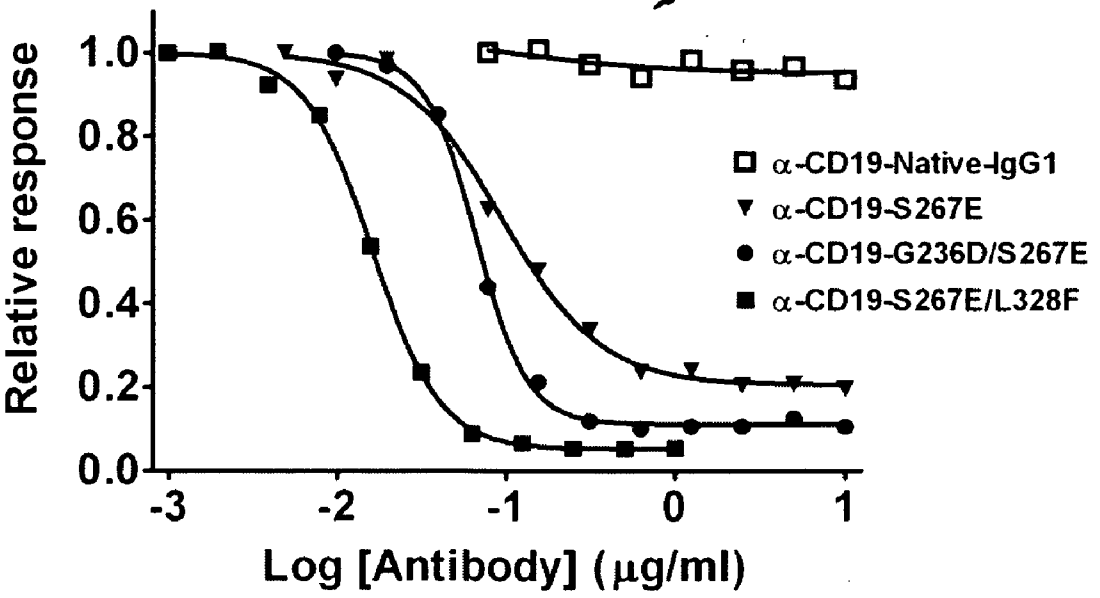


Figure 62

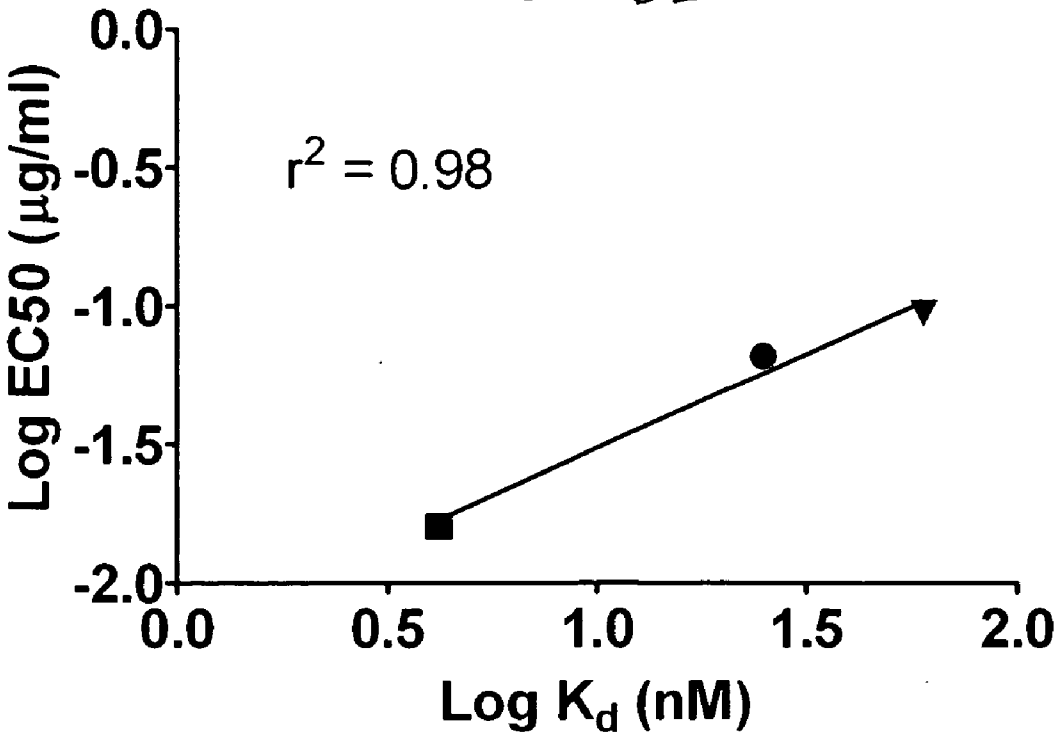


Figure 63

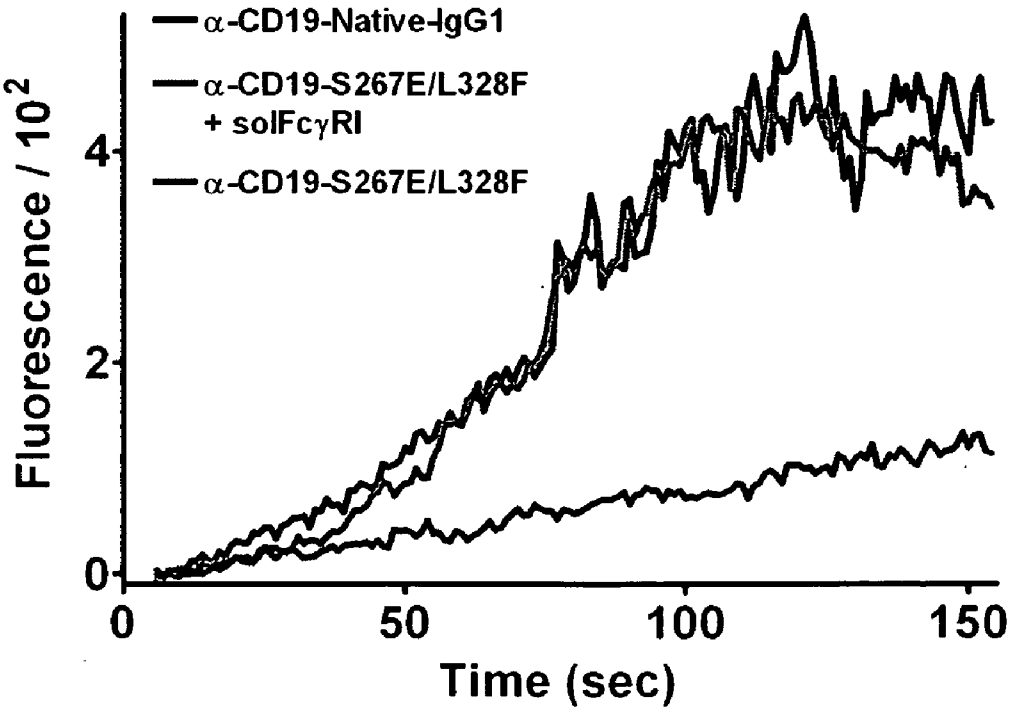


Figure 64

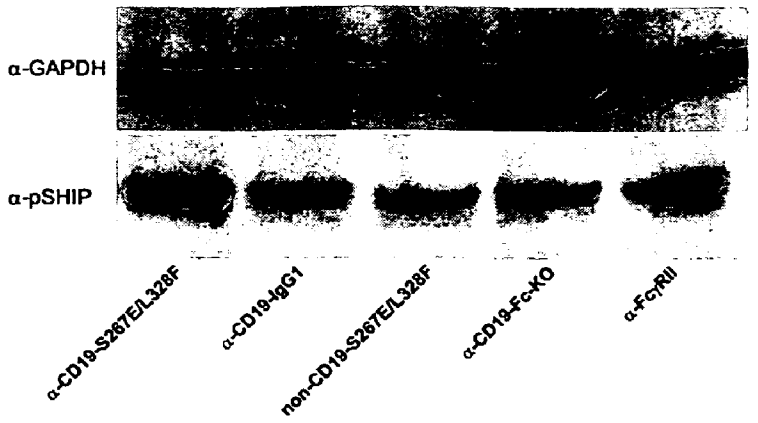


Figure 65

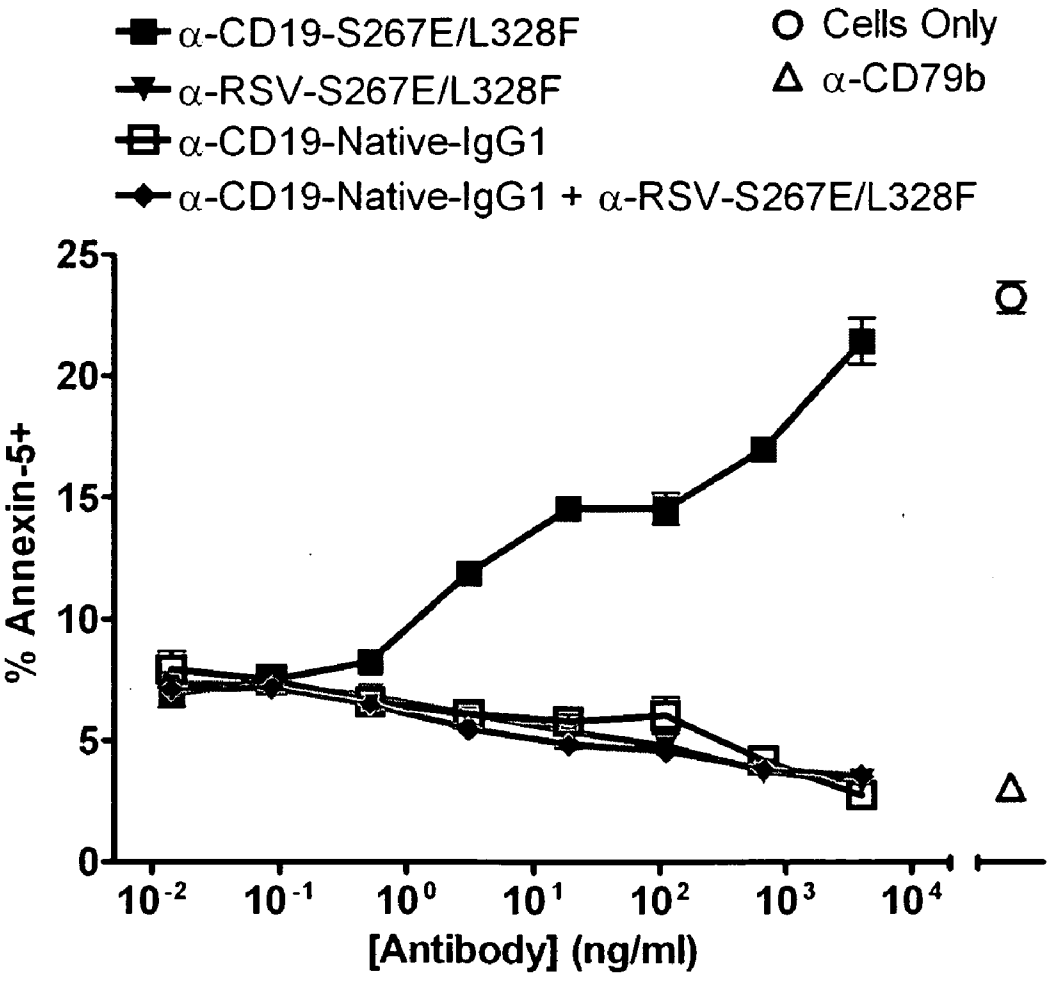


Figure 66

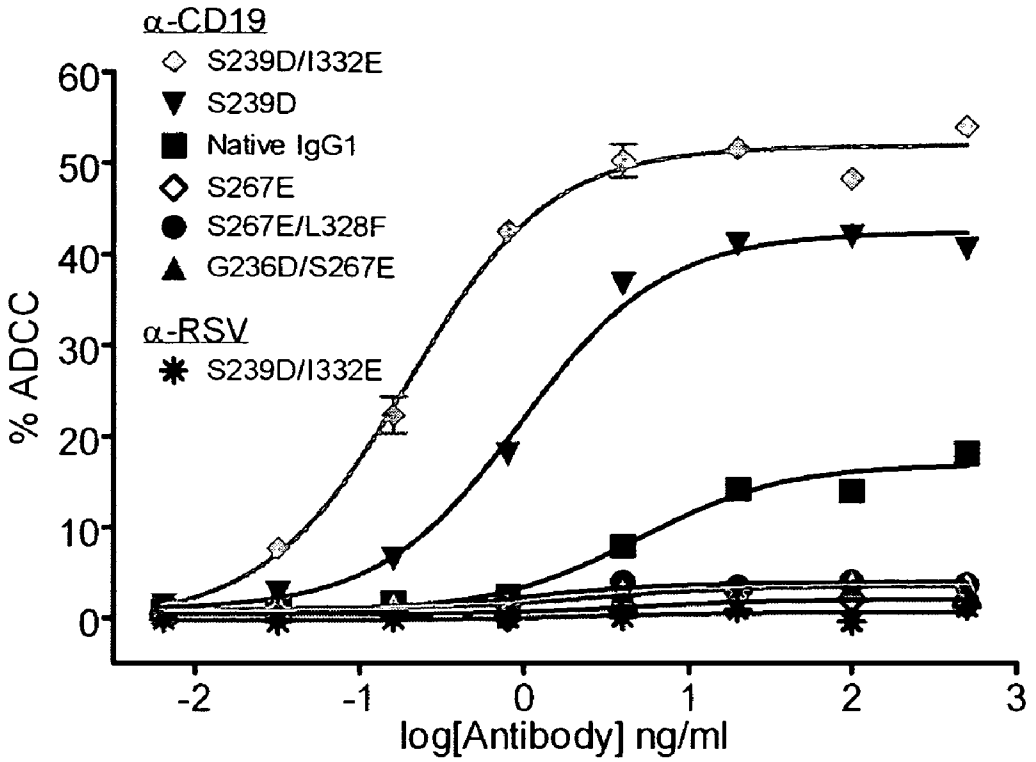


Figure 67

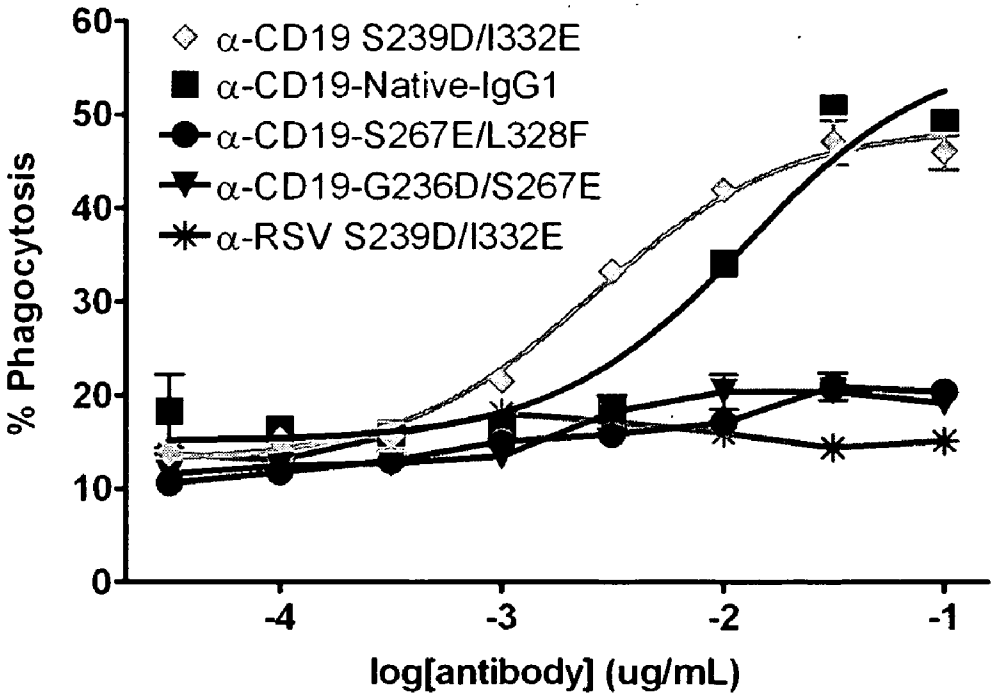


Figure 68

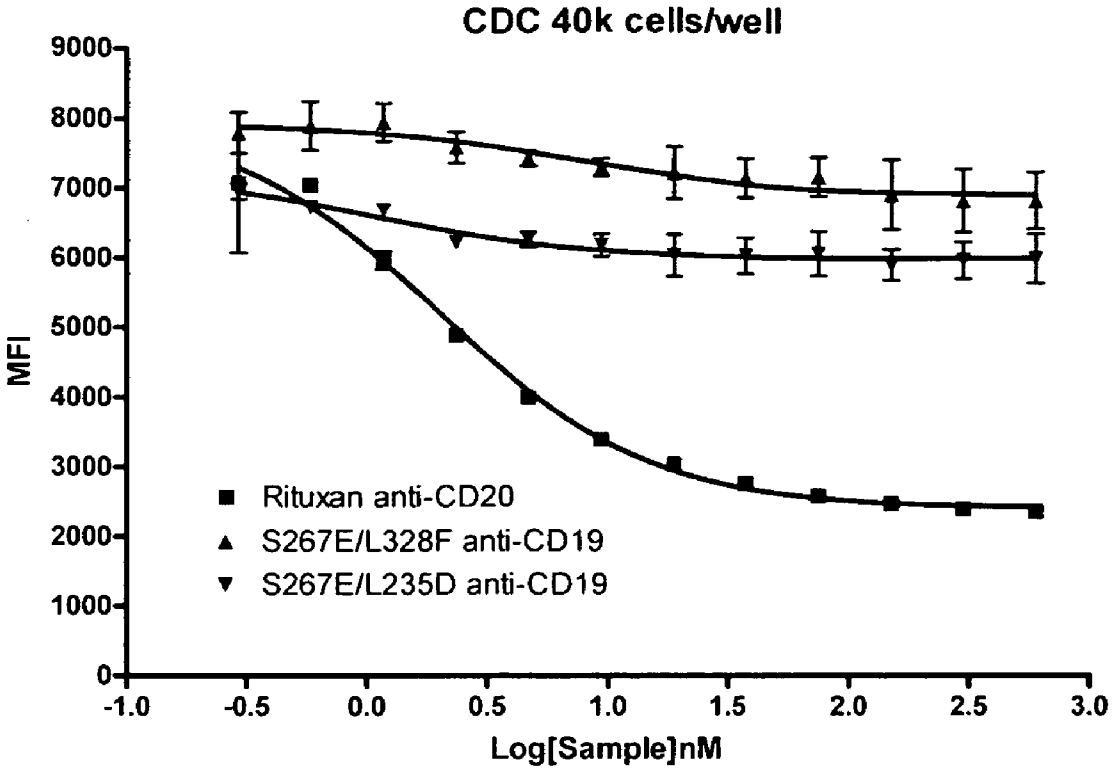

CDC 40k cells/well
MFI
9000
8000
7000
6000
5000
4000
3000
2000
1000
0
-1.0
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
Log[Sample]nM
Rituxan anti-CD20
S267E/L328F anti-CD19
S267E/L235D anti-CD19

Figure 69 A

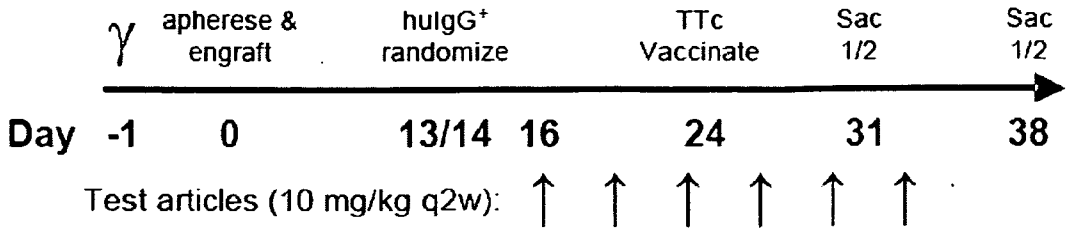


Figure 69 B

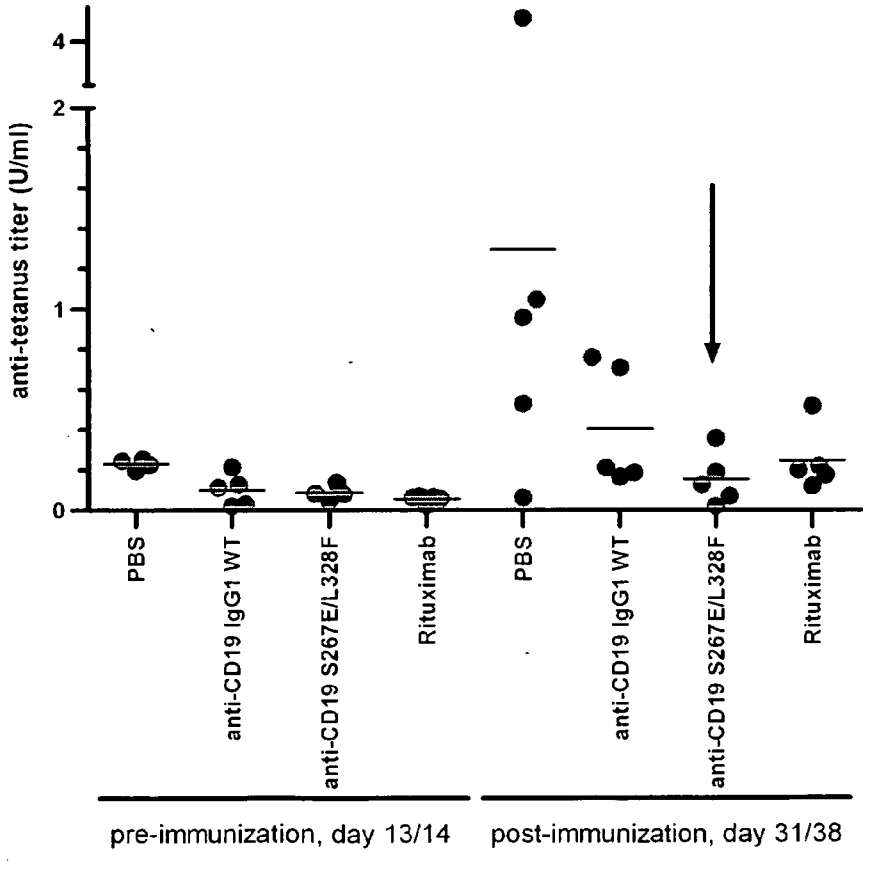


Figure 70

Antigen	Expression	Function
CD19	B, DC	BCR co-receptor
CD20	B	Membrane Ca^{++} regulator
CD21 (CR2)	B, DC	BCR co-receptor
CD22	B	BCR co-receptor, negative regulator
CD23 / FcεRII	B, MΦ, Eos, DC	IgE receptor
FcεRI (α, β, and γ subunits)	Mast, Baso	IgE receptor
CD24 / BBA-1 / HSA	B	Cell adhesion and motility
CD27	Memory B cells	T-cell interface
CD35 (CR1)	B	Complement receptor
CD38	B, plasma	Cell adhesion
CD40	B, DC	T-cell interface, T-cell co-stimulator
CD45RA	B	Membrane phosphatase
CD52 / CAMPATH -1 / HE5	B	Cellular signaling
CD72	B	BCR signaling modulator
CD79a (Igα)	B, DC	BCR signaling component
CD79b (Igβ)	B, DC	BCR signaling component
IgM (μ)	B	BCR antigen recognition component
CD80	B, DC	T-cell interface
CD81	B	BCR co-receptor
CD86	B, DC	T-cell interface
Leu13	B	BCR co-receptor
HLA-DR, -DP, -DQ	B, MΦ, DC	T-cell interface
CD138	Plasma	Cellular adhesion and growth factor co-receptor
CD317 / HM1.24	Plasma	Bone marrow stromal cell antigen (BST2)
CD11a	MΦ	integrin alpha L
CD11b	MΦ	integrin alpha M
CD11c	MΦ	integrin alpha X
CD14	MΦ, PMN	LPS receptor
CD68	MΦ	KP1, macrosialin
CD163	MΦ	hemoglobin/haptoglobin scavenger receptor
CD172a	MΦ	SIRP-alpha
CD200R	MΦ	OX2 receptor
CD206	MΦ	MΦ mannose receptor

Figure 71

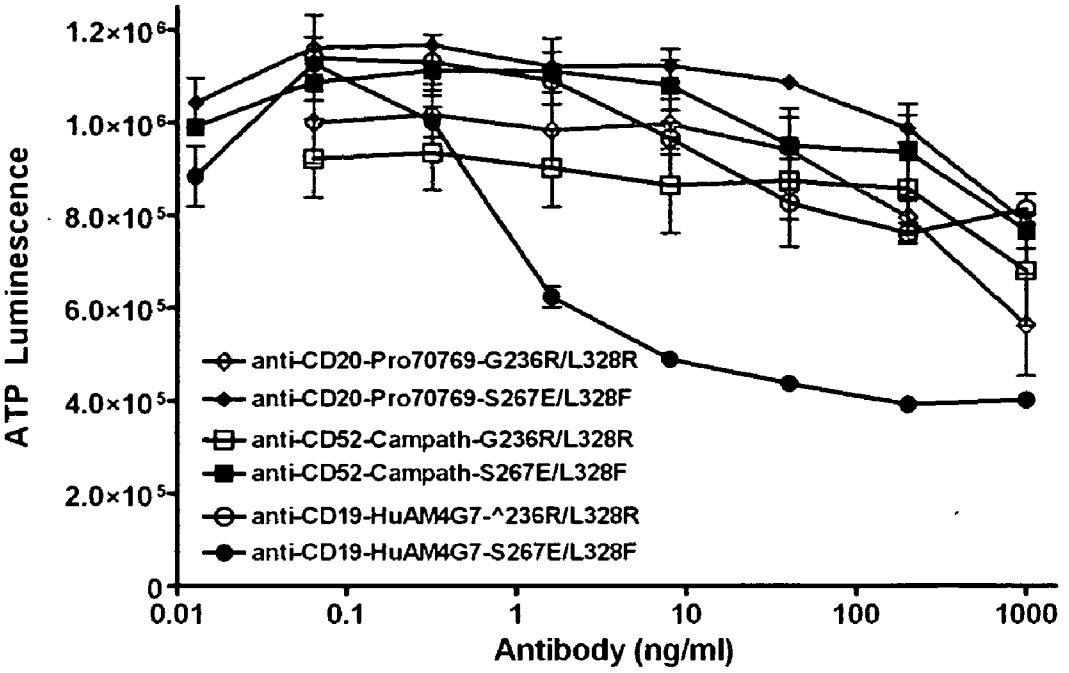


Figure 72

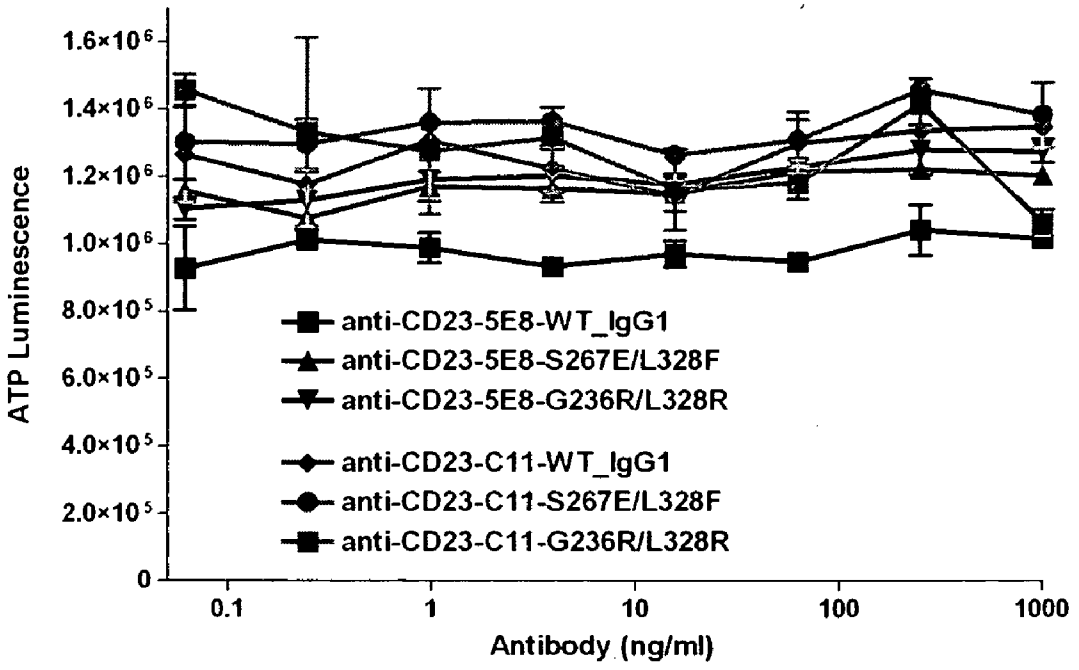


Figure 73

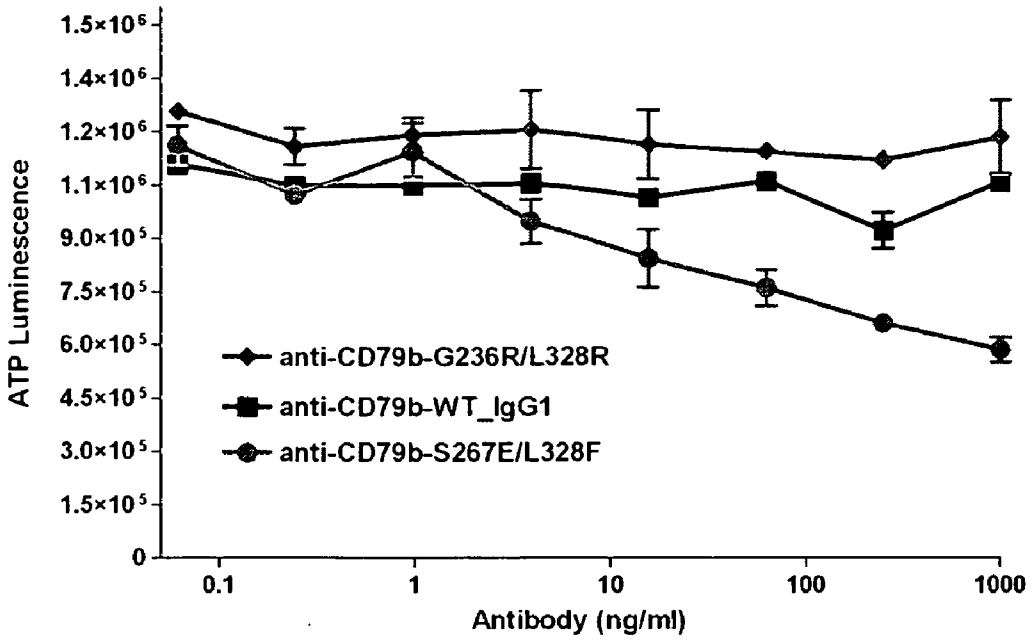


Figure 74

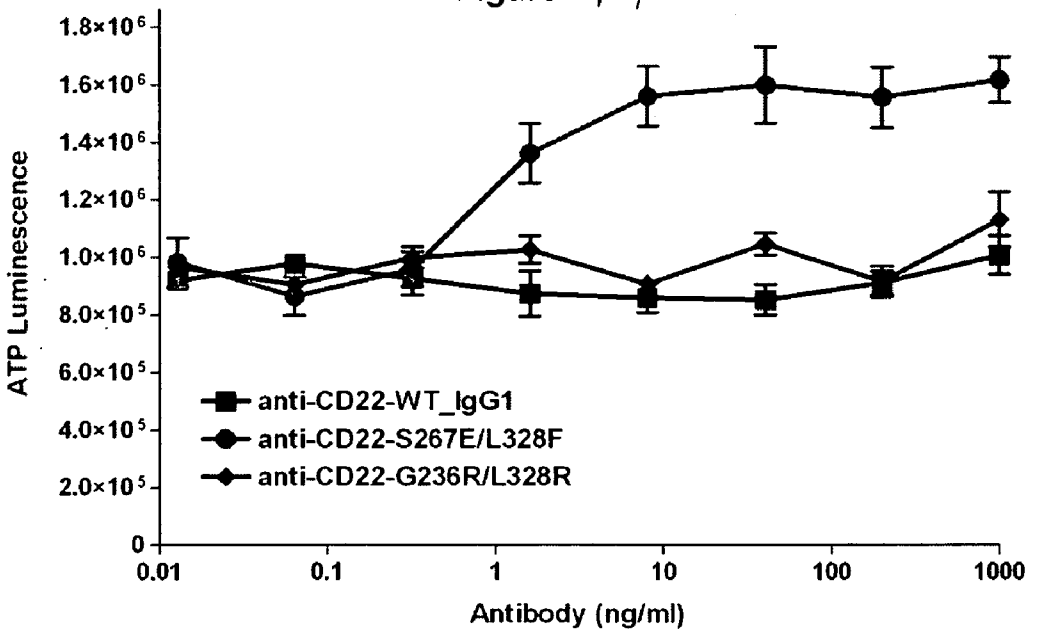


Figure 75A

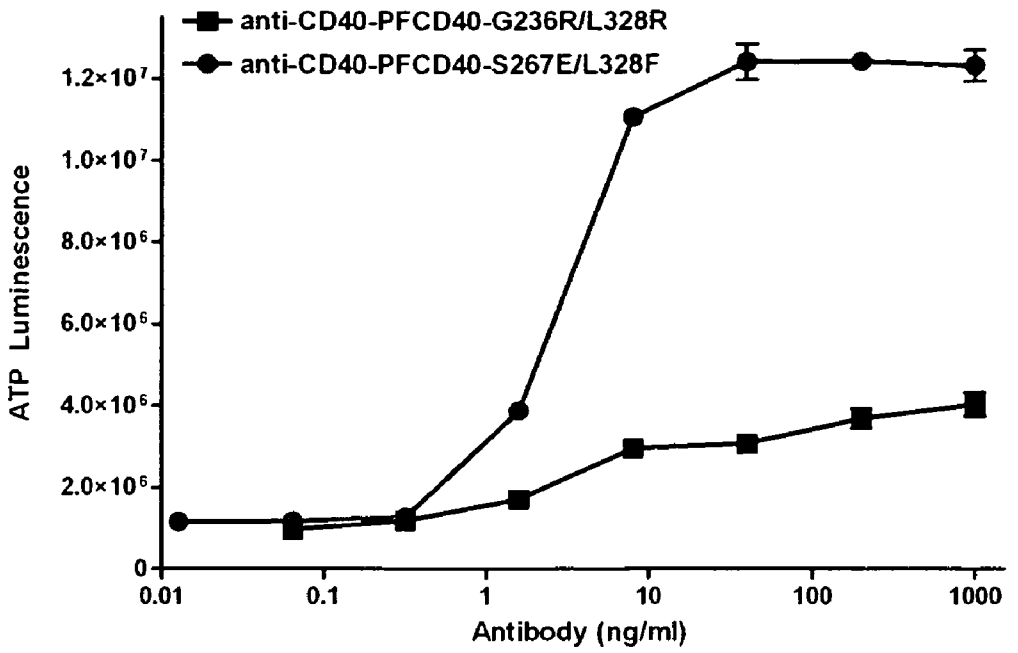


Figure 75B

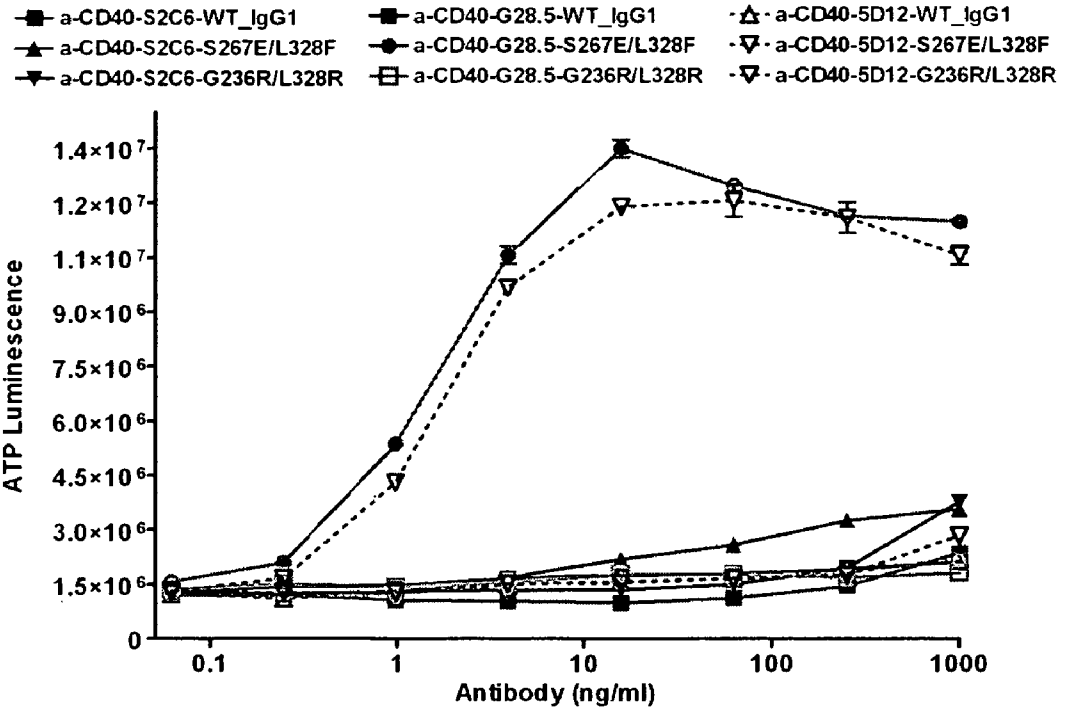


Figure 76

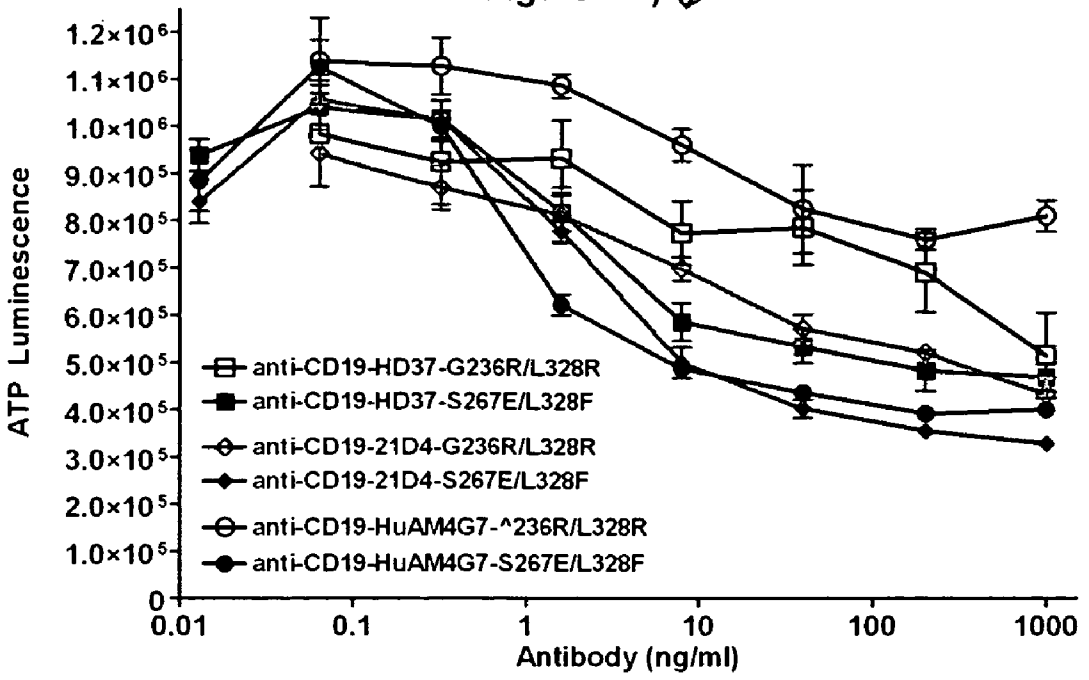

ATP Luminescence
1.2×10⁶
1.1×10⁶
1.0×10⁶
9.0×10⁵
8.0×10⁵
7.0×10⁵
6.0×10⁵
5.0×10⁵
4.0×10⁵
3.0×10⁵
2.0×10⁵
1.0×10⁵
0
0.01
0.1
1
10
100
1000
Antibody (ng/ml)
anti-CD19-HD37-G236R/L328R
anti-CD19-HD37-S267E/L328F
anti-CD19-21D4-G236R/L328R
anti-CD19-21D4-S267E/L328F
anti-CD19-HuAM4G7-^236R/L328R
anti-CD19-HuAM4G7-S267E/L328F

Figure 77A

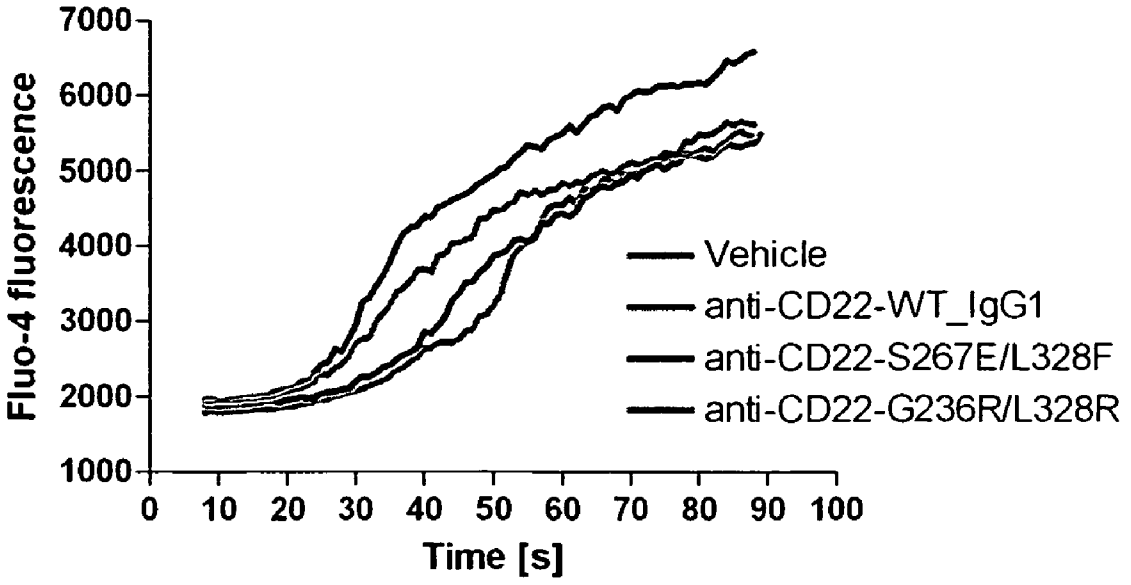


Figure 77B

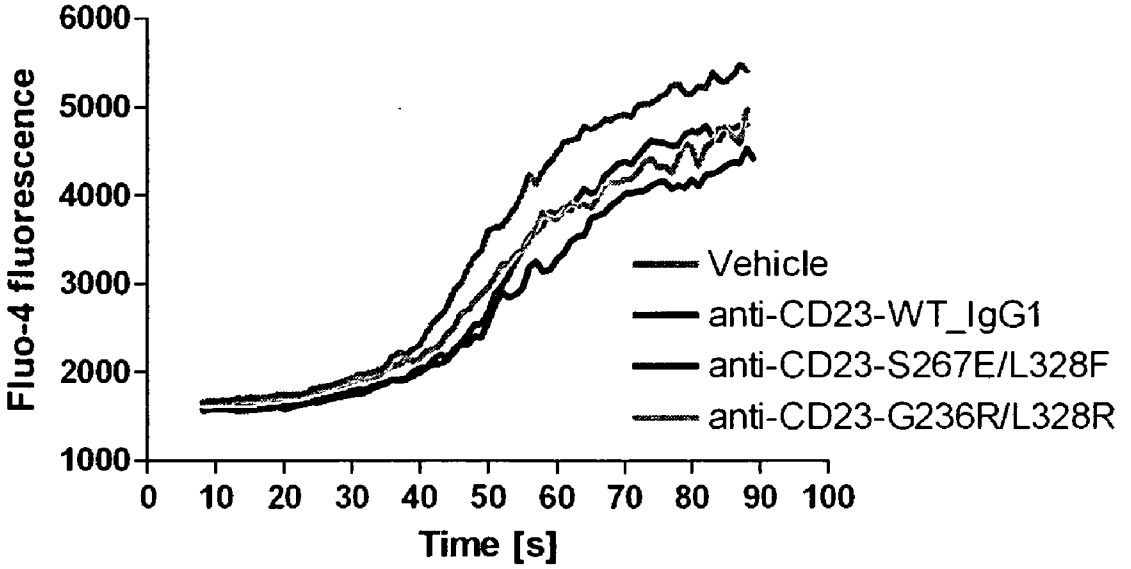


Figure 77C

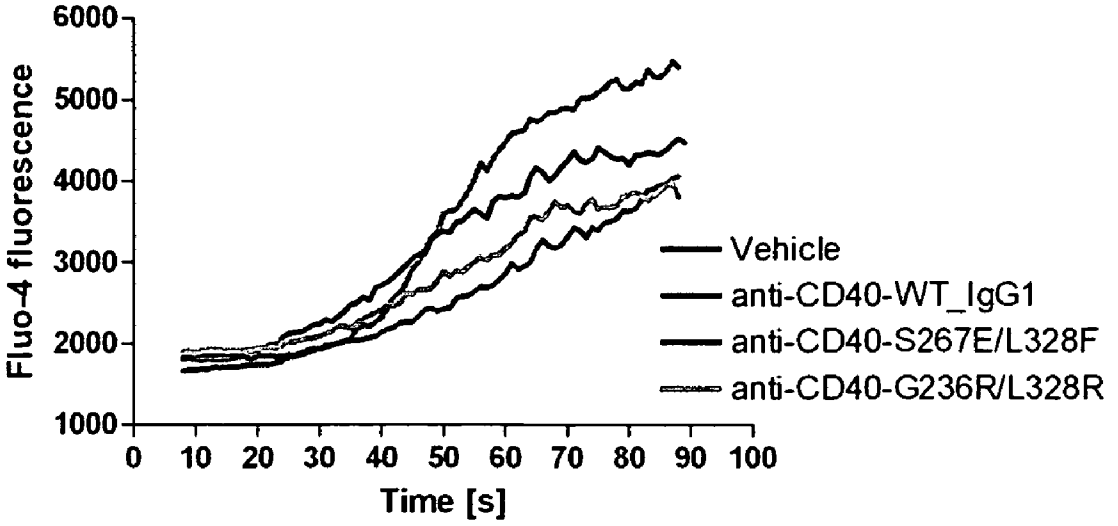


Figure 77D

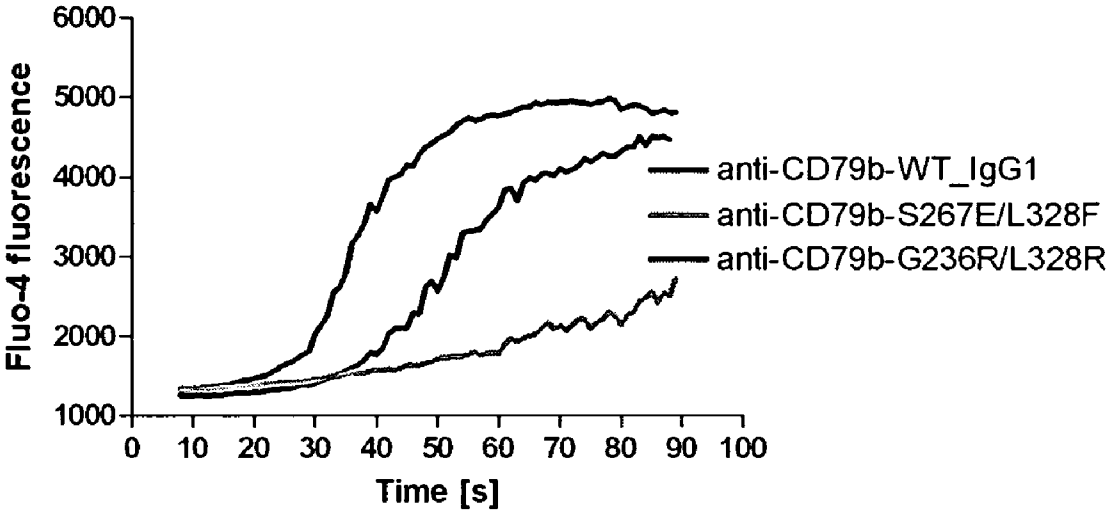


Figure 78

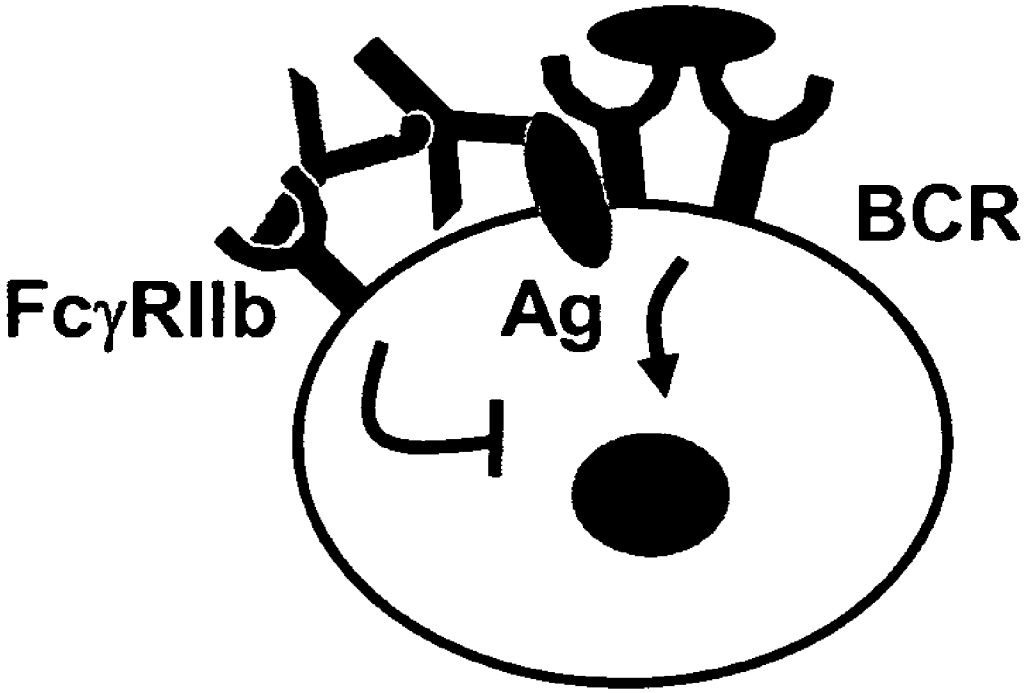


Figure 79

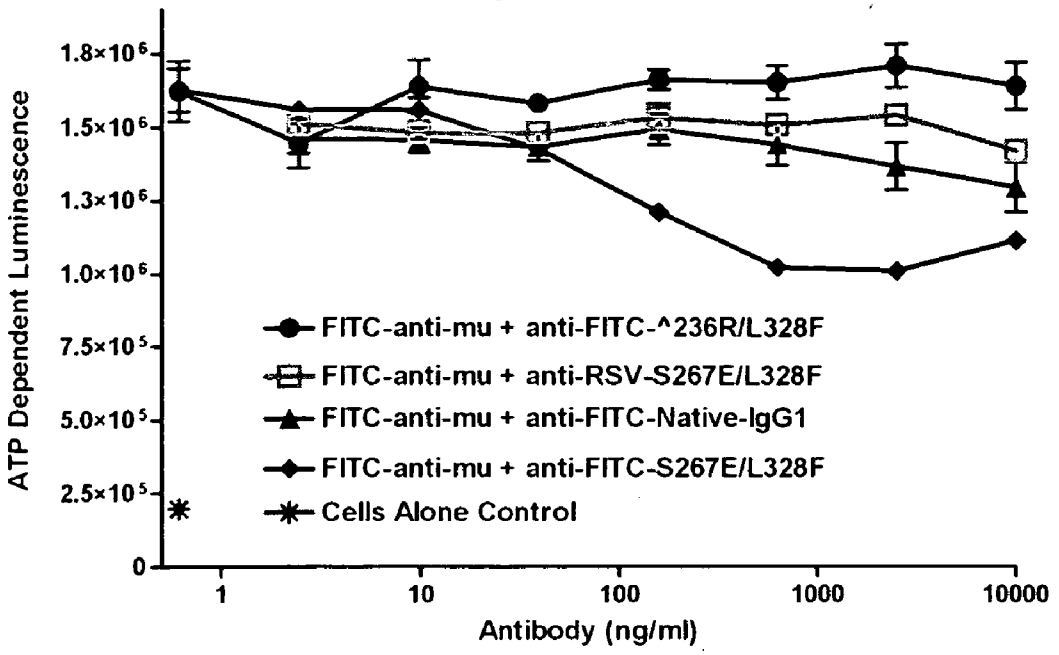


Figure 80

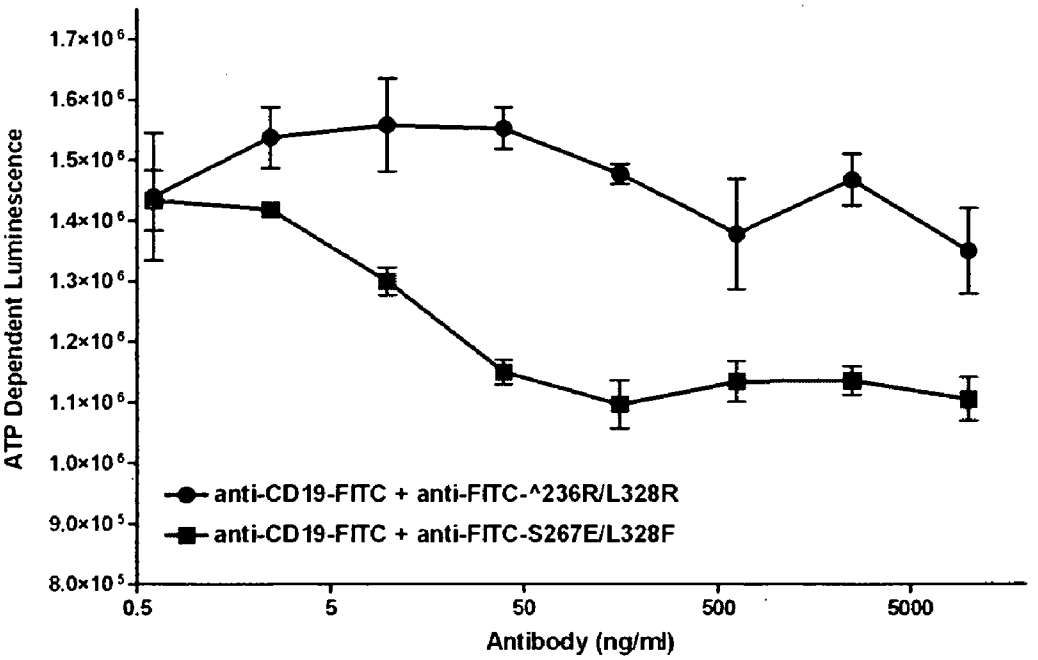


Figure 81A

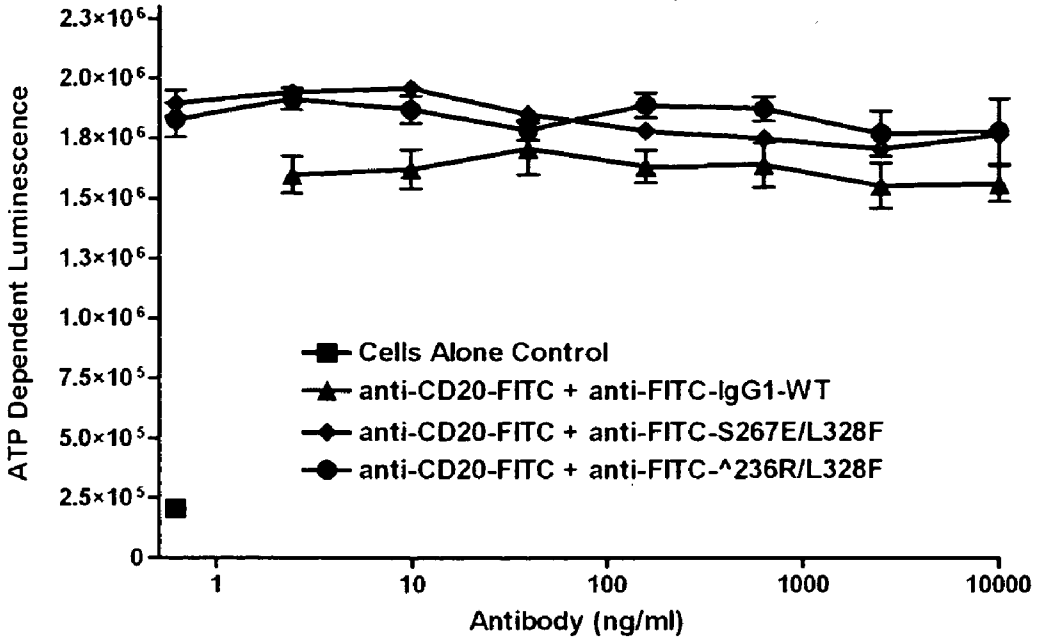


Figure 81B

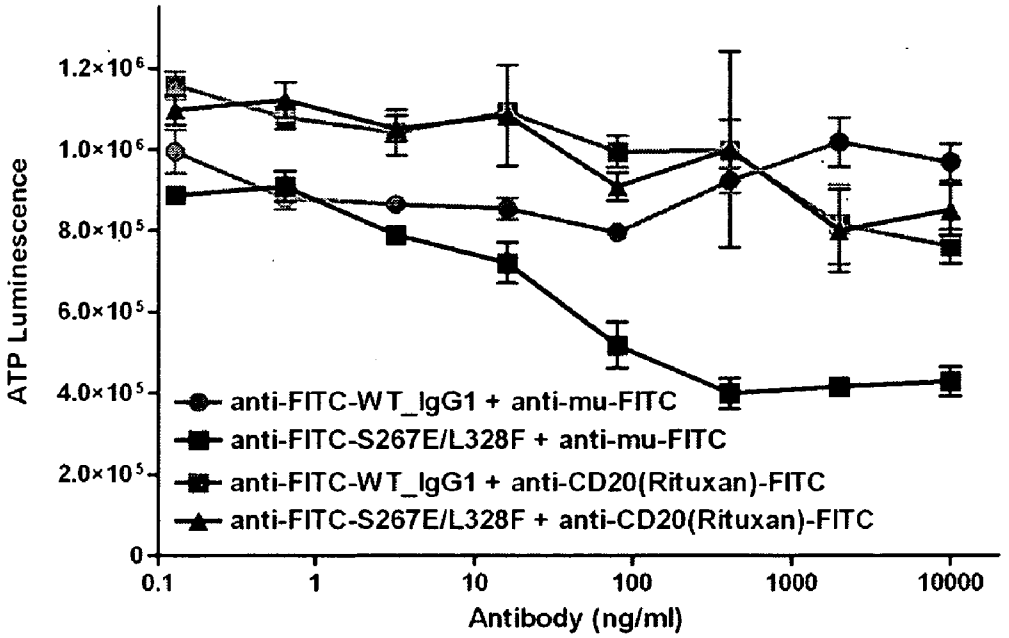


Figure 82

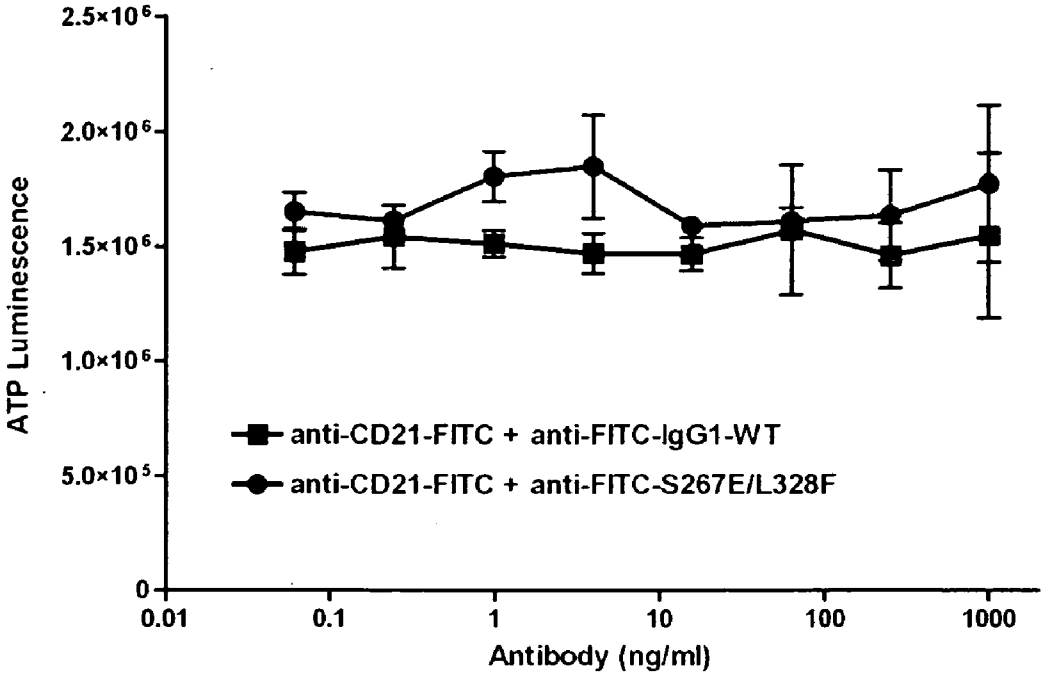


Figure 83

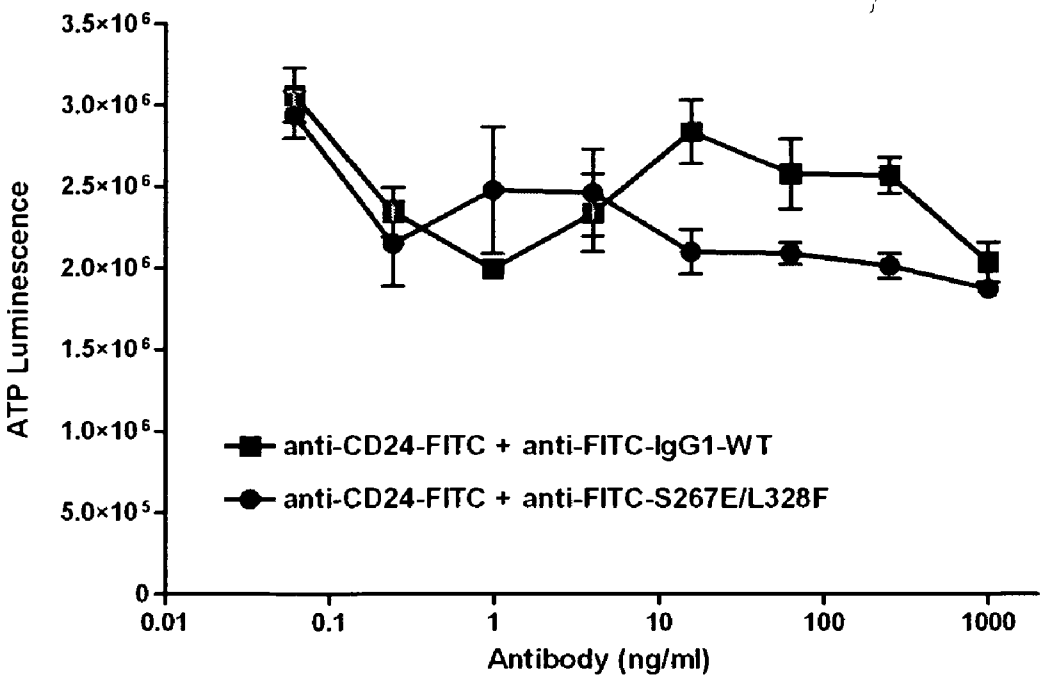


Figure 84

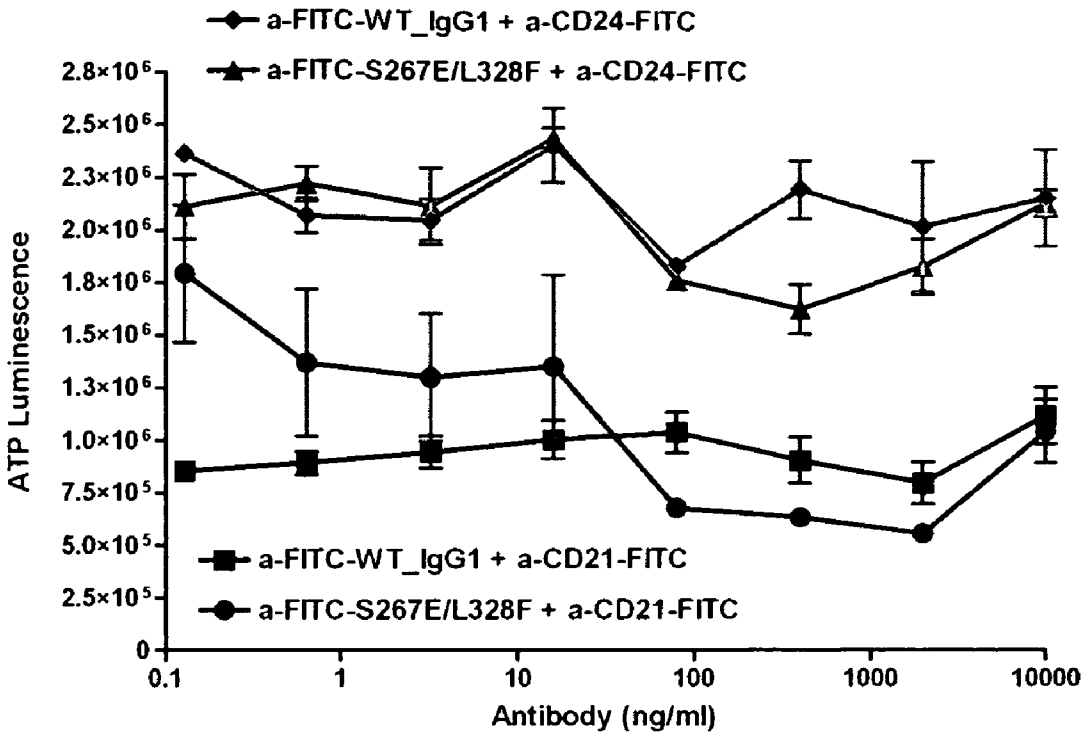


Figure 85

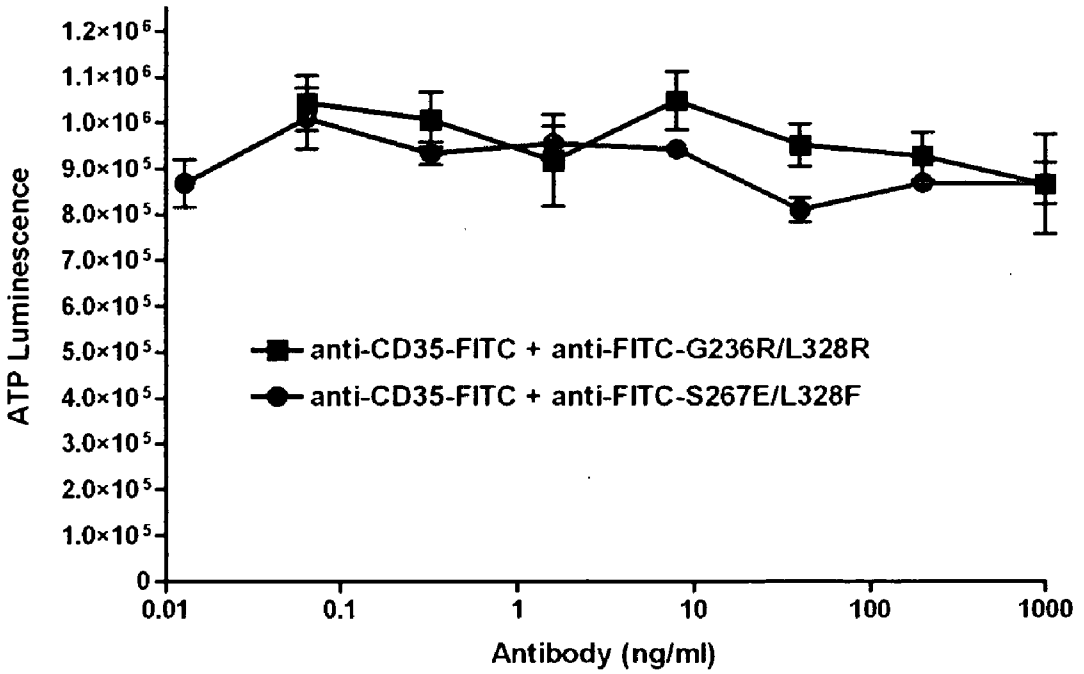


Figure 86

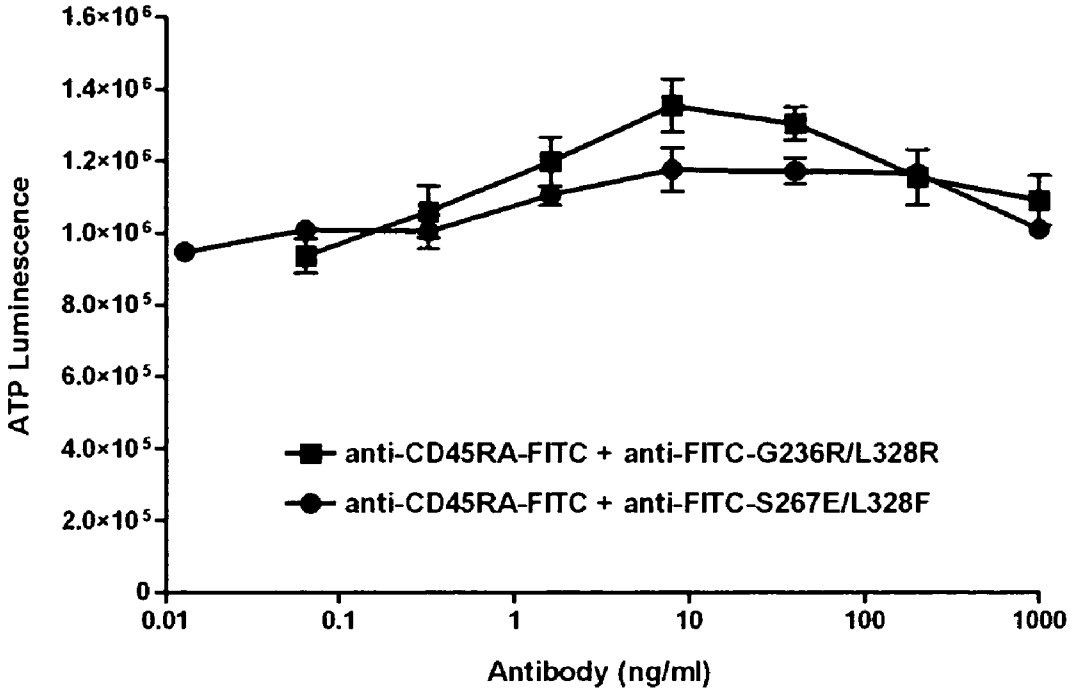


Figure 87

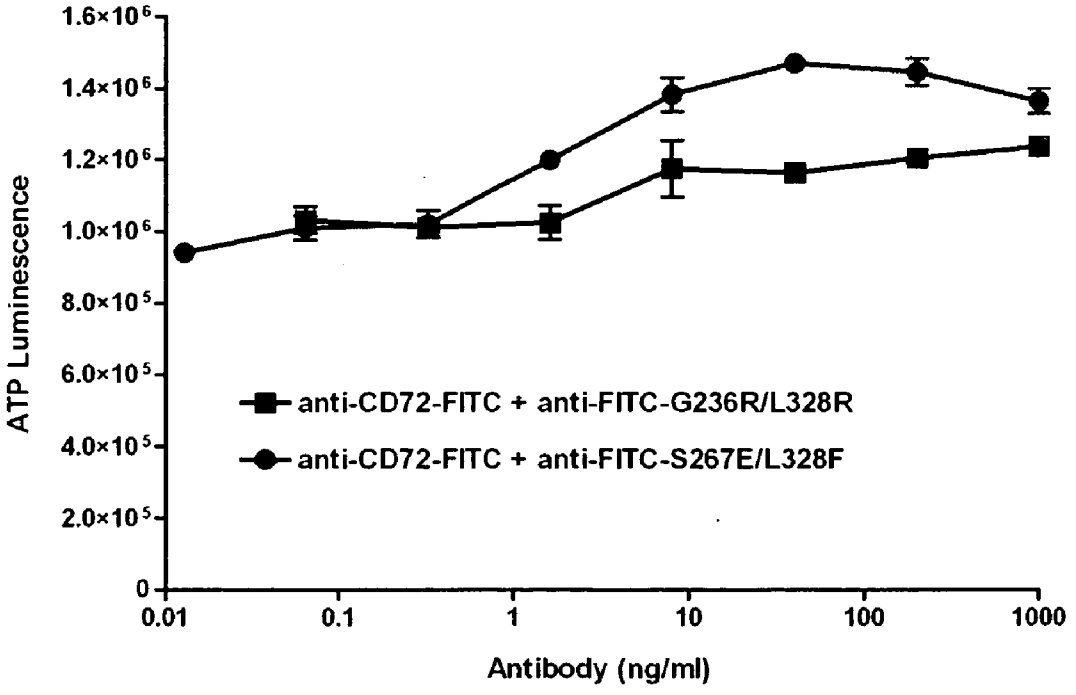


Figure 88

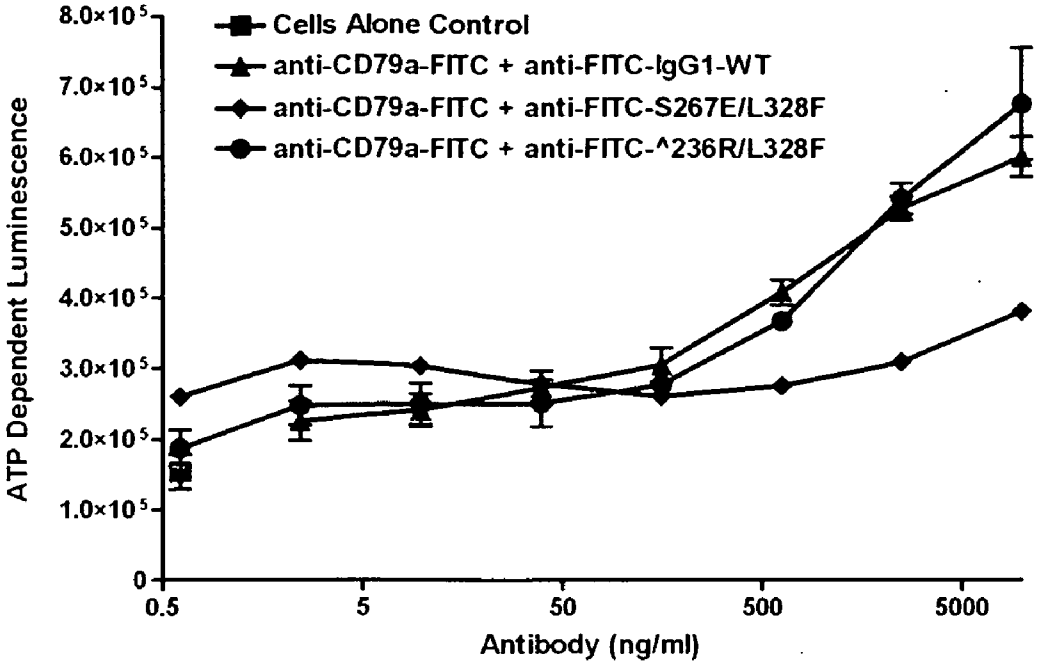


Figure 89

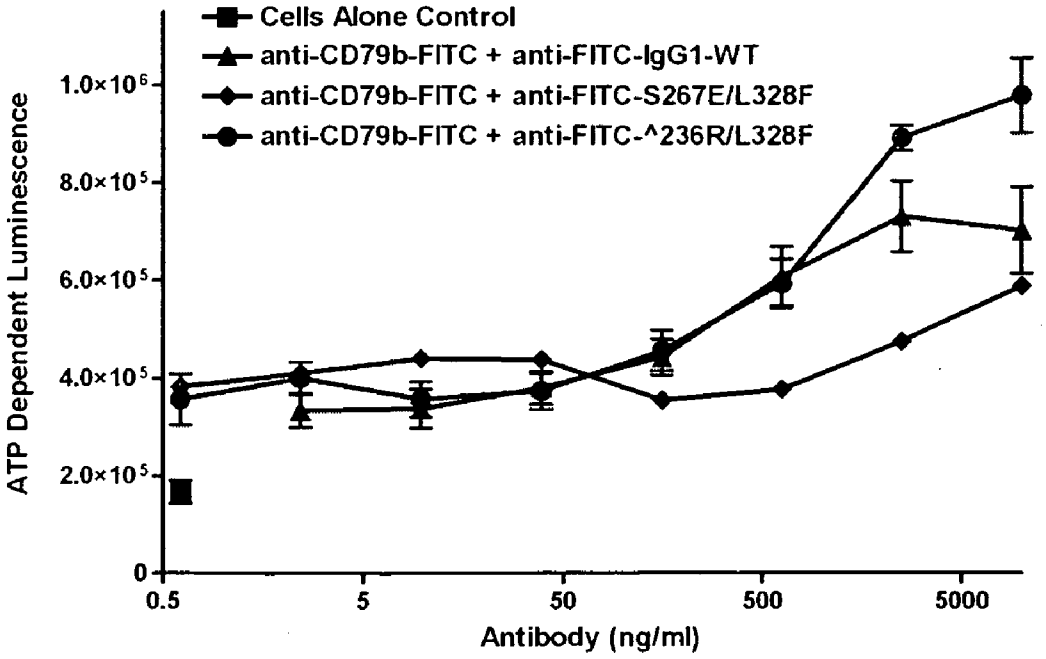


Figure 90

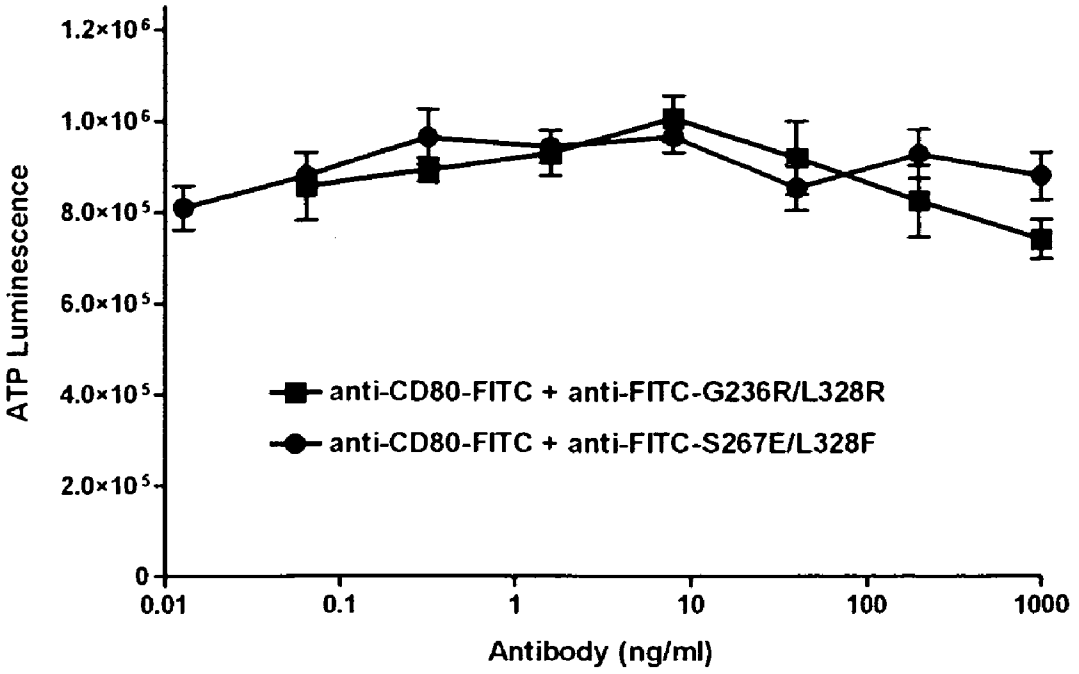


Figure 91

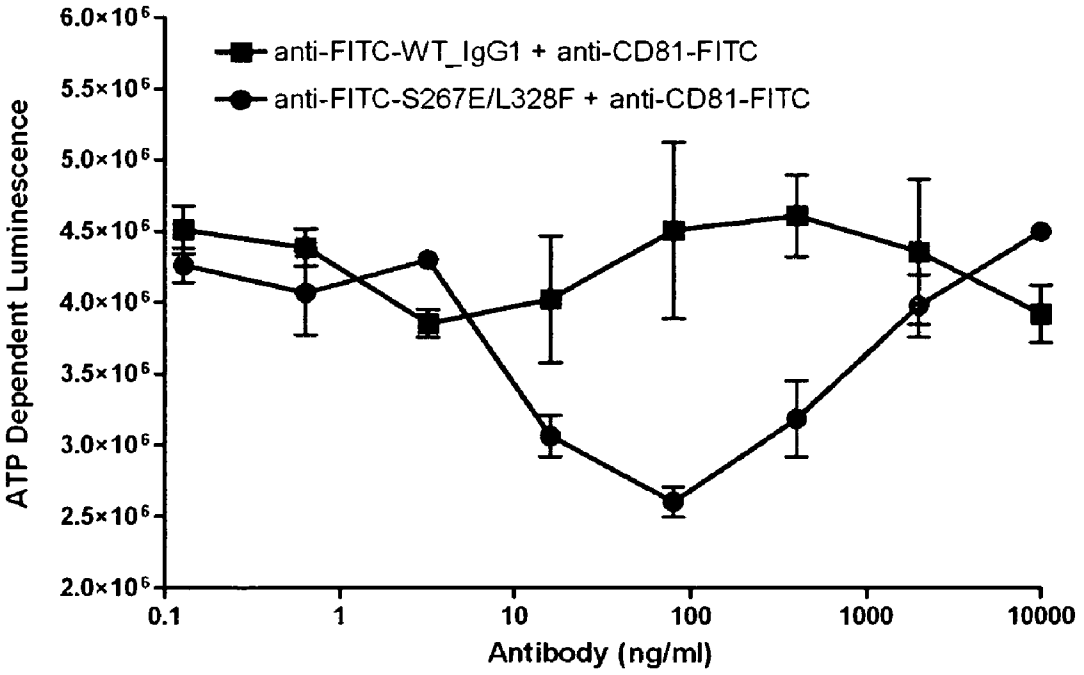


Figure 92

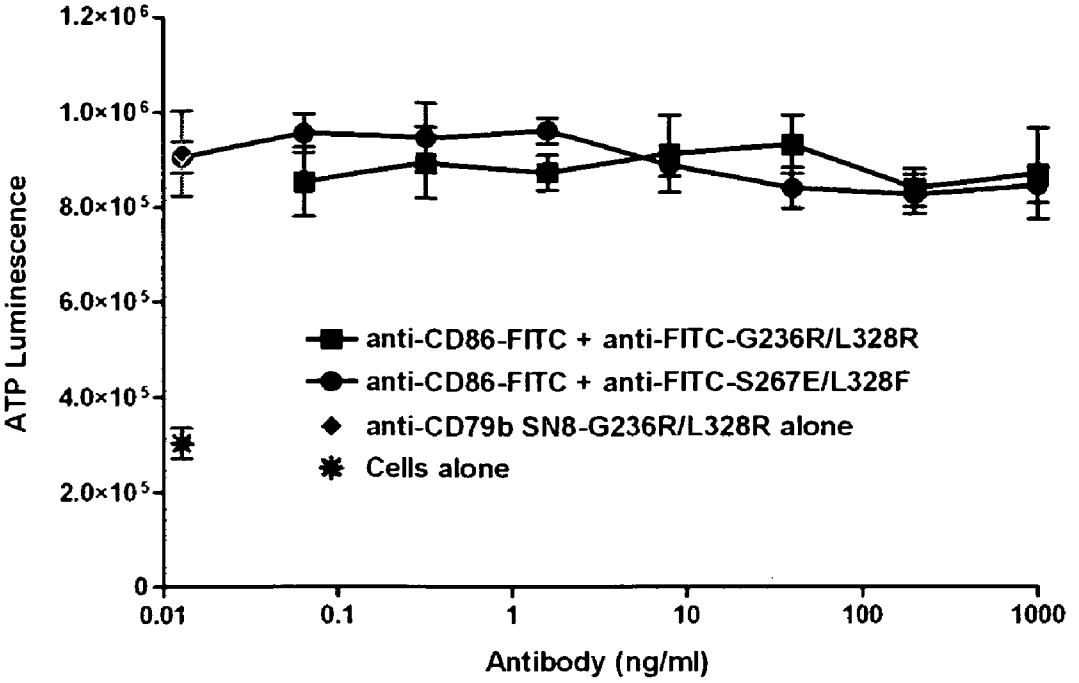


Figure 93

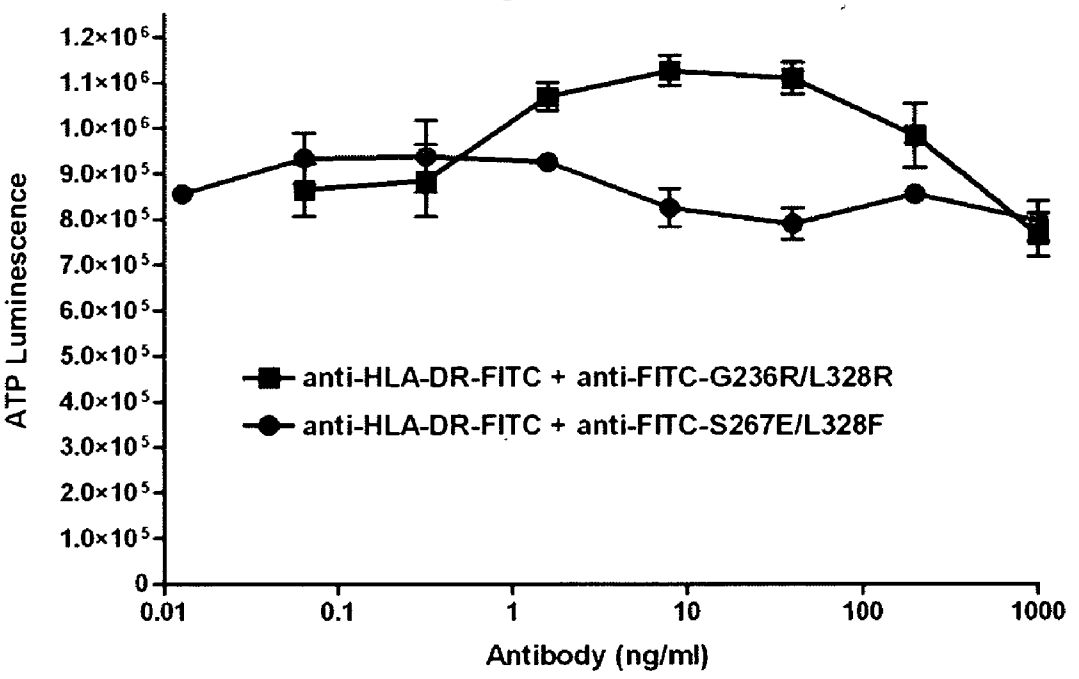


Figure 94

Antigen	Approach	B cell viability	Calcium release
μ	Hapten	Inhibitory	ND
CD19	Fc variant	Inhibitory	Inhibitory
	Hapten	Inhibitory	ND
CD20	Fc variant	Not active	ND
	Hapten	Not active	ND
CD21	Hapten	Not active	ND
CD22	Fc variant	Stimulatory	Stimulatory
CD23	Fc variant	Not active	Not active
CD24	Hapten	Not active	ND
CD35	Hapten	Not active	ND
CD40	Fc variant	Stimulatory	Stimulatory
CD45RA	Hapten	Not active	ND
CD72	Hapten	Stimulatory	ND
CD79a	Hapten	Inhibitory	ND
CD79b	Fc variant	Inhibitory	Inhibitory
	Hapten	Inhibitory	ND
CD80	Hapten	Not active	ND
CD81	Hapten	Possibly inhibitory	ND
CD86	Hapten	Not active	ND
HLA-DR	Hapten	Possibly inhibitory	ND
ND = not determined			

Figure 95

HuAM4G7 VL (SEQ ID NO:1)
DIVMTQSPATLSLSPGERATLSCRSSKSLQNVNGNTYLYWFQQKPGQSPQLLIYRMSNLNSGV
PDRFSGSGSGTEFTLTISSLEPEDFAVYYCMQHLEYPITFGAGTKLEIK
HuAM4G7 VH (SEQ ID NO:2)
EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYNDGTKYNE
KFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSS

Ckappa light chain (SEQ ID NO:3)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Native IgG1 constant chain (SEQ ID NO:4)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK
S267E/L328F IgG1 constant chain (SEQ ID NO:5)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK
G236D/S267E IgG1 constant chain (SEQ ID NO:6)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLDGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
HNHYTQKSLSLSPGK

HuAM4G7 light chain (VH-Cκ) (SEQ ID NO:7)
DIVMTQSPATLSLSPGERATLSCRSSKSLQNVNGNTYLYWFQQKPGQSPQLLIYRMSNLNSGV
PDRFSGSGSGTEFTLTISSLEPEDFAVYYCMQHLEYPITFGAGTKLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

HuAM4G7 IgG1 heavy chain (SEQ ID NO:8)
EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYNDGTKYNE
KFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK

HuAM4G7 S267E/L328F heavy chain (SEQ ID NO:9)

EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYNDGTKYNE
KFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKAFPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK

HuAM4G7 G236D/S267E heavy chain (SEQ ID NO:10)
EVQLVESGGGLVKPGGSLKLSCAASGYTFTSYVMHWVRQAPGKGLEWIGYINPYNDGTKYNE
KFQGRVTISSDKSISTAYMELSSLRSEDTAMYYCARGTYYYGTRVFDYWGQGTLVTVSSASTK
GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLDGPSVFLFPPKPK
DTLMISRTPEVTCVVVDVEHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP
SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK

anti-RSV Numax VL (SEQ ID NO:11)
DIQMTQSPSTLSASVGDRVTITCSASSRVGYMHWYQQKPGKAPKLLIYDTSKLASGVPSRFSG
SGSGTEFTLTISSLQPDDFATYYCFQGSGYPFTFGGGTKVEIK
anti-RSV Numax VH (SEQ ID NO:12)
QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKKHYN
PSLKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARDMIFNFYFDVWGQGTTVTVSS

anti-FITC VL (SEQ ID NO:13)
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLRWYLQKPGQSPKVLIYKVSNRFSGV
PDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK
anti-FITC VH (SEQ ID NO:14)
EVKLDETGGGLVQPGRPMKLSCVASGFTFSDYWMNWVRQSPEKGLEWVAQIRNKPYNYETY
YSDSVKGRFTISRDDSKSSVYLQMNNLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS

anti-CD79b SN8 VL (SEQ ID NO:15)
DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSFLNWYQQKPGQPPKLFIYAASNLESGIPA
RFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPLTFGAGTELELK
anti-CD79b SN8 VH (SEQ ID NO:16)
EVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGGGDTNYNEI
FKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCTRRVPVYFDYWGQGTSVTVSS

anti-CD20 Pro70769 VL (SEQ ID NO:17)
DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKPLIYAPSNLASGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQWSFNPPTFGQGTKVEIK
anti-CD20 Pro70769 VH (SEQ ID NO:18)
EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTSYN
QKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYWYFDVWGQGTLVTVSS

anti-CD52 Campath VL (SEQ ID NO:19)
DIQMTQSPSSLSASVGDRVTITCKASQNIDKYLNWYQQKPGKAPKLLIYNTNNLQTGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCLQHISRPRTFGQGTKVEIK
anti-CD52 Campath VH (SEQ ID NO:20)

QVQLQESGPGLVRPSQTLSLTCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKAKGYTTEY
NPSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAPFDYWGQGSLVTVSS

anti-CD23 5E8 VL (SEQ ID NO:21)
DIQMTQSPSSLSASVGDRVTITCRASQDIRYYLNWYQQKPGKAPKLLIYVASSLQSGVPSRFSG
SGSGTEFTLTVSSLQPEDFATYYCLQVYSTPRTFGQGTKVEIK
anti-CD23 5E8 VH (SEQ ID NO:22)
EVQLVESGGGLAKPGGSLRLSCAASGFRFTFNNYYMDWVRQAPGQGLEWVSRISSSGDPTW
YADSVKGRFTISRENANNTLFLQMNSLRAEDTAVYYCASLTTGSDSWGQGVLVTVSS

anti-CD23 C11 VL (SEQ ID NO:23)
DIVITQDELSNPVTSGESVSISCRSSKSLLYKDGKTYLNWFLQRPGQSPQLLMYLMSTRASGVS
DRFSGSGSGTDFTLEISRVKAEDVGVYYCQQLVEYPFTFGSGTKLEIK
anti-CD23 C11 VH (SEQ ID NO:24)
EVKLEESGGGLVQPGGSMKLSCVASGFTFSGYWMSWVRQSPEKGLEWVAEIRLKSDNYATH
YAESVKGKFTISRDDSKSRLYLQMNSLRAEDSGVYYCTDFIDWGQGTLVTVSS

anti-CD22 RFB4 VL (SEQ ID NO:25)
DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSILHSGVPSRFSGS
GSGTDYSLTISNLEQEDFATYFCQQGNTLPWTFGGGTKLEIK
anti-CD22 RFB4 VH (SEQ ID NO:26)
EVQLVESGGGLVKPGGSLKLSCAASGFAFSIYDMSWVRQTPEKRLEWVAYISSGGGTTYYPD
TVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHSGYGSSYGVLFAYWGQGTLVTTSA

anti-CD40 PFCD40 VL (SEQ ID NO:27)
DIQMTQSPSSVSASVGDRVTITCRASQGIYSWLAWYQQKPGKAPNLLIYTASTLQSGVPSRFS
GSGSGTDFTLTISSLQPEDFATYYCQQANIFPLTFGGGTKVEIK
anti-CD40 PFCD40 VH (SEQ ID NO:28)
QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPDSGGTNY
AQKFQGRVTMTRDTSISTAYMELNRLRSDDTAVYYCARDQPLGYCTNGVCSYFDYWGQGTLV
TVSS

anti-CD40 S2C6 VL (SEQ ID NO:29)
DVVVTQTPLSLPVSLGAQASISCRSSQSLVHSNGNTFLHWYLQKPGQSPKLLIYTVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPWTFGGGTKLEIQ
anti-CD40 S2C6 VH (SEQ ID NO:30)
EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYIHWVKQSHGKSLEWIGRVIPNNGGTSYNQK
FKGKAILTVDKSSSTAYMELRSLTSEDSAVYYCAREGIYWWGHGTTLTVSS

anti-CD40 G28.5 VL (SEQ ID NO:31)
DAVMTQNPLSLPVSLGDEASISCRSSQSLENSNGNTFLNWFFQKPGQSPQLLIYRVSNRFSGV
PDRFSGSGSGTDFTLKISRVEAEDLGVYFCLQVTHVPYTFGGGTTLEIK
anti-CD40 G28.5 VH (SEQ ID NO:32)
DIQLQQSGPGLVKPSQSLSLTCSVTGYSITTNYNWNWIRQFPGNKLEWMGYIRYDGTSEYTPS
LKNRVSITRDTSMNQFFLRLTSVTPEDTATYYCARLDYWGQGTSVTVSS

anti-CD40 5D12 VL (SEQ ID NO:33)
ELQLTQSPLSLPVSLGDQASISCRSSQSLVNSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK
anti-CD40 5D12 VH (SEQ ID NO:34)

QVKLEESGPGLVAPSQSLSITCTVSGFSLSRYSVYWVRQPPGKGLEWLGMMWGGGSTDYNS
ALKSRLSISKDTSKSQVFLKMNSLQTDDTAMYYCVRTDGDYWGQGTSVTVSS

anti-CD19 HD37 VL (SEQ ID NO:35)
DILLTQTPASLAVSLGQRATISCKASQSVDYDGDSYLNWYQQIPGQPPKLLIYDASNLVSGIPPR
FSGSGSGTDFTLNIHPVEKVDAATYHCQQSTEDPWTFGGGTKLEIK
anti-CD19 HD37 VH (SEQ ID NO:36)
QVQLQQSGAELVRPGSSVKISCKASGYAFSSYWMNWVKQRPGQGLEWIGQIWPGDGDTNYN
GKFKGKATLTADESSSTAYMQLSSLASEDSAVYFCARRETTTVGRYYYAMDYWGQGTSVTVS
S

anti-CD19 21D4 VL (SEQ ID NO:37)
AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQFNSYPYTFGQGTKLEIK
anti-CD19 21D4 VH (SEQ ID NO:38)
EVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGWVRQMPGKGLEWMGIIYPDDSDTRYSP
SFQGQVTISADKSIRTAYLQWSSLKASDTAMYYCARHVTMWGVIIDFWGQGTLVTVSS

anti-CD19 murine 4G7 VL (SEQ ID NO:39)
DIVMTQAAPSIPVTPGESVSISCRSSKSLLNSNGNTYLYWFLQRPGQSPQLLIYRMSNLASGVP
DRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYPFTFGAGTKLELK
anti-CD19 murine 4G7 VH (SEQ ID NO:40)
EVQLQQSGPELIKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKYNE
KFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCARGTYYYGSRVFDYWGQGTTLTVSS

OPTIMIZED FC VARIANTS

[0001] This application claims benefit under 35 U.S.C. §119(e) to U.S. Provisional Application Nos. 60/940,776 (filed May 30, 2007); 60/953,174 (filed Jul. 31, 2007); 60/970,413 (filed Sep. 6, 2007); 60/976,279 (filed Sep. 28, 2007); 60/990,509 (filed Nov. 27, 2007); 61/012,035 (filed Dec. 6, 2007); 61/013,775 (filed Dec. 14, 2007), 61/019,395 (filed Jan. 7, 2008), 61/032,059 (filed Feb. 27, 2008), 61/043,585 (filed Apr. 9, 2008), and 61/046,397 (filed Apr. 18, 2008); and is a continuation-in-part of U.S. patent application Ser. No. 11/124,620, filed May 5, 2005, which claims benefit under 35 U.S.C. §119(e) to U.S. Provisional Patent Application Nos. 60/568,440, filed May 5, 2004; 60/589,906, filed Jul. 20, 2004; 60/627,026, filed Nov. 9, 2004; 60/626,991 filed Nov. 10, 2004; and 60/627,774 filed Nov. 12, 2004. U.S. patent application Ser. No. 11/124,620 is a continuation-in-part of U.S. patent application Ser. No. 10/822,231 filed Mar. 26, 2004 (now U.S. Pat. No. 7,317,091), which claims benefit under 35 U.S.C. §119(e) to U.S. Provisional Patent Application Nos. 60/477,839 filed Jun. 12, 2003, and 60/467,606, filed May 2, 2003. U.S. patent application Ser. No. 10/822,231 is a continuation-in-part of U.S. patent application Ser. No. 10/672,280 filed Sep. 26, 2003, which claims benefit under 35 U.S.C. §119(e) to U.S. Provisional Patent Application Nos. 60/477,839 filed Jun. 12, 2003; 60/467,606, filed May 2, 2003; 60/414,433 filed Sep. 27, 2002; and 60/442,301 filed Jan. 23, 2003. U.S. patent application Ser. No. 10/672,280 is a continuation-in-part of U.S. patent application Ser. No. 10/379,392 filed Mar. 3, 2003 (now abandoned), which claims benefit under 35 U.S.C. §119(e) to U.S. Provisional Patent Application Nos. 60/360,843, filed Mar. 1, 2002, and 60/384,197, filed May 29, 2002; and 60/414,433, filed Sep. 27, 2002. All of the above referenced patent application are each incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention relates to novel optimized Fc variants, engineering methods for their generation, and their application, particularly for therapeutic purposes.

BACKGROUND OF THE INVENTION

[0003] Antibodies are immunological proteins that bind a specific antigen. In most mammals, including humans and mice, antibodies are constructed from paired heavy and light polypeptide chains. Each chain is made up of individual immunoglobulin (Ig) domains, and thus the generic term immunoglobulin is used for such proteins. Each chain is made up of two distinct regions, referred to as the variable and constant regions. The light and heavy chain variable regions show significant sequence diversity between antibodies, and are responsible for binding the target antigen. The constant regions show less sequence diversity, and are responsible for binding a number of natural proteins to elicit important biochemical events. In humans there are five different classes of antibodies including IgA (which includes subclasses IgA1 and IgA2), IgD, IgE, IgG (which includes subclasses IgG1, IgG2, IgG3, and IgG4), and IgM. The distinguishing features between these antibody classes are their constant regions, although subtler differences may exist in the variable region. FIG. **1** shows an IgG1 antibody, used here as an example to describe the general structural features of immunoglobulins. IgG antibodies are tetrameric proteins composed of two heavy chains and two light chains. The IgG heavy chain is composed of four immunoglobulin domains linked from N- to C-terminus in the order V_H-C_H1-C_H2-C_H3, referring to the variable heavy domain, constant heavy domain 1, constant heavy domain 2, and constant heavy domain 3. The IgG C_H1, C_H2, and C_H3 domains are also referred to as constant gamma 1 domain (Cγ1), constant gamma 2 domain (Cγ2), and constant gamma 3 domain (Cγ3) respectively. The IgG light chain is composed of two immunoglobulin domains linked from N- to C-terminus in the order V_L-C_L, referring to the light chain variable domain and the light chain constant domain respectively.

[0004] The variable region of an antibody contains the antigen binding determinants of the molecule, and thus determines the specificity of an antibody for its target antigen. The variable region is so named because it is the most distinct in sequence from other antibodies within the same class. The majority of sequence variability occurs in the complementarity determining regions (CDRs). There are 6 CDRs total, three each per heavy and light chain, designated V_H CDR1, V_H CDR2, V_H CDR3, V_L CDR1, V_L CDR2, and V_L CDR3. The variable region outside of the CDRs is referred to as the framework (FR) region. Although not as diverse as the CDRs, sequence variability does occur in the FR region between different antibodies. Overall, this characteristic architecture of antibodies provides a stable scaffold (the FR region) upon which substantial antigen binding diversity (the CDRs) can be explored by the immune system to obtain specificity for a broad array of antigens. A number of high-resolution structures are available for a variety of variable region fragments from different organisms, some unbound and some in complex with antigen. The sequence and structural features of antibody variable regions are well characterized (Morea et al., 1997, Biophys Chem 68:9-16; Morea et al., 2000, Methods 20:267-279, incorporated by reference), and the conserved features of antibodies have enabled the development of a wealth of antibody engineering techniques (Maynard et al., 2000, Annu Rev Biomed Eng 2:339-376, incorporated by reference). For example, it is possible to graft the CDRs from one antibody, for example a murine antibody, onto the framework region of another antibody, for example a human antibody. This process, referred to in the art as "humanization", enables generation of less immunogenic antibody therapeutics from nonhuman antibodies. Fragments comprising the variable region can exist in the absence of other regions of the antibody, including for example the antigen binding fragment (Fab) comprising V_H-Cγ1 and V_H-C_L, the variable fragment (Fv) comprising V_H and V_L, the single chain variable fragment (scFv) comprising V_H and V_L linked together in the same chain, as well as a variety of other variable region fragments (Little et al., 2000, Immunol Today 21:364-370, incorporated by reference).

[0005] The Fc region of an antibody interacts with a number of Fc receptors and ligands, imparting an array of important functional capabilities referred to as effector functions. For IgG the Fc region, as shown in FIG. **1**, comprises Ig domains Cγ2 and Cγ3 and the N-terminal hinge leading into Cγ2. An important family of Fc receptors for the IgG class are the Fc gamma receptors (FcγRs). These receptors mediate communication between antibodies and the cellular arm of the immune system (Raghavan et al., 1996, Annu Rev Cell Dev Biol 12:181-220; Ravetch et al., 2001, Annu Rev Immunol 19:275-290). In humans this protein family includes

FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and FcγRIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIIb-NA1 and FcγRIIIb-NA2) (Jefferis et al., 2002, Immunol Lett 82:57-65, incorporated by reference). These receptors typically have an extracellular domain that mediates binding to Fc, a membrane spanning region, and an intracellular domain that may mediate some signaling event within the cell. These receptors are expressed in a variety of immune cells including monocytes, macrophages, neutrophils, dendritic cells, eosinophils, mast cells, platelets, B cells, large granular lymphocytes, Langerhans' cells, natural killer (NK) cells, and γδ T cells. Formation of the Fc/FcγR complex recruits these effector cells to sites of bound antigen, typically resulting in signaling events within the cells and important subsequent immune responses such as release of inflammation mediators, B cell activation, endocytosis, phagocytosis, and cytotoxic attack. The ability to mediate cytotoxic and phagocytic effector functions is a potential mechanism by which antibodies destroy targeted cells. The cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell is referred to as antibody dependent cell-mediated cytotoxicity (ADCC) (Raghavan et al., 1996, Annu Rev Cell Dev Biol 12:181-220; Ghetie et al., 2000, Annu Rev Immunol 18:739-766; Ravetch et al., 2001, Annu Rev Immunol 19:275-290, incorporated by reference). The cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause phagocytosis of the target cell is referred to as antibody dependent cell-mediated phagocytosis (ADCP). A number of structures have been solved of the extracellular domains of human FcγRs, including FcγRIIa (pdb accession code 1H9V) (Sondermann et al., 2001, J Mol Biol 309:737-749) (pdb accession code 1 FCG) (Maxwell et al., 1999, Nat Struct Biol 6:437-442), FcγRIIb (pdb accession code 2FCB) (Sondermann et al., 1999, Embo J 18:1095-1103); and FcγRIIIb (pdb accession code 1E4J) (Sondermann et al., 2000, Nature 406:267-273, incorporated by reference). All FcγRs bind the same region on Fc, at the N-terminal end of the Cγ2 domain and the preceding hinge, shown in FIG. **2**. This interaction is well characterized structurally (Sondermann et al., 2001, J Mol Biol 309:737-749 incorporated by reference), and several structures of the human Fc bound to the extracellular domain of human FcγRIIIb have been solved (pdb accession code 1E4K)(Sondermann et al., 2000, Nature 406:267-273) (pdb accession codes 1IIS and 1IIX) (Radaev et al., 2001, J Biol Chem 276:16469-16477, incorporated by reference), as well as has the structure of the human IgE Fc/FcεRIα complex (pdb accession code 1F6A) (Garman et al., 2000, Nature 406:259-266, incorporated by reference).

[0006] The different IgG subclasses have different affinities for the FcγRs, with IgG1 and IgG3 typically binding substantially better to the receptors than IgG2 and IgG4. All FcγRs bind the same region on IgG Fc, yet with different affinities: the high affinity binder FcγRI has a Kd for IgG1 of 10^{-8} M^{-1}, whereas the low affinity receptors FcγRII and FcγRIII generally bind at 10^{-6} and 10^{-5} respectively. The extracellular domains of FcγRIIIa and FcγRIIIb are 96% identical, however FcγRIIIb does not have a intracellular signaling domain. Furthermore, whereas FcγRI, FcγRIIa/c, and FcγRIIIa are positive regulators of immune complex-triggered activation, characterized by having an intracellular domain that has an immunoreceptor tyrosine-based activation motif (ITAM), FcγRIIb has an immunoreceptor tyrosine-based inhibition motif (ITIM) and is therefore inhibitory. Thus the former are referred to as activation receptors, and FcγRIIb is referred to as an inhibitory receptor. The receptors also differ in expression pattern and levels on different immune cells. Yet another level of complexity is the existence of a number of FcγR polymorphisms in the human proteome. A particularly relevant polymorphism with clinical significance is V158/F158 FcγRIIIa. Human IgG1 binds with greater affinity to the V158 allotype than to the F158 allotype. This difference in affinity, and presumably its effect on ADCC and/or ADCP, has been shown to be a significant determinant of the efficacy of the anti-CD20 antibody rituximab (Rituxan®, a registered trademark of IDEC Pharmaceuticals Corporation). Patients with the V158 allotype respond favorably to rituximab treatment; however, patients with the lower affinity F158 allotype respond poorly (Cartron et al., 2002, Blood 99:754-758, incorporated by reference). Approximately 10-20% of humans are V158/V158 homozygous, 45% are V158/F158 heterozygous, and 35-45% of humans are F158/F158 homozygous (Lehrnbecher et al., 1999, Blood 94:4220-4232; Cartron et al., 2002, Blood 99:754-758, incorporated by reference). Thus 80-90% of humans are poor responders, that is they have at least one allele of the F158 FcγRIIIa.

[0007] An overlapping but separate site on Fc, shown in FIG. **1**, serves as the interface for the complement protein C1q. In the same way that Fc/FcγR binding mediates ADCC, Fc/C1q binding mediates complement dependent cytotoxicity (CDC). C1q forms a complex with the serine proteases C1r and C1s to form the C1 complex. C1q is capable of binding six antibodies, although binding to two IgGs is sufficient to activate the complement cascade. Similar to Fc interaction with FcγRs, different IgG subclasses have different affinity for C1q, with IgG1 and IgG3 typically binding substantially better to the FcγRs than IgG2 and IgG4. There is currently no structure available for the Fc/C1q complex; however, mutagenesis studies have mapped the binding site on human IgG for C1q to a region involving residues D270, K322, K326, P329, and P331, and E333 (Idusogie et al., 2000, *J Immunol* 164:4178-4184; Idusogie et al., 2001, *J Immunol* 166:2571-2575, incorporated by reference).

[0008] A site on Fc between the Cγ2 and Cγ3 domains, shown in FIG. **1**, mediates interaction with the neonatal receptor FcRn, the binding of which recycles endocytosed antibody from the endosome back to the bloodstream (Raghavan et al., 1996, *Annu Rev Cell Dev Biol* 12:181-220; Ghetie et al., 2000, *Annu Rev Immunol* 18:739-766, incorporated by reference). This process, coupled with preclusion of kidney filtration due to the large size of the full length molecule, results in favorable antibody serum half-lives ranging from one to three weeks. Binding of Fc to FcRn also plays a key role in antibody transport. The binding site for FcRn on Fc is also the site at which the bacterial proteins A and G bind. The tight binding by these proteins is typically exploited as a means to purify antibodies by employing protein A or protein G affinity chromatography during protein purification. Thus the fidelity of this region on Fc is important for both the clinical properties of antibodies and their purification. Available structures of the rat Fc/FcRn complex (Martin et al., 2001, *Mol Cell* 7:867-877, incorporated by reference), and of

the complexes of Fc with proteins A and G (Deisenhofer, 1981, *Biochemistry* 20:2361-2370; Sauer-Eriksson et al., 1995, *Structure* 3:265-278; Tashiro et al., 1995, *Curr Opin Struct Biol* 5:471-481, incorporated by reference) provide insight into the interaction of Fc with these proteins.

[0009] A key feature of the Fc region is the conserved N-linked glycosylation that occurs at N297, shown in FIG. **1**. This carbohydrate, or oligosaccharide as it is sometimes referred, plays a critical structural and functional role for the antibody, and is one of the principle reasons that antibodies must be produced using mammalian expression systems. While not wanting to be limited to one theory, it is believed that the structural purpose of this carbohydrate may be to stabilize or solubilize Fc, determine a specific angle or level of flexibility between the Cγ3 and Cγ2 domains, keep the two Cγ2 domains from aggregating with one another across the central axis, or a combination of these. Efficient Fc binding to FcγR and C1q requires this modification, and alterations in the composition of the N297 carbohydrate or its elimination affect binding to these proteins (Umaña et al., 1999, *Nat Biotechnol* 17:176-180; Davies et al., 2001, *Biotechnol Bioeng* 74:288-294; Mimura et al., 2001, *J Biol Chem* 276: 45539-45547.; Radaev et al., 2001, *Biol Chem* 276:16478-16483; Shields et al., 2001, *J Biol Chem* 276:6591-6604; Shields et al., 2002, *J Biol Chem* 277:26733-26740; Simmons et al., 2002, *J Immunol Methods* 263:133-147, incorporated by reference). Yet the carbohydrate makes little if any specific contact with FcγRs (Radaev et al., 2001, *J Biol Chem* 276: 16469-16477, incorporated by reference), indicating that the functional role of the N297 carbohydrate in mediating Fc/FcγR binding may be via the structural role it plays in determining the Fc conformation. This is supported by a collection of crystal structures of four different Fc glycoforms, which show that the composition of the oligosaccharide impacts the conformation of Cγ2 and as a result the Fc/FcγR interface (Krapp et al., 2003, *J Mol Biol* 325:979-989, incorporated by reference).

[0010] Antigen recognition by B cells is mediated by the B cell receptor (BCR), a surface-bound immunoglobulin in complex with signaling components CD79a (Igα) and CD79b (Igβ). Crosslinking of BCR upon engagement of antigen results in phosphorylation of immunoreceptor tyrosine-based activation motifs (ITAMs) within CD79a and CD79b, initiating a cascade of intracellular signaling events that recruit downstream molecules to the membrane and stimulate calcium mobilization. This leads to the induction of diverse B cell responses (e.g., cell survival, proliferation, antibody production, antigen presentation, and differentiation, etc.) which lead to a humoral immune response (DeFranco, A. L., 1997, Curr. Opin. Immunol. 9, 296-308; Pierce, S. K., 2002, Nat. Rev. Immunol. 2, 96-105; Ravetch, J. V. & Lanier, L. L., 2000, Science 290, 84-89). Other components of the BCR coreceptor complex enhance (e.g., CD19, CD21, and CD81) or suppress (e.g., CD22 and CD72) BCR activation signals (Doody, G. M. et al., 1996, Curr. Opin. Immunol. 8, 378-382; L1, D. H. et al., 2006, J. Immunol. 176, 5321-5328). In this way, the immune system maintains multiple BCR regulatory mechanisms to ensure that B cell responses including antibody production and antigen presentation are tightly controlled.

[0011] When antibodies are produced to an antigen, the circulating level of immune complexes (e.g., antigen bound to antibody) increases. These immune complexes downregulate antigen-induced B cell activation. It is believed that these immune complexes downregulate antigen-induced B cell activation by coengaging cognate BCR with the low-affinity inhibitory receptor Fc□RIIb, the only IgG receptor on B cells (Heyman, B., 2003, Immunol. Lett. 88, 157-161). It is also believed that this negative feedback of antibody production requires interaction of the antibody Fc domain with FcγRIIb since immune complexes containing F(ab')2 antibody fragments are not inhibitory (Chan, P. L. & Sinclair, N. R., 1973, Immunology 24, 289-301). The intracellular immunoreceptor tyrosine-based inhibitory motif (ITIM) of Fc□RIIb is necessary to inhibit BCR-induced intracellular signals (Amigorena, S. et al., 1992, Science 256, 1808-1812; Muta, T., et al., 1994, Nature 368, 70-73). This inhibitory effect occurs through phosphorylation of the Fc□RIIb ITIM, which recruits SH2-containing inositol polyphosphate 5-phosphatase (SHIP) to neutralize ITAM-induced intracellular calcium mobilization (Kiener, P. A., et al., 1997, J. Biol. Chem. 272, 3838-3844; Ono, M., et al., 1996, Nature 383, 263-266; Ravetch, J. V. & Lanier, L. L., 2000, Science 290, 84-89). In addition, FcγRIIb-mediated SHIP phosphorylation inhibits the downstream Ras-MAPK proliferation pathway (Tridandapani, S. et al., 1998, Immunol. 35, 1135-1146).

[0012] The features of antibodies discussed above—specificity for target, ability to mediate immune effector mechanisms, and long half-life in serum—make antibodies powerful therapeutics. Monoclonal antibodies are used therapeutically for the treatment of a variety of conditions including cancer, inflammation, and cardiovascular disease. There are currently over ten antibody products on the market and hundreds in development. In addition to antibodies, an antibody-like protein that is finding an expanding role in research and therapy is the Fc fusion (Chamow et al., 1996, *Trends Biotechnol* 14:52-60; Ashkenazi et al., 1997, *Curr Opin Immunol* 9:195-200, incorporated by reference). An Fc fusion is a protein wherein one or more polypeptides is operably linked to Fc. An Fc fusion combines the Fc region of an antibody, and thus its favorable effector functions and pharmacokinetics, with the target-binding region of a receptor, ligand, or some other protein or protein domain. The role of the latter is to mediate target recognition, and thus it is functionally analogous to the antibody variable region. Because of the structural and functional overlap of Fc fusions with antibodies, the discussion on antibodies in the present invention extends directly to Fc fusions.

[0013] There are a number of possible mechanisms by which antibodies destroy tumor cells, including anti-proliferation via blockage of needed growth pathways, intracellular signaling leading to apoptosis, enhanced down regulation and/or turnover of receptors, CDC, ADCC, ADCP, and promotion of an adaptive immune response (Cragg et al., 1999, *Curr Opin Immunol* 11:541-547; Glennie et al., 2000, *Immunol Today* 21:403-410. incorporated by reference). Anti-tumor efficacy may be due to a combination of these mechanisms, and their relative importance in clinical therapy appears to be cancer dependent. Despite this arsenal of anti-tumor weapons, the potency of antibodies as anti-cancer agents is unsatisfactory, particularly given their high cost. Patient tumor response data show that monoclonal antibodies provide only a small improvement in therapeutic success over normal single-agent cytotoxic chemotherapeutics. For example, just half of all relapsed low-grade non-Hodgkin's lymphoma patients respond to the anti-CD20 antibody rituximab (McLaughlin et al., 1998, *J Clin Oncol* 16:2825-2833. incorporated by reference). Of 166 clinical patients, 6% showed a complete response and 42% showed a partial

response, with median response duration of approximately 12 months. Trastuzumab (Herceptin®), a registered trademark of Genentech), an anti-HER2/neu antibody for treatment of metastatic breast cancer, has less efficacy. The overall response rate using trastuzumab for the 222 patients tested was only 15%, with 8 complete and 26 partial responses and a median response duration and survival of 9 to 13 months (Cobleigh et al., 1999, *J Clin Oncol* 17:2639-2648, incorporated by reference). Currently for anticancer therapy, any small improvement in mortality rate defines success. Thus there is a significant need to enhance the capacity of antibodies to destroy targeted cancer cells.

[0014] The role of FcγR-mediated effector functions in the anti-cancer activity of antibodies has been demonstrated in mice (Clynes et al., 1998, *Proc Natl Acad Sci USA* 95:652-656; Clynes et al., 2000, Nat Med 6:443-446, incorporated by reference), and the affinity of interaction between Fc and certain FcγRs correlates with targeted cytotoxicity in cell-based assays (Shields et al., 2001, *J Biol Chem* 276:6591-6604; Presta et al., 2002, *Biochem Soc Trans* 30:487-490; Shields et al., 2002, *J Biol Chem* 277:26733-26740, incorporated by reference): Additionally, a correlation has been observed between clinical efficacy in humans and their allotype of high (V158) or low (F158) affinity polymorphic forms of FcγRIIIa (Cartron et al., 2002, *Blood* 99:754-758, incorporated by reference).

[0015] Mutagenesis studies have been carried out on Fc towards various goals, with substitutions typically made to alanine (referred to as alanine scanning) or guided by sequence homology substitutions (Duncan et al., 1988, *Nature* 332:563-564; Lund et al., 1991, *J Immunol* 147:2657-2662; Lund et al., 1992, *Mol Immunol* 29:53-59; Jefferis et al., 1995, *Immunol Lett* 44:111-117; Lund et al., 1995, *Faseb J* 9:115-119; Jefferis et al., 1996, *Immunol Lett* 54:101-104; Lund et al., 1996, *J Immunol* 157:4963-4969; Armour et al., 1999, *Eur J Immunol* 29:2613-2624; Shields et al., 2001, *J Biol Chem* 276:6591-6604) (U.S. Pat. No. 5,624,821; U.S. Pat. No. 5,885,573; PCT WO 00/42072; PCT WO 99/58572), all incorporated by reference. The majority of substitutions reduce or ablate binding with FcγRs. However some success has been achieved at obtaining Fc variants with higher FcγR affinity. (See for example U.S. Pat. No. 5,624,821 and PCT WO 00/42072). For example, Winter and colleagues substituted the human amino acid at position 235 of mouse IgG2b antibody (a glutamic acid to leucine mutation) that increased binding of the mouse antibody to human FcγRI by 100-fold (Duncan et al., 1988; *Nature* 332:563-564) (U.S. Pat. No. 5,624,821). Shields et al. used alanine scanning mutagenesis to map Fc residues important to FcγR binding, followed by substitution of select residues with non-alanine mutations (Shields et al., 2001, *J Biol Chem* 276:6591-6604; Presta et al., 2002, *Biochem Soc Trans* 30:487-490) (PCT WO 00/42072), incorporated by reference.

[0016] Enhanced affinity of Fc for FcγR has also been achieved using engineered glycoforms generated by expression of antibodies in engineered or variant cell lines (Umaña et al., 1999, *Nat Biotechnol* 17:176-180; Davies et al., 2001, *Biotechnol Bioeng* 74:288-294; Shields et al., 2002, *J Biol Chem* 277:26733-26740; Shinkawa et al., 2003, *J Biol Chem* 278:3466-3473, incorporated by reference). This approach has generated enhancement of the capacity of antibodies to bind FcγRIIIa and to mediate ADCC.

[0017] Another major shortcoming of antibodies is their demanding production requirements (Garber, 2001, *Nat Biotechnol* 19:184-185; Dove, 2002, *Nat Biotechnol* 20:777-779, incorporated by reference). Antibodies must be expressed in mammalian cells, and the currently marketed antibodies together with other high-demand biotherapeutics consume essentially all of the available manufacturing capacity. With hundreds of biologics in development, the majority of which are antibodies, there is an urgent need for more efficient and cheaper methods of production. The downstream effects of insufficient antibody manufacturing capacity are three-fold. First, it dramatically raises the cost of goods to the producer, a cost that is passed on to the patient. Second, it hinders industrial production of approved antibody products, limiting availability of high demand therapeutics to patients. Finally, because clinical trials require large amounts of a protein that is not yet profitable, the insufficient supply impedes progress of the growing antibody pipeline to market.

[0018] Alternative production methods have been explored in attempts at alleviating this problem. Transgenic plants and animals are being pursued as potentially cheaper and higher capacity production systems (Chadd et al., 2001, *Curr Opin Biotechnol* 12:188-194, incorporated by reference). Such expression systems, however, can generate glycosylation patterns significantly different from human glycoproteins. This may result in reduced or even lack of effector function because, as discussed above, the carbohydrate structure can significantly impact FcγR and complement binding. A potentially greater problem with nonhuman glycoforms may be immunogenicity; carbohydrates are a key source of antigenicity for the immune system, and the presence of nonhuman glycoforms has a significant chance of eliciting antibodies that neutralize the therapeutic, or worse cause adverse immune reactions. Thus the efficacy and safety of antibodies produced by transgenic plants and animals remains uncertain. Bacterial expression is another attractive solution to the antibody production problem. Expression in bacteria, for example *E. coli*, provides a cost-effective and high capacity method for producing proteins. For complex proteins such as antibodies there are a number of obstacles to bacterial expression, including folding and assembly of these complex molecules, proper disulfide formation, and solubility, stability, and functionality in the absence of glycosylation because proteins expressed in bacteria are not glycosylated. Full length unglycosylated antibodies that bind antigen have been successfully expressed in *E. coli* (Simmons et al., 2002, *J Immunol Methods* 263:133-147, incorporated by reference), and thus, folding, assembly, and proper disulfide formation of bacterially expressed antibodies are possible in the absence of the eukaryotic chaperone machinery. However the ultimate utility of bacterially expressed antibodies as therapeutics remains hindered by the lack of glycosylation, which results in lack effector function and may result in poor stability and solubility. This will likely be more problematic for formulation at the high concentrations for the prolonged periods demanded by clinical use.

[0019] In summary, there is a need for antibodies with enhanced therapeutic properties.

SUMMARY OF THE INVENTION

[0020] The present invention provides Fc variants that are optimized for a number of therapeutically relevant properties. These Fc variants are generally contained within a variant protein, that preferably comprises an antibody or a Fc fusion protein.

[0021] It is an object of the present invention to provide novel Fc positions at which amino acid modifications may be made to generate optimized Fc variants. Said Fc positions include 230, 240, 244, 245, 247, 262, 263, 266, 273, 275, 299, 302, 313, 323, 325, 328, and 332, wherein the numbering of the residues in the Fc region is that of the EU index as in Kabat. The present invention describes any amino acid modification at any of said novel Fc positions in order to generate an optimized Fc variant.

[0022] It is a further object of the present invention to provide Fc variants that have been characterized herein. In one embodiment, said Fc variants comprise at least one amino acid substitution at a position selected from the group consisting of 221, 222, 223, 224, 225, 227, 228, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 243, 244, 245, 246, 247, 249, 255, 258, 260, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 278, 280, 281, 282, 283, 284, 285, 286, 288, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 313, 317, 318, 320, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, and 337, wherein the numbering of the residues in the Fc region is that of the EU index as in Kabat. In a preferred embodiment, said Fc variants comprise at least one substitution selected from the group consisting of D221K, D221Y, K222E, K222Y, T223E, T223K, H224E, H224Y, T225E, T225K, T225W, P227E, P227G, P227K, P227Y, P228E, P228G, P228K, P228Y, P230A, P230E, P230G, P230Y, A231E, A231G, A231K, A231P, A231Y, P232E, P232G, P232K, P232Y, E233A, E233D, E233F, E233G, E233H, E233I, E233K, E233L, E233M, E233N, E233Q, E233R, E233S, E233T, E233V, E233W, E233Y, L234A, L234D, L234E, L234F, L234G, L234H, L234I, L234K, L234M, L234N, L234P, L234Q, L234R, L234S, L234T, L234V, L234W, L234Y, L235A, L235D, L235E, L235F, L235G, L235H, L235I, L235K, L235M, L235N, L235P, L235Q, L235R, L235S, L235T, L235V, L235W, L235Y, G236A, G236D, G236E, G236F, G236H, G236I, G236K, G236L, G236M, G236N, G236P, G236Q, G236R, G236S, G236T, G236V, G236W, G236Y, G237D, G237E, G237F, G237H, G237I, G237K, G237L, G237M, G237N, G237P, G237Q, G237R, G237S, G237T, G237V, G237W, G237Y, P238D, P238E, P238F, P238G, P238H, P238I, P238K, P238L, P238M, P238N, P238Q, P238R, P238S, P238T, P238V, P238W, P238Y, S239D, S239E, S239F, S239G, S239H, S239I, S239K, S239L, S239M, S239N, S239P, S239Q, S239R, S239T, S239V, S239W, S239Y, V240A, V240I, V240M, V240T, F241D, F241E, F241L, F241R, F241S, F241W, F241Y, F243E, F243H, F243L, F2430, F243R, F243W, F243Y, P244H, P245A, K246D, K246E, K246H, K246Y, P247G, P247V, D249H, D249Q, D249Y, R255E, R255Y, E258H, E258S, E258Y, T260D, T260E, T260H, T260Y, V262A, V262E, V262F, V262I, V262T, V263A, V263I, V263M, V263T, V264A, V264D, V264E, V264F, V264G, V264H, V264I, V264K, V264L, V264M, V264N, V264P, V264Q, V264R, V264S, V264T, V264W, V264Y, D265F, D265G, D265H, D265I, D265K, D265L, D265M, D265N, D265P, D265Q, D265R, D265S, D265T, D265V, D265W, D265Y, V266A, V266I, V266M, V266T, S267D, S267E, S267F, S267H, S267I, S267K, S267L, S267M, S267N, S267P, S267Q, S267R, S267T, S267V, S267W, S267Y, H268D, H268E, H268F, H268G, H268I, H268K, H268L, H268M, H268P, H268Q, H268R, H268T, H268V, H268W, E269F, E269G, E269H, E269I, E269K, E269L, E269M, E269N, E269P, E269R, E269S, E269T, E269V, E269W, E269Y, D270F, D270G, D270H, D270I, D270L, D270M, D270P, D270Q, D270R, D270S, D270T, D270W, D270Y, P271A, P271D, P271E, P271F, P271G, P271H, P271I, P271K, P271L, P271M, P271N, P271Q, P271R, P271S, P271T, P271V, P271W, P271Y, E272D, E272F, E272G, E272H, E272I, E272K, E272L, E272M, E272P, E272R, E272S, E272T, E272V, E272W, E272Y, V273I, K274D, K274E, K274F, K274G, K274H, K274I, K274L, K274M, K274N, K274P, K274R, K274T, K274V, K274W, K274Y, F275L, F275W, N276D, N276E, N276F, N276G, N276H, N276I, N276L, N276M, N276P, N276R, N276S, N276T, N276V, N276W, N276Y, Y278D, Y278E, Y278G, Y278H, Y278I, Y278K, Y278L, Y278M, Y278N, Y278P, Y278Q, Y278R, Y278S, Y278T, Y278V, Y278W, D280G, D280K, D280L, D280P, D280W, G281D, G281E, G281K, G281N, G281P, G281Q, G281Y, V282E, V282G, V282K, V282P, V282Y, E283G, E283H, E283K, E283L, E283P, E283R, E283Y, V284D, V284E, V284L, V284N, V284Q, V284T, V284Y, H285D, H285E, H285K, H285Q, H285W, H285Y, N286E, N286G, N286P, N286Y, K288D, K288E, K288Y, K290D, K290H, K290L, K290N, K290W, P291D, P291E, P291G, P291H, P291I, P291Q, P291T, R292D, R292E, R292T, R292Y, E293F, E293G, E293H, E293I, E293L, E293M, E293N, E293P, E293R, E293S, E293T, E293V, E293W, E293Y, E294F, E294G, E294H, E294I, E294K, E294L, E294M, E294P, E294R, E294S, E294T, E294V, E294W, E294Y, Q295D, Q295E, Q295F, Q295G, Q295H, Q295I, Q295M, Q295N, Q295P, Q295R, Q295S, Q295T, Q295V, Q295W, Q295Y, Y296A, Y296D, Y296E, Y296G, Y296H, Y296I, Y296K, Y296L, Y296M, Y296N, Y296Q, Y296R, Y296S, Y296T, Y296V, N297D, N297E, N297F, N297G, N297H, N297I, N297K, N297L, N297M, N297P, N297Q, N297R, N297S, N297T, N297V, N297W, N297Y, S298D, S298E, S298F, S298H, S298I, S298K, S298M, S298N, S298Q, S298R, S298T, S298W, S298Y, T299A, T299D, T299E, T299F, T299G, T299H, T299I, T299K, T299L, T299M, T299N, T299P, T299Q, T299R, T299S, T299V, T299W, T299Y, Y300A, Y300D, Y300E, Y300G, Y300H, Y300K, Y300M, Y300N, Y300P, Y300Q, Y300R, Y300S, Y300T, Y300V, Y300W, R301D, R301E, R301H, R301Y, V302I, V303D, V303E, V303Y, S304D, S304H, S304L, S304N, S304T, V305E, V305T, V305Y, W313F, K317E, K317Q, E318H, E318L, E318Q, E318R, E318Y, K320D, K320F, K320G, K320H, K320I, K320L, K320N, K320P, K320S, K320T, K320V, K320W, K320Y, K322D, K322F, K322G, K322H, K322I, K322P, K322S, K322T, K322V, K322W, K322Y, V323I, S324D, S324F, S324G, S324H, S324I, S324L, S324M, S324P, S324R, S324T, S324V, S324W, S324Y, N325A, N325D, N325E, N325F, N325G, N325H, N325I, N325K, N325L, N325M, N325P, N325Q, N325R, N325S, N325T, N325V, N325W, N325Y, K326I, K326L, K326P, K326T, A327D, A327E, A327F, A327H, A327I, A327K, A327L, A327M, A327N, A327P, A327R, A327S, A327T, A327V, A327W, A327Y, L328A, L328D, L328E, L328F, L328G, L328H, L328I, L328K, L328M, L328N, L328P, L328Q, L328R, L328S, L328T, L328V, L328W, L328Y, P329D, P329E, P329F, P329G, P329H, P329I, P329K, P329L, P329M, P329N, P329Q, P329R, P329S, P329T, P329V, P329W, P329Y, A330E, A330F, A330G, A330H, A330I, A330L, A330M, A330N, A330P, A330R, A330S, A330T, A330V, A330W, A330Y, P331D, P331F, P331H, P331I, P331L, P331M, P331Q, P331R, P331T, P331V, P331W, P331Y, I332A, I332D, I332E, I332F, I332H, I332K, I332L,

I332M, I332N, I332P, I332Q, I332R, I332S, I332T, I332V, I332W, I332Y, E333F, E333H, E333I, E333L, E333M, E333P, E333T, E333Y, K334F, K334I, K334L, K334P, K334T, T335D, T335F, T335G, T335H, T335I, T335L, T335M, T335N, T335P, T335R, T335S, T335V, T335W, T335Y, I336E, I336K, I336Y, S337E, S337H, and S337N, wherein the numbering of the residues in the Fc region is that of the EU index as in Kabat. This set of variants is sometimes referenced to as "the single variant set" of the invention.

[0023] It is an additional aspect of the invention to provide Fc variants (and proteins containing these variants) that have at least 1, 2, 3, 4, 5, 6, 7, 8, 9 and 10 or more amino acid substitutions as compared to the parent Fc polypeptide, for example the Fc region SEQ ID NO:X. In some embodiments, 1, 2, 3 and 4 substitutions find particular use.

[0024] It is a further aspect of the invention to provide Fc variants (and proteins containing these variants) that exhibit altered Fc ligand binding as compared to the parent Fc polypeptide, for example the Fc region of SEQ ID NO:X, and that are encoded by nucleic acids that hybridize under high stringency conditions to a gene that encodes a human Fc polypeptide. High stringency conditions are known in the art; see for example U.S. Pat. No. 6,875,846, hereby incorporated by reference, particularly for high stringency conditions. Genes that encode human Fc polypeptides are usually fragments of larger genes, and are also known in the art, as well as genes that due to the degeneracy of the genetic code will encode a naturally occurring Fc polypeptide even if not naturally occurring themselves.

[0025] It is an additional aspect of the invention to provide for variant Fc polypeptides that exhibit altered ADCC activity, particularly increased ADCC activity. In some aspects, these variants comprise an amino acid substitution at position 239, optionally amino acid substitutions at positions 239 and 332, and optionally can include any other substitutions outlined in the single variant set above, to create variants comprising multiple substitutions.

[0026] It is a further object of the present invention to provide Fc variants that have been characterized herein, wherein said Fc variants are selected from the group consisting of D221K, D221Y, K222E, K222Y, T223E, T223K, H224E, H224Y, T225E, T225K, T225W, P227E, P227G, P227K, P227Y, P228E, P228G, P228K, P228Y, P230A, P230A/E233D, P230A/E233D/I332E, P230E, P230G, P230Y, A231E, A231G, A231K, A231P, A231Y, P232E, P232G, P232K, P232Y, E233A, E233D, E233F, E233G, E233H, E233I, E233K, E233L, E233M, E233N, E233Q, E233R, E233S, E233T, E233V, E233W, E233Y, L234A, L234D, L234E, L234F, L234G, L234H, L234I, L234I/L235D, L234K, L234M, L234N, L234P, L234Q, L234R, L234S, L234T, L234V, L234W, L234Y, L235A, L235D, L235D/S239D/A330Y/I332E, L235D/S239D/N297D/I332E, L235E, L235F, L235G, L235H, L235I, L235K, L235M, L235N, L235P, L235Q, L235R, L235S, L235T, L235V, L235W, L235Y, G236A, G236D, G236E, G236F, G236H, G236I, G236K, G236L, G236M, G236N, G236P, G236Q, G236R, G236S, G236T, G236V, G236W, G236Y, G237D, G237E, G237F, G237H, G237I, G237K, G237L, G237M, G237N, G237P, G237Q, G237R, G237S, G237T, G237V, G237W, G237Y, P238D, P238E, P238F, P238G, P238H, P238I, P238K, P238L, P238M, P238N, P2380, P238R, P238S, P238T, P238V, P238W, P238Y, S239D, S239D/A330L/I332E, S239D/A330Y/I332E/L234I, S239D/A330Y/I332E/V266I, S239D/D265F/N297D/I332E, S239D/D265H/N297D/I332E, S239D/D265I/N297D/I332E, S239D/D265L/N297D/I332E, S239D/D265T/N297D/I332E, S239D/D265Y/N297D/I332E, S239D/E272I/A330L/I332E, S239D/E272I/I332E, S239D/E272K/A330L/I332E, S239D/E272K/I332E, S239D/E272S/A330L/I332E, S239D/E272S/I332E, S239D/E272Y/A330L/I332E, S239D/E272Y/I332E, S239D/F241S/F243H/V262T/N264T/N297D/A330Y/I332E, S239D/H268D, S239D/H268E, S239D/I332D, S239D/I332E, S239D/I332E/A327D, S239D/I332E/A330I, S239D/I332E/A330Y, S239D/I332E/E272H, S239D/I332E/E272R, S239D/I332E/E283H, S239D/I332E/E283L, S239D/I332E/G236A, S239D/I332E/G236S, S239D/I332E/H268D, S239D/I332E/H268E, S239D/I332E/K246H, S239D/I332E/R255Y, S239D/I332E/S267E, S239D/I332E/V264I, S239D/I332E/V264I/A330L, S239D/I332E/V264I/S298A, S239D/I332E/V284D, S239D/I332E/V284E, S239D/I332E/V284E, S239D/I332N, S239D/I332Q, S239D/K274E/A330L/I332E, S239D/K274E/I332E, S239D/K326E/A330L/I332E, S239D/K326E/A330Y/I332E, S239D/K326E/I332E, S239D/K326T/A330Y/I332E, S239D/K326T/I332E, S239D/N297D/A330Y/I332E, S239D/N297D/I332E, S239D/N297D/K326E/I332E, S239D/S267E/A330Y/I332E, S239D/S267E/I332E, S239D/S298A/K326E/I332E, S239D/S298A/K326T/I332E, S239D/V240I/A330Y/I332E, S239D/V264T/A330Y/I332E, S239D/Y278T/A330L/I332E, S239D/Y278T/I332E, S239E, S239E/D265G, S239E/D265N, S239E/D265Q, S239E/I332D, S239E/I332E, S239E/I332N, S239E/I332Q, S239E/N297D/I332E, S239E/V264I/A330Y/I332E, S239E/V264I/I332E, S239E/V264I/S298A/A330Y/I332E, S239F, S239G, S239H, S239I, S239K, S239L, S239M, S239N, S239N/I332D, S239N/I332E, S239N/I332E/A330L, S239N/I332E/A330Y, S239N/I332N, S239N/I332Q, S239P, S239Q, S239Q/I332D, S239Q/I332E, S239Q/I332N, S239Q/I332Q, S239Q/V264I/I332E, S239R, S239T, S239V, S239W, S239Y, V240A, V240I, V2401N266I, V240M, V240T, F241D, F241E, F241E/F243Q/V262T/V264E/I332E, F241E/F243Q/V262T/V264E, F241E/F243R/V262E/V264R/I332E, F241E/F243R/V262E/V264R, F241E/F243Y/V262T/V264R/I332E, F241E/F243Y/V262T/V264R, F241L, F241L/F243L/V262I/V264I, F241L/V262I, F241R/F243Q/V262T/V264R/I332E, F241R/F243Q/V262T/V264R, F241W, F241W/F243W, F241W/F243W/V262A/V264A, F241Y, F241Y/F243Y/V262T/V264T/N297D/I332E, F241Y/F243Y/V262T/V264T, F243E, F243L, F243L/V262I/V264W, F243L/V264I, F243W, P244H, P244H/P245A/P247V, P245A, K246D, K246E, K246H, K246Y, P247G, P247V, D249H, D249Q, D249Y, R255E, R255Y, E258H, E258S, E258Y, T260D, T260E, T260H, T260Y, V262E, V262F, V263A, V263I, V263M, V263T, V264A, V264D, V264E, V264E/N297D/I332E, V264F, V264G, V264H, V264I, V264I/A330Y/I332E, V264I/A330Y/I332E, V264I/I332E, V264K, V264L, V264M, V264N, V264P, V264Q, V264R, V264S, V264T, V264W, V264Y, D265F, D265F/N297E/I332E, D265G, D265H, D265I, D265K, D265L, D265M, D265N, D265P, D265Q, D265R, D265S, D265T, D265V, D265W, D265Y, D265Y/N297D/I332E, D265Y/N297D/T299L/I332E, V266A, V266I, V266M, V266T, S267D, S267E, S267E, S267E/A327D, S267E/P331D, S267E/S324I, S267E/V282G, S267F, S267H, S267I, S267K, S267L, S267L/A327S, S267M, S267N, S267P, S2670, S267Q/A327S, S267R, S267T, S267V, S267W, S267Y, H268D, H268E, H268F, H268G, H268I, H268K,

H268L, H268M, H268P, H268Q, H268R, H268T, H268V, H268W, E269F, E269G, E269H, E269I, E269K, E269L, E269M, E269N, E269P, E269R, E269S, E269T, E269V, E269W, E269Y, D270F, D270G, D270H, D270I, D270L, D270M, D270P, D270Q, D270R, D270S, D270T, D270W, D270Y, P271A, P271D, P271E, P271F, P271G, P271H, P271I, P271K, P271L, P271M, P271N, P271Q, P271R, P271S, P271T, P271V, P271W, P271Y, E272D, E272F, E272G, E272H, E272I, E272K, E272L, E272M, E272P, E272R, E272S, E272T, E272V, E272W, E272Y, V273I, K274D, K274E, K274F, K274G, K274H, K274I, K274L, K274M, K274N, K274P, K274R, K274T, K274V, K274W, K274Y, F275L, F275W, N276D, N276E, N276F, N276G, N276H, N276I, N276L, N276M, N276P, N276R, N276S, N276T, N276V, N276W, N276Y, Y278D, Y278E, Y278G, Y278H, Y278I, Y278K, Y278L, Y278M, Y278N, Y278P, Y278Q, Y278R, Y278S, Y278T, Y278V, Y278W, Y278W, Y278W/E283R/V302I, Y278W/V302I, D280G, D280K, D280L, D280P, D280W; G281D, G281D/V282G, G281E, G281K, G281N, G281P, G281Q, G281Y, V282E, V282G, V282G/P331D, V282K, V282P, V282Y, E283G, E283H, E283K, E283L, E283P, E283R, E283R/V302I/Y278W/E283R, E283Y, V284D, V284E, V284L, V284N, V284Q, V284T, V284Y, H285D, H285E, H285K, H285Q, H285W, H285Y, N286E, N286G, N286P, N286Y, K288D, K288E, K288Y, K290D, K290H, K290L, K290N, K290W, P291D, P291E, P291G, P291H, P291I, P291Q, P291T, R292D, R292E, R292T, R292Y, E293F, E293G, E293H, E293I, E293L, E293M, E293N, E293P, E293R, E293S, E293T, E293V, E293W, E293Y, E294F, E294G, E294H, E294I, E294K, E294L, E294M, E294P, E294R, E294S, E294T, E294V, E294W, E294Y, Q295D, Q295E, Q295F, Q295G, Q295H, Q295I, Q295M, Q295N, Q295P, Q295R, Q295S, Q295T, Q295V, Q295W, Q295Y, Y296A, Y296D, Y296E, Y296G, Y296I, Y296K, Y296L, Y296M, Y296N, Y296Q, Y296R, Y296S, Y296T, Y296V, N297D, N297D/I332E, N297D/I332E/A330Y, N297D/I332E/S239D/A330L, N297D/I332E/S239D/D265V, N297D/I332E/S298A/A330Y, N297D/I332E/T299E, N297D/I332E/T299F, N297D/I332E/T299H, N297D/I332E/T299I, N297D/I332E/T299L, N297D/I332E/T299V, N297D/I332E/Y296D, N297D/I332E/Y296E, N297D/I332E/Y296H, N297D/I332E/Y296N, N297D/I332E/Y296Q, N297D/I332E/Y296T, N297E/I332E, N297F, N297G, N297H, N297I, N297K, N297L, N297M, N297P, N297Q, N297R, N297S, N297S/I332E, N297T, N297V, N297W, N297Y, S298A/I332E, S298A/K326E, S298A/K326E/K334L, S298A/K334L, S298D, S298E, S298F, S298H, S298I, S298K, S298M, S298N, S298Q, S298R, S298T, S298W, S298Y, T299A, T299D, T299E, T299F, T299G, T299H, T299I, T299K, T299L, T299M, T299N, T299P, T299Q, T299R, T299S, T299V, T299W, T299Y, Y300A, Y300D, Y300E, Y300G, Y300H, Y300K, Y300M, Y300N, Y300P, Y300Q, Y300R, Y300S, Y300T, Y300V, Y300W, R301D, R301E, R301H, R301Y, V302I, V303D, V303E, V303Y, S304D, S304H, S304L, S304N, S304T, V305E, V305T, V305Y, W313F, K317E, K317Q, E318H, E318L, E318Q, E318R, E318Y, K320D, K320F, K320G, K320H, K320I, K320L, K320N, K320P, K320S, K320T, K320V, K320W, K320Y, K322D, K322F, K322G, K322H, K322I, K322P, K322S, K322T, K322V, K322W, K322Y, V323I, S324D, S324F, S324G, S324H, S324I, S324I/A327D, S324L, S324M, S324P, S324R, S324T, S324V, S324W, S324Y, N325A, N325D, N325E, N325F, N325G, N325H, N325I, N325K, N325L, N325M, N325P, N325Q, N325R, N325S, N325T, N325V, N325W, N325Y, K326I, K326L, K326P, K326T, A327D, A327E, A327F, A327H, A327I, A327K, A327L, A327M, A327N, A327P, A327R, A327S, A327T, A327V, A327W, A327Y, L328A, L328D, L328D/I332E, L328E, L328E/I332E, L328F, L328G, L328H, L328H/I332E, L328I, L328I/I332E, L328I/I332E, L328K, L328M, L328M/I332E, L328N, L328N/I332E, L328P, L328Q, L328Q/I332E, L328Q/I332E, L328R, L328S, L328T, L328T/I332E, L328V, L328V/I332E, L328W, L328Y, P329D, P329E, P329F, P329G, P329H, P329I, P329K, P329L, P329M, P329N, P329Q, P329R, P329S, P329T, P329V, P329W, P329Y, A330E, A330F, A330G, A330H, A330I, A330L, A330L/I332E, A330M, A330N, A330P, A330R, A330S, A330T, A330V, A330W, A330Y, A330Y/I332E, P331D, P331F, P331H, P331I, P331L, P331M, P331Q, P331R, P331T, P331V, P331W, P331Y, I332A, I332D, I332E, I332E/G281D, I332E/H268D, I332E/H268E, I332E/S239D/S298A, I332E/S239N/S298A, I332E/V264I/S298A, I332E/V284E, I332F, I332H, I332K, I332L, I332M, I332N, I332P, I332Q, I332R, I332S, I332T, I332V, I332W, I332Y, E333F, E333H, E333I, E333L, E333M, E333P, E333T, E333Y, K334F, K334I, K334P, K334T, T335D, T335F, T335G, T335H, T335I, T335L, T335M, T335N, T335P, T335R, T335S, T335V, T335W, T335Y, I336E, I336K, I336Y, S337E, S337H, and S337N, wherein the numbering of the residues in the Fc region is that of the EU index as in Kabat.

[0027] It is a further object of the present invention to provide an Fc variant that binds with greater affinity to one or more FcγRs. In one embodiment, said Fc variants have affinity for an FcγR that is more than 1-fold greater than that of the parent Fc polypeptide. In an alternate embodiment, said Fc variants have affinity for an FcγR that is more than 5-fold greater than that of the parent Fc polypeptide. In a preferred embodiment, said Fc variants have affinity for an FcγR that is between about 5-fold and 300-fold greater than that of the parent Fc polypeptide.

[0028] It is a further object of the present invention to provide Fc variant that have a FcγRIIIa-fold:FcγRIIb-fold ratio greater than 1:1. In one embodiment, said Fc variants have a FcγRIIIa-fold:FcγRIIb-fold ratio greater than 11:1. In a preferred embodiment, said Fc variants have a FcγRIIIa-fold:FcγRIIb-fold ratio between 11:1 and 86:1.

[0029] It is a further object of the present invention to provide Fc variants that mediate effector function more effectively in the presence of effector cells. In one embodiment, said Fc variants mediate ADCC that is greater than that mediated by the parent Fc polypeptide. In a preferred embodiment, said Fc variants mediate ADCC that is more than 5-fold greater than that mediated by the parent Fc polypeptide. In a mostly preferred embodiment, said Fc variants mediate ADCC that is between 5-fold and 1000-fold greater than that mediated by the parent Fc polypeptide.

[0030] It is a further object of the present invention to provide Fc variants that bind with weaker affinity to one or more FcγRs. It is a further object of the present invention to provide Fc variants that mediate ADCC in the presence of effector cells less effectively.

[0031] It is a further object of the present invention to provide Fc variants that have improved function and/or solution properties as compared to the aglycosylated form of the parent Fc polypeptide. Improved functionality herein includes but is not limited to binding affinity to an Fc ligand. Improved solution properties herein includes but is not lim-

ited to stability and solubility. In an one embodiment, said Fc variants bind to an FcγR with an affinity that is within about 0.5-fold of the glycosylated form of the parent Fc polypeptide. In an alternate embodiment, said aglycosylated Fc variants bind to an FcγR with an affinity that is comparable to the glycosylated parent Fc polypeptide. In an alternate embodiment, said Fc variants bind to an FcγR with an affinity that is greater than the glycosylated form of the parent Fc polypeptide.

[0032] Also provided herein are methods of promoting anti-proliferative effects in a cell comprising contacting the cell with an Fv variant, wherein said contacting results in co-engagement of a target antigen and an FcγR on the surface of the cell. In one embodiment, the anti-proliferative effects include cell growth inhibition and/or apoptosis. In one embodiment of the invention, the FcγR is FcγRIIb. In another embodiment, the cell is a cancer cell. In another embodiment, the cell is an immune cell. In one embodiment, the Fv variant that results in coengagement of a target antigen and an FcγR on the cell's surface comprises at least one amino acid modification in the Fc region compared to a parent polypeptide, wherein said modification is at a position selected from 234, 235, 236, 237, 239, 266, 267, 268, 298, 327, 328, 329, 330, and 332, wherein numbering is according to the EU index. In another embodiment the modification is an amino acid substitution selected from the group consisting of 234F, 234G, 234I, 234K, 234N, 234P, 234Q, 234S, 234V, 234W, 234Y, 235H, 235I, 235N, 235P, 235Q, 235R, 235S, 235W, 235Y, 236D, 236F, 236H, 236I, 236K, 236L, 236M, 236P, 236Q, 236R, 236S, 236T, 236V, 236W, 236Y, 237E, 237H, 237K, 237L, 237P, 237Q, 237S, 237V, 237Y, 239D, 239E, 239N, 239Q, 266I, 266M, 267D, 267E, 268D, 268E, 268Q, 298D, 298E, 298M, 298Q, 327D, 327L, 327N, 328E, 328F, 329E, 330H, 330S, 267E/327D, 239D/267E, 239D/268D, 239D/332E, and 239D/267E/332E, wherein numbering is according to the EU index.

[0033] The present invention also provides methods for engineering optimized Fc variants. It is a further object of the present invention to provide experimental production and screening methods for obtaining optimized Fc variants.

[0034] The present invention provides isolated nucleic acids encoding the Fc variants described herein. The present invention provides vectors comprising said nucleic acids, optionally, operably linked to control sequences. The present invention provides host cells containing the vectors, and methods for producing and optionally recovering the Fc variants.

[0035] The present invention provides novel Fc polypeptides, including antibodies, Fc fusions, isolated Fc, and Fc fragments, that comprise the Fc variants disclosed herein. Said novel Fc polypeptides may find use in a therapeutic product.

[0036] The present invention provides compositions comprising Fc polypeptides that comprise the Fc variants described herein, and a physiologically or pharmaceutically acceptable carrier or diluent.

[0037] The present invention contemplates therapeutic and diagnostic uses for Fc polypeptides that comprise the Fc variants disclosed herein.

[0038] The present disclosure provides novel immunoglobulins, compositions comprising such immunoglobulins, and methods of using the immunoglobulin to inhibit cells that express FcγRIIb. The FcγRIIb+ cell inhibitory methods disclosed herein comprise contacting FcγRIIb+ cells with an immunoglobulin that binds FcγRIIb and coengages a target antigen on the cell's surface and an FcγRIIb on the cell's surface. In one embodiment, the immunoglobulin binds with FcγRIIb, wherein the affinity of said binding has a Kd less than about 100 nM, e.g., less than or equal to about 95 nM, less than or equal to about 90 nM, less than or equal to about 85 nM, less than or equal to about 80 nM, less than or equal to about 75 nM, less than or equal to about 74 nM. In one embodiment, the immunoglobulin comprises an Fc region, wherein said Fc region comprises one or more modifications compared to a parent Fc region, wherein said modifications are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In another embodiment, the immunoglobulin is a bispecific antibody comprising a first Fv region and a second Fv region, wherein said first Fv region binds the target antigen, and said second Fv region binds FcγRIIb with a Kd of less than about 100 nM. In another embodiment, the immunoglobulin is an Fc fusion comprising an Fc region, wherein said Fc region binds FcγRIIb with a Kd of less than about 100 nM. FcγRIIb+ cells as disclosed herein may be cancer cells, B cells, plasma cells, dendritic cells, macrophages, neutrophils, mast cells, basophils, eosinophils, and a combination thereof.

[0039] Also disclosed herein are novel methods of inhibiting activation of B cells. The B cell inhibitory methods disclosed herein comprise contacting B cells with an immunoglobulin that binds FcγRIIb and coengages a target antigen on the B cell's surface and an FcγRIIb on the B cell's surface. In one embodiment, the immunoglobulin binds with FcγRIIb, wherein the affinity of said binding has a Kd less than about 100 nM, e.g., less than or equal to about 95 nM, less than or equal to about 90 nM, less than or equal to about 85 nM, less than or equal to about 80 nM, less than or equal to about 75 nM, less than or equal to about 74 nM. In one embodiment, the immunoglobulin comprises an Fc region, wherein said Fc region comprises one or more modifications compared to a parent Fc region, wherein said modifications are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In another embodiment, the immunoglobulin is a bispecific antibody comprising a first Fv region and a second Fv region, wherein said first Fv region binds the target antigen, and said second Fv region binds FcγRIIb with a Kd of less than about 100 nM. In another embodiment, the immunoglobulin is an Fc fusion comprising an Fc region, wherein said Fc region binds FcγRIIb with a Kd of less than about 100 nM. In one embodiment, the immunoglobulin binds at least two B cell proteins, e.g., at least two proteins bound, or that may be bound, on the surface of B cells. In one embodiment, the first of said B cell proteins is FcγRIIb and the second of said B cell proteins is part of the B cell receptor (BCR) complex. In another embodiment, the second of said B cell proteins is not involved directly in antigen recognition. In another embodiment, the second of said B cell proteins is an antigen bound to the BCR complex. In some embodiments, the immunoglobulins inhibit release of calcium from the B cells upon their stimulation through the B cell receptor. In another embodiment, an immunoglobulin disclosed herein binds at least two B cell proteins bound on the surface of the same B cell.

[0040] Also disclosed herein are novel methods of treating B cell-mediated disorders, e.g., autoimmune diseases, inflammatory diseases, hematological malignancies, etc. The

treatment methods disclosed herein comprise administration to a patient in need of such administration a therapeutic amount of an immunoglobulin that binds FcγRIIb+ cells and coengages a target antigen on the cell's surface and an FcγRIIb on cell's surface. In one embodiment, the immunoglobulin binds with FcγRIIb, wherein the affinity of said binding has a Kd less than about 100 nM, e.g., less than or equal to about 95 nM, less than or equal to about 90 nM, less than or equal to about 85 nM, less than or equal to about 80 nM, less than or equal to about 75 nM, less than or equal to about 74 nM. In one embodiment, the immunoglobulin comprises an Fc region, wherein said Fc region comprises one or more modifications compared to a parent Fc region, wherein said modifications are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In another embodiment, the immunoglobulin is a bispecific antibody comprising a first Fv region and a second Fv region, wherein said first Fv region binds the target antigen, and said second Fv region binds FcγRIIb with a Kd of less than about 100 nM. In another embodiment, the immunoglobulin is an Fc fusion comprising an Fc region, wherein said Fc region binds FcγRIIb with a Kd of less than about 100 nM. In some embodiments, autoimmune and inflammatory diseases that may be treated by the methods disclosed herein include Systemic Lupus Erythematosus, Rheumatoid arthritis, Sjogren's syndrome, Multiple sclerosis, Idiopathic thrombocytopenic purpura (ITP), Graves disease, Inflammatory bowel disease, Psoriasis, Type I diabetes, and Asthma.

[0041] Disclosed herein are novel FcγRIIb+ cell inhibitory immunoglobulin compositions. The compositions disclosed herein include immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface. In one embodiment, the immunoglobulin binds with FcγRIIb, wherein the affinity of said binding has a Kd less than about 100 nM, e.g., less than or equal to about 95 nM, less than or equal to about 90 nM, less than or equal to about 85 nM, less than or equal to about 80 nM, less than or equal to about 75 nM, less than or equal to about 74 nM. In one embodiment, the immunoglobulin comprises an Fc region, wherein said Fc region comprises one or more modifications compared to a parent Fc region, wherein said modifications are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In another embodiment, the immunoglobulin is a bispecific antibody comprising a first Fv region and a second Fv region, wherein said first Fv region binds the target antigen, and said second Fv region binds FcγRIIb with a Kd of less than about 100 nM. In another embodiment, the immunoglobulin is an Fc fusion comprising an Fc region, wherein said Fc region binds FcγRIIb with a Kd of less than about 100 nM.

[0042] In some embodiments, the immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage a target antigen selected from the group consisting of: CD19, CD20, CD21 (CR2), CD22, CD23/FcεRII, FcεRI, (α, β, and γ subunits), CD24/BBA-1/HSA, CD27, CD35 (CR1), CD38, CD40, CD45RA, CD52/CAMPATH-1/HE5, CD72, CD79a (Igo), CD79b (Igβ), IgM (μ), CD80, CD81, CD86, Leu13, HLA-DR, -DP, -DQ, CD138, CD317/HM1.24, CD11a, CD11b, CD11c, CD14, CD68, CD163, CD172a, CD200R, and CD206. In other embodiments, the immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage a target antigen selected from the group consisting of: IgM (μ), CD19, CD20, CD21, CD22, CD23, CD24, CD35, CD40, CD45RA, CD72, CD79a, CD79b, CD80, CD81, CD86, and HLA-DR. In one embodiment, immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage a target antigen selected from the group consisting of: IgM (μ), CD79a, CD79b, CD19, CD21, CD22, CD72, CD81, and Leu13. In one embodiment, immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage a target antigen selected from the group consisting of: IgM (μ), CD19, CD79a, CD79b, CD81, and HLA-DR. In another embodiment, immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage a target antigen selected from the group consisting of: CD22, CD40, and CD72.

[0043] In one embodiment, the immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may bind and/or coengage an autoantigen or allergen. In an alternate embodiment, an immunoglobulin disclosed herein may be an Fc fusion that is covalently linked to an autoantigen or allergen. In one embodiment, the autoantigen is selected from the group consisting citrullinated proteins and peptides such as CCP-1, CCP-2 (cyclical citrullinated peptides), fibrinogen, fibrin, vimentin, fillaggrin, collagen I and II peptides, alpha-enolase, translation initiation factor 4G1, perinuclear factor, keratin, Sa (cytoskeletal protein vimentin), components of articular cartilage such as collagen II, IX, and XI, circulating serum proteins such as RFs (IgG, IgM), fibrinogen, plasminogen, ferritin, nuclear components such as RA33/hnRNP A2, Sm, eukaryotic translation elongation factor 1 alpha 1, stress proteins such as HSP-65, -70, -90, BiP, inflammatory/immune factors such as B7-H1, IL-1 alpha, and IL-8, enzymes such as calpastatin, alpha-enolase, aldolase-A, dipeptidyl peptidase, osteopontin, glucose-6-phosphate isomerase, receptors such as lipocortin 1, neutrophil nuclear proteins such as lactoferrin and 25-35 kD nuclear protein, granular proteins such as bactericidal permeability increasing protein (BPI), elastase, cathepsin G, myeloperoxidase, proteinase 3, platelet antigens, myelin protein antigen, islet cell antigen, rheumatoid factor, histones, ribosomal P proteins, cardiolipin, vimentin, nucleic acids such as dsDNA, ssDNA, and RNA, ribonuclear particles and proteins such as Sm antigens (including but not limited to SmD's and SmB'/B), U1RNP, A2/B1 hnRNP, Ro (SSA), and La (SSB) antigens.

[0044] In one embodiment, immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may be variant immunoglobulins relative to a parent immunoglobulin. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according

to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332, according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 266, 267, 268, 327, 328, according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 235, 236, 266, 267, 268, 328, according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 235, 236, 239, 266, 267, 268, and 328, according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 266, 267, 268, 327, 328, according to the EU index

[0045] In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234F, 234G, 234I, 234K, 234N, 234P, 234O, 234S, 234V, 234W, 234Y, 234D, 234E, 235A, 235E, 235H, 235I, 235N, 235P, 235Q, 235R, 235S, 235W, 235Y, 235D, 235F, 235T, 236D, 236F, 236H, 236I, 236K, 236L, 236M, 236P, 236Q, 236R, 236S, 236T, 236V, 236W, 236Y, 236A, 236E, 236N, 237A, 237E, 237H, 237K, 237L, 237P, 237Q, 237S, 237V, 237Y, 237D, 237N, 239D, 239E, 239N, 239Q, 265E, 266D, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298D, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327G, 327L, 327N, 327Q, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 329E, 330D, 330H, 330K, 330S, 331S, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234N, 234F, 234D, 234E, 234W, 235Q, 235R, 235W, 235Y, 235D, 235F, 235T, 236D, 236H, 236I, 236L, 236S, 236Y, 236E, 236N, 237H, 237L, 237D, 237N, 239D, 239N, 239E, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327L, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 330D, 330H, 330K, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234D, 234E, 234W, 235D, 235F, 235R, 235Y, 236D, 236N, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of L234E, L235Y, L235R, G236D, G236N, G237N, V266M, S267E, H268E, H268D, A327D, A327E, L328F, L328Y, L328W, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 235Y, 236D, 239D, 266M, 267E, 268D, 268E, 328F, 328W, and 328Y, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of L235Y, G236D, V266M, S267E, H268E, H268D, L328F, L328Y, and L328W, wherein numbering is according to an EU index.

[0046] In one embodiment, said modification(s) is at least two modifications (e.g., a combination of modifications) at positions selected from the group consisting of 234/239, 234/267, 234/328, 235/236, 235/239, 235/267, 235/268, 235/328, 236/239, 236/267, 236/268, 236/328, 237/267, 239/267, 239/268, 239/327, 239/328, 239/332, 266/267, 267/268, 267/325, 267/327, 267/328, 267/332, 268/327, 268/328, 268/332, 326/328, 327/328, and 328/332, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least two modifications (e.g., a combination of modifications) at positions selected from the group consisting of 235/267, 236/267, 239/268, 239/267, 267/268, and 267/328, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least two substitutions (e.g., a combination of substitutions) selected from the group consisting of 234D/267E, 234E/267E, 234F/267E, 234E/328F, 234W/239D, 234W/239E, 234W/267E, 234W/328Y, 235D/267E, 235D/328F, 235F/239D, 235F/267E, 235F/328Y, 235Y/236D, 235Y/239D, 235Y/267D, 235Y/267E, 235Y/268E, 235Y/328F, 236D/239D, 236D/267E, 236D/268E, 236D/328F, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 239D/268D, 239D/268E, 239D/327D, 239D/328F, 239D/328W, 239D/328Y, 239D/332E, 239E/267E, 266M/267E, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267E/327D, 267E/327E, 267E/328F, 267E/328I, 267E/328Y, 267E/332E, 268D/327D, 268D/328F, 268D/328W, 268D/328Y, 268D/332E, 268E/328F, 268E/328Y, 327D/328Y, 328F/332E, 328W/332E, and 328Y/332E, wherein numbering is according to an EU index.

[0047] In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y,

239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 239D/267E/332E, 234W/328Y/332 E, 235F/328Y/332 E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 266D, 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 266M/267E, 234E/268D, 236D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 234N, 235Q, 235R, 235W, 235Y, 236D, 236H, 236I, 236L, 236S, 236Y, 237H, 237L, 239D, 239N, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 326A, 326E, 326W, 327D, 327L, 328E, 328F, 330D, 330H, 330K, 234F/236N, 234F/236D, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 239D/267E/268E, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332 E, 268E/328Y/332 E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E

[0048] In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 235Y/267E, 236D/267E, 239D/268D, 239D/267E, 267E/268D, 267E/268E, and 267E/328F, wherein numbering is according to an EU index.

[0049] In one embodiment, the modifications disclosed herein reduce affinity to at least one receptor relative to the parent immunoglobulin, wherein said receptor is selected from the group consisting of FcγRI, FcγRIIa, and FcγRIIIa. In an alternate embodiment, immunoglobulin variants disclosed herein mediate reduced ADCC or ADCP relative to the parent immunoglobulin.

[0050] Also disclosed herein are methods for engineering the novel immunoglobulin compositions.

[0051] Also disclosed herein are methods for screening target antigens for their capacity to mediate cellular inhibition via an FcγRIIb-dependent mechanism. In one embodiment, the antigen screening methods disclosed herein comprise the step of binding a cell that expresses the target antigen and FcγRIIb with an immunoglobulin that binds with enhanced affinity, e.g., the Kd of the immunoglobulin may be less than about 100 nM to at least FcγRIIb. In another embodiment, simultaneous binding of both target antigen and FcγRIIb by the immunoglobulin results in an inhibitory cellular response. In one embodiment of the screening methods disclosed herein, the cell is selected from the group consisting of: B cells, plasma cells, dendritic cells, macrophages, neutrophils, mast cells, basophils, or eosinophils. In another some screening methods disclosed herein, the immunoglobulin may be specific for the target antigen. In an alternate embodiment, immunoglobulin is specific for an antibody, wherein said antibody is specific for the target antigen. In an alternate embodiment, the immunoglobulin is specific for a hapten, and wherein either the target antigen, or an antibody or protein that is specific for the target antigen is haptenized.

[0052] Also disclosed herein are isolated nucleic acids encoding the immunoglobulins described herein. Also disclosed herein are vectors comprising the nucleic acids, optionally, operably linked to control sequences. Also disclosed herein are host cells containing the vectors, and methods for producing and optionally recovering the immunoglobulin compositions.

[0053] Also disclosed herein are immunoglobulin polypeptides, that comprise the immunoglobulins disclosed herein. The immunoglobulin polypeptides may find use in a therapeutic product. In one embodiment, the immunoglobulin polypeptides disclosed herein may be antibodies.

[0054] Also disclosed are compositions comprising immunoglobulin polypeptides described herein, and a physiologically or pharmaceutically acceptable carrier or diluent.

[0055] Also described are therapeutic and diagnostic uses for the immunoglobulin polypeptides disclosed herein. In one embodiment, the immunoglobulins disclosed herein are used to treat one or more autoimmune disease or inflammatory disease. In an alternate embodiment, the immunoglobulins disclosed herein are used to treat one or more hematological malignancies.

BRIEF DESCRIPTION OF THE DRAWINGS

[0056] FIG. **1**. Antibody structure and function. Shown is a model of a full length human IgG1 antibody, modeled using a humanized Fab structure from pdb accession code 1CE1

(James et al., 1999, J Mol Biol 289:293-301) and a human IgG1 Fc structure from pdb accession code 1 DN2 (DeLano et al., 2000, Science 287:1279-1283). The flexible hinge that links the Fab and Fc regions is not shown. IgG1 is a homodimer of heterodimers, made up of two light chains and two heavy chains. The Ig domains that comprise the antibody are labeled, and include V_L and C_L for the light chain, and V_H, Cgamma1 (Cγ1), Cgamma2 (Cγ2), and Cgamma3 (Cγ3) for the heavy chain. The Fc region is labeled. Binding sites for relevant proteins are labeled, including the antigen binding site in the variable region, and the binding sites for FcγRs, FcRn, C1q, and proteins A and G in the Fc region.

[0057] FIG. **2**. The Fc/FcγRIIIb complex structure 1IIS. Fc is shown as a gray ribbon diagram, and FcγRIIb is shown as a black ribbon. The N297 carbohydrate is shown as black sticks.

[0058] FIGS. **3***a*-**3***b*. Alignment of the amino acid sequences of the human IgG immunoglobulins IgG1, IgG2, IgG3, and IgG4. FIG. **3***a* provides the sequences of the CH1 (Cγ1) and hinge domains, and FIG. **3***b* provides the sequences of the CH2 (Cγ2) and CH3 (Cγ3) domains. Positions are numbered according to the EU index of the IgG1 sequence, and differences between IgG1 and the other immunoglobulins IgG2, IgG3, and IgG4 are shown in grey. Polymorphisms exist at a number of positions (Kim et al., 2001, J. Mol. Evol. 54:1-9), and thus slight differences between the presented sequences and sequences in the prior art may exist. The possible beginnings of the Fc region are labeled, defined herein as either EU position 226 or 230.

[0059] FIG. **4**. Residues at which amino acid modifications were made in the Fc variants of the present invention, mapped onto the Fc/FcγRIIIb complex structure 1IIS. Fc is shown as a gray ribbon diagram, and FcγRIIIb is shown as a black ribbon. Experimental library residues are shown in black, the N297 carbohydrate is shown in grey.

[0060] FIG. **5**. Expression of Fc variant and wild type (WT) proteins of alemtuzumab in 293T cells. Plasmids containing alemtuzumab heavy chain genes (WT or variants) were co-transfected with plasmid containing the alemtuzumab light chain gene. Media were harvested 5 days after transfection. For each transfected sample, 10 ul medium was loaded on a SDS-PAGE gel for Western analysis. The probe for Western was peroxidase-conjugated goat-anti human IgG (Jackson Immuno-Research, catalog #109-035-088). WT: wild type alemtuzumab; 1-10: alemtuzumab variants. H and L indicate antibody heavy chain and light chain, respectively.

[0061] FIG. **6**. Purification of alemtuzumab using protein A chromatography. WT alemtuzumab proteins was expressed in 293T cells and the media was harvested 5 days after transfection. The media were diluted 1:1 with PBS and purified with protein A (Pierce, Catalog #20334). O: original sample before purification; FT: flow through; E: elution; C: concentrated final sample. The left picture shows a Simple Blue-stained SDS-PAGE gel, and the right shows a western blot labeled using peroxidase-conjugated goat-anti human IgG.

[0062] FIG. **7**. Production of deglycosylated antibodies. Wild type and variants of alemtuzumab were expressed in 293T cells and purified with protein A chromatography. Antibodies were incubated with peptide-N-glycosidase (PNGase F) at 37° C. for 24 h. For each antibody, a mock treated sample (−PNGase F) was done in parallel. WT: wild-type alemtuzumab; #15, #16, #17, #18, #22: alemtuzumab variants F241E/F243R/V262E/V264R, F241E/F243Q/V262T/V264E, F241R/F243Q/V262T/V264R, F241 E/F243Y/V262T/V264R, and I332E respectively. The faster migration of the PNGase F treated versus the mock treated samples represents the deglycosylated heavy chains.

[0063] FIG. **8**. Alemtuzumab expressed from 293T cells binds its antigen. The antigenic CD52 peptide, fused to GST, was expressed in *E. coli* BL21 (DE3) under IPTG induction. Both uninduced and induced samples were run on a SDS-PAGE gel, and transferred to PVDF membrane. For western analysis, either alemtuzumab from Sotec (a-CD52, Sotec) (final concentration 2.5 ng/ul) or media of transfected 293T cells (Campath, Xencor) (final alemtuzumab concentration approximately 0.1-0.2 ng/ul) were used as primary antibody, and peroxidase-conjugated goat-anti human IgG was used as secondary antibody. M: pre-stained marker; U: un-induced sample for GST-CD52; I: induced sample for GST-CD52.

[0064] FIG. **9**. Expression and purification of extracellular region of human V158 FcγRIIIa. Tagged FcγRIIIa was transfected in 293T cells, and media containing secreted FcγRIIIa were harvested 3 days later and purified using affinity chromatography. 1: media; 2: flow through; 3: wash; 4-8: serial elutions. Both simple blue-stained SDS-PAGE gel and western result are shown. For the western blot, membrane was probed with anti-GST antibody.

[0065] FIG. **10**. Binding to human V158 FcγRIIIa by select alemtuzumab Fc variants from the experimental library as determined by the AlphaScreen™ assay, described in Example 2. In the presence of competitor antibody (Fc variant or WT alemtuzumab) a characteristic inhibition curve is observed as a decrease in luminescence signal. Phosphate buffer saline (PBS) alone was used as the negative control. The binding data were normalized to the maximum and minimum luminescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a one site competition model using nonlinear regression. These fits provide IC50s for each antibody, illustrated for WT and S239D by the dotted lines.

[0066] FIGS. **11***a* and **11***b*. AlphaScreen assay showing binding of select alemtuzumab (FIG. **11***a*) and trastuzumab (FIG. **11***b*) Fc variants to human Vail 58 FcγRIIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0067] FIG. **12**. AlphaScreen assay showing binding of select alemtuzumab Fc variants to human FcγRIIb. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0068] FIG. **13**. AlphaScreen assay showing binding of select alemtuzumab Fc variants to human R131 FcγRIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model.

[0069] FIG. **14**. AlphaScreen assay measuring binding of select alemtuzumab Fc variants to human FcRn, as described in Example 2. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0070] FIG. **15**. AlphaScreen assay measuring binding of select alemtuzumab Fc variants to bacterial protein A, as described in Example 2. The binding data were normalized to

the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0071] FIGS. **16***a*-**16***b*. AlphaScreen assay comparing binding of select alemtuzumab Fc variants to human V158 FcγRIIIa (FIG. **16***a*) and human FcγRIIb (FIG. **16***b*). The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0072] FIGS. **17***a*-**17***b*. AlphaScreen assay measuring binding to human V158 FcγRIIIa (FIGS. **17***a* and **17***b*) and human FcγRIIb (FIG. **17***c*) by select Fc variants in the context of trastuzumab. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0073] FIG. **18**. AlphaScreen assay measuring binding to human V158 FcγRIIIa by select Fc variants in the context of rituximab. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0074] FIG. **19**. AlphaScreen assay measuring binding to human V158 FcγRIIIa by select Fc variants in the context of cetuximab. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0075] FIGS. **20***a*-**20***b*. AlphaScreen assay showing binding of select alemtuzumab Fc variants to the V158 (FIG. **20***a*) and F158 (FIG. **20***b*) allotypes of human FcγRIIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0076] FIGS. **21***a*-**21***d*. FIGS. **21***a* and **21***b* show the correlation between SPR Kd's and AlphaScreen IC50's from binding of select alemtuzumab Fc variants to V158 FcγRIIIa (FIG. **21***a*) and F158 FcγRIIIa (FIG. **21***b*). FIGS. **21***c* and **21***d* show the correlation between SPR and AlphaScreen fold-improvements over WT for binding of select alemtuzumab Fc variants to V158 FcγRIIIa (FIG. **21***c*) and F158 FcγRIIIa (FIG. **21***d*). Binding data are presented in Table 3. The lines through the data represent the linear fits of the data, and the r^2 values indicate the significance of these fits.

[0077] FIGS. **22***a* and **22***b*. AlphaScreen assay showing binding of select alemtuzumab Fc variants to human V158 FcγRIIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0078] FIGS. **23***a*-**23***b*. Cell-based ADCC assays of select Fc variants in the context of alemtuzumab. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay (Perkin Elmer, MA), as described in Example 3, using DoHH-2 lymphoma target cells and 50-fold excess human PBMCs. FIG. **23***a* is a bar graph showing the raw fluorescence data for the indicated alemtuzumab antibodies at 10 ng/ml. The PBMC bar indicates basal levels of cytotoxicity in the absence of antibody. FIG. **23***b* shows the dose-dependence of ADCC on antibody concentration for the indicated alemtuzumab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0079] FIGS. **24***a*-**24***c*. Cell-based ADCC assays of select Fc variants in the context of trastuzumab. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay, as described in Example 3, using BT474 and Sk-Br-3 breast carcinoma target cells and 50-fold excess human PBMCs. FIG. **24***a* is a bar graph showing the raw fluorescence data for the indicated trastuzumab antibodies at 1 ng/ml. The PBMC bar indicates basal levels of cytotoxicity in the absence of antibody. FIGS. **24***b* and **24***c* show the dose-dependence of ADCC on antibody concentration for the indicated trastuzumab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0080] FIGS. **25***a*-**25***c*. Cell-based ADCC assays of select Fc variants in the context of rituximab. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay, as described in Example 3, using WIL2-S lymphoma target cells and 50-fold excess human PBMCs. FIG. **25***a* is a bar graph showing the raw fluorescence data for the indicated rituximab antibodies at 1 ng/ml. The PBMC bar indicates basal levels of cytotoxicity in the absence of antibody. FIGS. **25***b* and **25***c* show the dose-dependence of ADCC on antibody concentration for the indicated rituximab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0081] FIGS. **26***a*-**26***b*. Cell-based ADCC assay of select trastuzumab (FIG. **26***a*) and rituximab (FIG. **26***b*) Fc variants showing enhancements in potency and efficacy. Both assays used homozygous F158/F158 FcγRIIIa PBMCs as effector cells at a 25-fold excess to target cells, which were Sk-Br-3 for the trastuzumab assay and WIL2-S for the rituximab assay. Data were normalized according to the absolute minimal lysis for the assay, provided by the fluorescence signal of target cells in the presence of PBMCs alone (no antibody), and the absolute maximal lysis for the assay, provided by the fluorescence signal of target cells in the presence of Triton X1000, as described in Example 3.

[0082] FIG. **27**. AlphaScreen assay showing binding of select alemtuzumab Fc variants to human V158 FcγRIIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0083] FIG. **28**. ADCC. Cell-based ADCC assays of select Fc variant trastuzumab antibodies as compared to WT trastuzumab. Purified human peripheral blood monocytes (PBMCs) were used as effector cells, and Sk-Br-3 breast carcinoma cells were used as target cells. Lysis was monitored by measuring LDH activity using the Cytotoxicity Detection Kit (LDH, Roche Diagnostic Corporation, Indianapolis, Ind.). Samples were run in triplicate to provide error estimates (n=3, +/−S.D.). The figure shows the dose dependence of ADCC at various antibody concentrations, normalized to the minimum and maximum levels of lysis for the assay. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0084] FIGS. **29***a*-**29***b*. Cell-based ADCC assay of select trastuzumab Fc variants against different cell lines expressing varying levels of the Her2/neu target antigen. ADCC assays were run as described in Example 5, with various cell lines expressing amplified to low levels of Her2/neu receptor, including Sk-Br-3 (1×106 copies), SkOV3 (~1×105), OVCAR3(~1×104), and MCF-7 (~3×103 copies). FIG. **29***a* provides a western blot showing the Her2 expression level for each cell line; equivalent amounts of cell lysate were loaded on an SDS-PAGE gel, and Her2 was detected using trastuzumab. Human PBMCs allotyped as homozygous F158/F158 FcγRIIIa were used at 25-fold excess to target cells. The bar graph in FIG. **29***b* provides ADCC data for WT and Fc variant against the indicated cell lines, normalized to the minimum and maximum fluorescence signal provided by minimal lysis (PBMCs alone) and maximal lysis (Triton X1000).

[0085] FIG. **30**. Cell-based ADCC assays of select Fc variants in the context of trastuzumab using natural killer (NK) cells as effector cells and measuring LDH release to monitor cell lysis. NK cells, allotyped as heterozygous F158/F158 FcγRIIIa, were at an 4-fold excess to Sk-Br-3 breast carcinoma target cells, and the level of cytotoxicity was measured using the LDH Cytotoxicity Detection Kit, according to the manufacturer's protocol (Roche Diagnostics GmbH, Penzberg, Germany). The graph shows the dose-dependence of ADCC on antibody concentration for the indicated trastuzumab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0086] FIG. **31**. Cell-based ADCP assay of select variants. The ADCP assay was carried out as described in Example 7, using a co-labeling strategy coupled with flow cytometry. Differentiated macrophages were used as effector cells, and Sk-Br-3 cells were used as target cells. Percent phagocytosis represents the number of co-labeled cells (macrophage+Sk-Br-3) over the total number of Sk-Br-3 in the population (phagocytosed+non-phagocytosed).

[0087] FIGS. **32***a*-**32***c*. Capacity of select Fc variants to mediate binding and activation of complement. FIG. **32***a* shows an AlphaScreen assay measuring binding of select alemtuzumab Fc variants to C1q. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. FIGS. **32***b* and **31***c* show a cell-based assay measuring capacity of select rituximab Fc variants to mediate CDC. CDC assays were performed using Alamar Blue to monitor lysis of Fc variant and WT rituximab-opsonized WIL2-S lymphoma cells by human serum complement (Quidel, San Diego, Calif.). The dose-dependence on antibody concentration of complement-mediated lysis is shown for the indicated rituximab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0088] FIGS. **33***a*-**33***c*. Enhanced B cell depletion by Fc variants in macaques, as described in Example 9. FIG. **33***a* shows the percent B cells remaining in *Macaca Fascicularis* monkeys during treatment with anti-CD20 WT and S239D/I332E rituximab antibodies, measured using markers CD20+ and CD40+. FIG. **33***b* shows the percent natural killer (NK) cells remaining in the monkeys during treatment, measured using markers CD3−/CD16+ and CD3−/CD8+. FIG. **33***c* shows the dose response of CD20+ B cell levels to treatment with S239D/I332E rituximab. Data are presented as the average of 3 monkeys/sample.

[0089] FIGS. **34***a* and **34***b*. AlphaScreen assay measuring binding of select alemtuzumab (FIG. **34***a*) and trastuzumab (FIG. **34***b*) Fc variants to mouse FcγRIII, as described in Example 10. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0090] FIG. **35**. Cell-based ADCC assays of select Fc variants in the context of trastuzumab using mouse PBMCs as effector cells. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay using Sk-Br-3 breast carcinoma target cells and 8-fold excess mouse PBMCs. The bar graph shows the raw fluorescence data for the indicated trastuzumab antibodies at 10 ng/ml. The PBMC bar indicates basal levels of cytotoxicity in the absence of antibody, and TX indicates complete cell lysis in the presence of Triton X1000.

[0091] FIG. **36**. AlphaScreen assay measuring binding to human V158 FcγRIIIa by select trastuzumab Fc variants expressed in 293T and CHO cells, as described in Example 11. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0092] FIGS. **37***a*-**37***b*. Synergy of Fc variants and engineered glycoforms. FIG. **37***a* presents an AlphaScreen assay showing V158 FcγRIIIa binding by WT and Fc variant (V209, S239/1332E/A330L) trastuzumab expressed in 293T, CHO, and Lec-13 CHO cells. The data were normalized to the upper and lower baselines for each antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control. FIG. **37***b* presents a cell-based ADCC assay showing the ability of 239T, CHO, and Lec-13 CHO expressed WT and V209 trastuzumab to mediate ADCC. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay as described previously, with Sk-Br-3 breast carcinoma target cells. The data show the dose-dependence of ADCC on antibody concentration for the indicated trastuzumab antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[0093] FIG. **38**. AlphaScreen assay showing binding of aglycosylated alemtuzumab Fc variants to human V158 FcγRIIIa. The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model. PBS was used as a negative control.

[0094] FIG. **39**. AlphaScreen assay comparing human V158 FcγRIIIa binding by select alemtuzumab Fc variants in glycosylated (solid symbols, solid lines) and deglycosylated (open symbols, dotted lines). The binding data were normalized to the upper and lower baselines for each particular antibody, and the curves represent the fits of the data to a one site competition model.

[0095] FIGS. **40***a*-**40***c*. Sequences showing improved anti-CD20 antibodies. The light and heavy chain sequences of rituximab are presented in FIG. **40***a* and FIG. **40***b* respec-

tively, and are taken from translated Sequence 3 of U.S. Pat. No. 5,736,137. Relevant positions in FIG. **40***b* are bolded, including S239, V240, V264I, H268, E272, K274, N297, S298, K326, A330, and I332. FIG. **40***c* shows the improved anti-CD20 antibody heavy chain sequences, with variable positions designated in bold as X1, X2, X3, X4, X5, X6, X7, X8, X9, Z1, and Z2. The table below the sequence provides possible substitutions for these positions. The improved anti-CD20 antibody sequences comprise at least one non-WT amino acid selected from the group of possible substitutions for X1, X2, X3, X4, X5, X6, X7, X8, and X9. These improved anti-CD20 antibody sequences may also comprise a substitution Z1 and/or Z2. These positions are numbered according to the EU index as in Kabat, and thus do not correspond to the sequential order in the sequence.

[0096] FIG. **41** depicts the set of Fc variants that were constructed and experimentally tested.

[0097] FIG. **42** depicts SEQ ID NO:5; the particular Xaa residues are as shown in Table 10.

[0098] FIG. **43**. Common haplotypes of the human gamma1 (FIG. **43**A) and gamma2 (FIG. **43**B) chains.

[0099] FIG. **44**. Novel methods of inhibiting B cell activation. Here CR represents a co-receptor of the BCR complex, but could be any antigen expressed on any FcγRIIb+ cell.

[0100] FIG. **45**. FcγR positions that contribute to FcγRIIIb and FcγRIIIa binding selectivity. Positions were identified by evaluating proximity to the FcγR/Fc interface and amino acid dissimilarity between FcγRIIb and FcγRIIIa.

[0101] FIG. **46**. Fc positions proximal to FcγR positions contributing to FcγRIIb and FcγRIIIa binding selectivity, as listed in FIG. **47**.

[0102] FIG. **47**. Biacore surface plasmon resonance sensorgrams showing binding of Fc variant anti-CD19 antibodies to human FcγRIIb.

[0103] FIG. **48**. Affinities of Fc variant antibodies for human FcγRs as determined by Biacore surface plasmon resonance. The table lists the dissociation constant (Kd) for binding anti-CD19 variant antibodies to human FcγRI, FcγRIIa (131R), FcγRIIa (131H), FcγRIIb, FcγRIIIa (158V), and FcγRIIIa (158F). Multiple observations have been averaged. n.d.=no detectable binding.

[0104] FIG. **49**. Fold affinities of Fc variant antibodies for human FcγRs as determined by Biacore surface plasmon resonance. The table lists the fold improvement or reduction in affinity relative to WT IgG1 for binding of anti-CD19 variant antibodies to human FcγRI, FcγRIIa (131R), FcγRIIa (131H), FcγRIIb, FcγRIIIa (158V), and FcγRIIIa (158F). Fold=KD(Native IgG1)/KD(variant). n.d.=no detectable binding.

[0105] FIG. **50**. Affinities of Fc variant antibodies for human FcγRs as determined by Biacore surface plasmon resonance. The graph shows the −log(KD) for binding of anti-CD19 variant and WT IgG1 antibodies to human FcγRI (I), R131 FcγRIIa (RIIa), H131 FcγRIIa (HIIa), FcγRIIb (IIb), and V158 FcγRIIIa (VIIIa). Binding of L235Y/S267E, G236D/S267E, and S267E/L328F to V158 FcγRIIIa was not detectable.

[0106] FIG. **51**. Affinities of Fc variant antibodies for human FcγRs as determined by Biacore surface plasmon resonance. The graph shows the −log(KD) for binding of anti-CD19 variant and WT IgG1 antibodies to human FcγRI (I), R131 FcγRIIa (RIIa), H131 FcγRIIa (HIIa), FcγRIIb (IIb), and V158 FcγRIIIa (VIIIa).

[0107] FIG. **52**. Analysis of combination variants (doubles, triples) for synergistic and non-additive effects in binding to human FcγRIIb (A), FcγRI (B), R131 FcγRIIa (C), H131 FcγRIIa (D), and V158 FcγRIIIa (E). The ratio between actual fold improvement measured by SPR and expected fold improvement calculated by multiplying the fold improvements of the single substitution variants is plotted. Ratios greater than one indicate a synergistic effect.

[0108] FIG. **53**. Binding of Fc variant antibodies to human FcγRs relative to WT IgG1 as measured by cell surface binding. Antibodies (variant and WT IgG1) were added to HEK293T cells transfected with FcγRIIb to assess cell surface binding. The binding curves were constructed by plotting MFI as a function of Fc variant concentration.

[0109] FIG. **54**. Affinities of Fc variant antibodies for mouse and cynologous monkey (*Macaca fascicularis*) FcγRs as determined by Biacore surface plasmon resonance, either by dissociation constant (Kd) or off-rate determination as indicated. The table lists the fold improvement relative to WT IgG1 for binding of anti-CD19 antibody variants to mouse FcγRI, mouse FcγRII, mouse FcγRIII, mouse FcγRIV, cynomolgus monkey FcγRI, cynomolgus monkey FcγRIIa, cynomolgus monkey FcγRIIb, and cynomolgus monkey FcγRIIIa. NB=no detectable binding.

[0110] FIG. **55**. Affinities of Fc variant antibodies for human FcγRs as determined by Biacore surface plasmon resonance. The graph shows the −log(KD) for binding of anti-CD19 variant and WT IgG1 antibodies to human FcγRI (I), R131 FcγRIIa (RIIa), H131 FcγRIIa (HIIa), FcγRIIb (IIb), and V158 FcγRIIIa (VIIIa).

[0111] FIG. **56**. ATP-dependent B cell viability assay demonstrating the survival of primary human B cells upon BCR activation, here carried out by crosslinking with anti-mu (A) or anti-CD79b (B) antibodies.

[0112] FIG. **57**. Inhibition of B cell proliferation by Fc variant anti-CD19 antibodies. Anti-RSV (Respiratory Syncytial Virus) S267E/L328F is used as a control (RSV is not expressed on B cells). An ATP-dependent luminescence assay was used to measure B cell proliferation in the presence of 10 μg/ml anti-CD79b activating antibody, and the effect of anti-CD19-S267E/L328F was compared to anti-CD19-IgG1 (native IgG1 Fv control) and anti-RSV-S267E/L328F (non-CD19 Fc control). To assess the importance of CD19 and FcγRIIb coengagement, anti-RSV-S267E/L328F alone or in combination with anti-CD19-IgG1 was used.

[0113] FIG. **58**. Inhibition of B cell proliferation by Fc variant anti-CD19 antibodies. An ATP-dependent luminescence assay was used to measure proliferation of primary human B cells in the presence of 1 μg/ml anti-CD79b activating antibody, and varying concentrations of the indicated anti-CD19 or anti-RSV control antibodies.

[0114] FIG. **59**. Inhibition of B cell proliferation by Fc variant anti-CD19 antibodies. An ATP-dependent luminescence assay was used to measure proliferation of primary human B cells in the presence of 2 μg/ml anti-μ (mu) antibody and varying concentrations of the indicated anti-CD19 antibodies.

[0115] FIG. **60**. Coengagement of FcγRIIb and CD19 by IIbE variants inhibits BCR activation-induced calcium mobilization in primary human B cells. Calcium mobilization was induced with 10 μg/ml anti-CD79b BCR-activating antibody. Calcium mobilization was measured in the presence of 10 μg/ml fixed concentration of anti-CD19 IIbE variants, α-CD19-IgG1 (native IgG1 Fv control), α-FITC-S267E/

L328F (non-CD19 Fc control), or PBS vehicle. The data are plotted as the change of MFI over time, or the area under the response curve normalized to the maximum measured signal intensity.

[0116] FIG. **61**. Coengagement of FcγRIIb and CD19 by IIbE variants inhibits BCR activation-induced calcium mobilization in primary human B cells. Calcium mobilization was induced with 10 μg/ml anti-CD79b BCR-activating antibody. Calcium mobilization was measured at multiple antibody concentrations for anti-CD19-IgG1 and three IIbE variants, and the areas under the curves were plotted to obtain dose-response relationships.

[0117] FIG. **62**. Correlation between affinity for FcγRIIb and inhibition of calcium release. EC50 data are from FIG. **61**, and symbols are the same as indicated in FIG. **63**. Affinities are from Biacore data presented in FIG. **48**.

[0118] FIG. **63**. Coengagement of FcγRIIIb and CD19 by IIbE variants inhibits BCR activation-induced calcium mobilization in primary human B cells. Calcium mobilization was induced with 10 μg/ml anti-CD79b BCR-activating antibody. Soluble FcγRI (50 μg/ml) added to 10 pg/ml α-CD19-S267E/L328F completely abolished the IIbE variant's inhibitory effect on calcium mobilization, confirming the importance of FcγRIIb engagement by anti-CD19 antibody.

[0119] FIG. **64**. IIbE variant anti-CD19-S267E/L328F activates FcγRIIb-mediated SHIP phosphorylation in primary human B cells. Anti-CD19-S267E/L328F, anti-CD19-IgG1 (Fv control), anti-RSV-S267E/L328F (Fc control), anti-CD19-Fc KO (Fv control), or anti-FcγRII (10 μg/ml each) were added to B cells in the presence of 20 μg/ml anti-CD79b antibody. As a positive control, 20 μg/ml goat anti-mouse IgG F(ab')2 fragment was used to crosslink anti-CD79b and anti-FcγRII antibodies. A blot of total cellular extracts was probed with anti-pSHIP, with anti-GAPDH used as a loading control. Relative to negative controls, anti-CD19-S267E/L328F induced greater SHIP1 phosphorylation than direct crosslinking of BCR and FcγRIIb by CD79b and FcγRIIb antibodies.

[0120] FIG. **65**. Anti-CD19-S267E/L328F inhibits the anti-apoptotic effects of BCR activation on primary human B cells. Inhibition of BCR-mediated survival signals by FcγRIIb and CD19 coengagement was examined using annexin-V staining in the presence of 10 μg/ml anti-CD79b. B cell apoptosis was stimulated by anti-CD19-S267E/L328F, but not anti-CD19-IgG1 (Fv control), anti-RSV-S267E/L328F (Fc control), or the two controls combined.

[0121] FIG. **66**. NK-cell mediated ADCC activity of Fc variant antibodies against Ramos B cells.

[0122] FIG. **67**. Macrophage mediated phagocytosis (ADCP) activity of Fc variant antibodies against RS4; 11 Bcells.

[0123] FIG. **68**. Fc variant anti-CD19 antibodies do not mediate CDC activity against Raji B cells.

[0124] FIG. **69**: Evaluation of the capacity of co-engagement of CD19 and FcγRIIb to inhibit human B cell activation in vivo. (A) Schematic representation of the experimental protocol. (B) Titer of anti-tetanus toxoid (TT) specific antibody in huPBL-SCID mice after TT immunization and treatment with vehicle (PBS), anti-CD19 IgG1 WT, anti-CD19 with enhanced FcγRIIb affinity (a-CD19 S267E/L328F), or anti-CD20 (Rituximab).

[0125] FIG. **70**. Target antigens that may be effective FcγRIIb co-targets for modulation of cellular activity. B=B cells, Plasma=plasma cells, DC=dendritic cells, MΦ=macrophages, PMN=neutrophils, Baso=basophils, Eos=eosinophils, and Mast=mast cells.

[0126] FIG. **71**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b-SN8-G236R/L328R antibody, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout variant (G236R/L328R or ^236R/L328R) versions of anti-CD20 (clone PRO70769), -CD52 (Campath), and -CD19 (HuAM4G7) antibodies.

[0127] FIG. **72**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ antibody, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R), or WT IgG1 versions of anti-CD23 antibodies (clone 5E8 or C11).

[0128] FIG. **73**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ antibody, and either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R), or WT IgG1 versions of the anti-CD79b antibody SN8.

[0129] FIG. **74** ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ antibody, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R), or WT IgG1 versions of anti-CD22 antibody.

[0130] FIG. **75** ATP-dependent luminescence assay measuring B cell proliferation in the presence of BCR stimulation by (A) 1 μg/ml anti-CD79b-SN8-G236R/L328R antibody or (B) 2 μg/ml anti-μ antibody, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R), or WT IgG1 versions of anti-CD40 antibodies (clones PFCD40, S2C6, G28.5, and 5D12).

[0131] FIG. **76**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b-SN8-G236R/L328R antibody, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout variant (G236R/L328R or ^236R/L328R) versions of anti-CD19 antibodies (clones HD37, 21D4, or HuAM4G7.

[0132] FIG. **77**. Calcium release assay measuring inhibition capacity of variant antibodies with specificity for CD22 (A), CD23 (B), CD40 (C), and CD79b (D). Calcium mobilization was induced with 10 μg/ml anti-CD79b-SN8-G236R/L328R antibody, and monitored in the presence of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout variant (G236R/L328R) versions of anti-CD22, —CD23, —CD40, and CD79b antibodies.

[0133] FIG. **78**. Hapten approach to screening target antigens for capacity to modulate cellular activity upon high affinity co-targeting with FcγRIIb.

[0134] FIG. **79**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml FITCylated anti-μ F(ab')2 and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R or ^236R/L328R), or WT IgG1 versions of anti-FITC antibody (clone 4-4-20). Anti-RSV was included as a control.

[0135] FIG. **80**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ F(ab')2, 0.5 pg/ml FITC-labeled anti-CD19 (clone murine 4G7 IgG1), and varying concentrations of either enhanced

FcγRIIb variant (S267E/L328F), FcγR knockout variant (ˆ236R/L328R), or WT IgG1 versions of anti-FITC antibody.

[0136] FIG. **81**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ F(ab')2, 0.5 pg/ml FITC-labeled anti-CD20 clone PDR-79 (A) or 1 pg/ml FITC-labeled Rituxan (B), and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (ˆ236R/L328R), or WT IgG1 versions of anti-FITC antibody. FITC-labeled anti-mu at 2 μg/ml is also included in (B) as a control.

[0137] FIG. **82**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, 0.5 μg/ml FITC-labeled anti-CD21, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or WT IgG1 versions of anti-FITC antibody.

[0138] FIG. **83**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, 0.5 μg/ml FITC-labeled anti-CD24, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or WT IgG1 versions of anti-FITC antibody.

[0139] FIG. **84**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ F(ab')2, 0.25 μg/ml FITC-labeled anti-CD1 or 0.5 μg/ml FITC-labeled anti-CD24, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or WT IgG1 versions of anti-FITC antibody.

[0140] FIG. **85**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, FITC-labeled anti-CD35, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0141] FIG. **86**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, FITC-labeled anti-CD45RA, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0142] FIG. **87**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, FITC-labeled anti-CD72, and varying concentrations of either enhanced FcγRIIb variant (S267 μL328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0143] FIG. **88**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ F(ab')2, 2 μg/ml FITC-labeled anti-CD79a (clone ZL7-4), and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout (1236R/L328R) or WT IgG1 versions of anti-FITC antibody.

[0144] FIG. **89**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 2 μg/ml anti-μ F(ab')2, 1.8 μg/ml FITC-labeled anti-CD79b (clone ZL9-3), and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout (A236R/L328R) or WT IgG1 versions of anti-FITC antibody.

[0145] FIG. **90**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b (SN8) antibody, FITC-labeled anti-CD80, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0146] FIG. **91**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of FITC-labeled anti-CD81, varying concentrations of either enhanced FcγRIIb variant (S267E/L328F), FcγR knockout variant (G236R/L328R), or WT IgG1 versions of anti-FITC antibody, and 2 μg/ml anti-μ antibody.

[0147] FIG. **92**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b(SN8)-G236R/L328R antibody, FITC-labeled anti-CD86, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0148] FIG. **93**. ATP-dependent luminescence assay measuring B cell proliferation in the presence of 1 μg/ml anti-CD79b(SN8)-G236R/L328R antibody, FITC-labeled anti-HLA-DR, and varying concentrations of either enhanced FcγRIIb variant (S267E/L328F) or FcγR knockout (G236R/L328R) versions of anti-FITC antibody.

[0149] FIG. **94**. Summary of results from target antigen screening for capacity of antigens to modulate B cell activation when co-targeted with high affinity FcγRIIb binding. Results are from the ATP-dependence luminescence B cell viability assay or calcium mobilization assay using either Fc variant versions of antibodies with specificity for the indicated target antigens (Fc variant approach) or Fc variant versions of the anti-FITC antibody together with commercial antibodies with specificity for the indicated target antigens (Hapten approach)

[0150] FIG. **95**. Amino acid sequences of variable regions, heavy chain constant regions, and full length antibodies in Example 16.

DETAILED DESCRIPTION OF THE INVENTION

[0151] The humoral immune response (e.g., the result of diverse B cell responses) may be initiated when B cells are activated by an antigen and subsequently differentiated into plasma cells. Binding of membrane bound B cell receptor (BCR) on B cells by an antigen activates an intracellular signaling cascade, including calcium mobilization, which leads to cell proliferation and differentiation. Coengagement of cognate BCR with the inhibitory Fc receptor (FcγRIIb) inhibits B cell activation signals through a negative feedback loop.

[0152] The importance of FcγRIIb in negative regulation of B cell responses has been demonstrated using FcγRIIb-deficient mice, which fail to regulate humoral responses (Wernersson, S. et al., 1999, J. Immunol. 163, 618-622), are sensitized to collagen-induced arthritis (Yuasa, T. et al., 1999, J. Exp. Med. 189, 187-194), and develop lupus-like disease (Fukuyama, H. et al., J. V., 2005, Nat. Immunol. 6, 99-106; McGaha, T. L. et al., 2005, Science 307, 590-593) and Goodpasture's syndrome (Nakamura, A. et al., 2000, J. Exp. Med. 191, 899-906). FcγRIIb dysregulation has also been associated with human autoimmune disease. For example, polymorphisms in the promoter (Blank, M. C. et al., 2005, Hum. Genet. 117, 220-227; Olferiev, M. et al., 2007, J. Biol. Chem. 282, 1738-1746) and transmembrane domain (Chen, J. Y. et al., 2006, Arthritis Rheum. 54, 3908-3917; Floto, R. A. et al., Nat. Med. 11, 1056-1058; Li, X. et al., 2003, Arthritis Rheum. 48, 3242-3252) of FcγRIIb have been linked with increased prevalence of systemic lupus erythematosus (SLE). SLE patients also show reduced FcγRIIb surface expression on B cells (Mackay, M. et al., 2006, J. Exp. Med. 203, 2157-2164; Su, K. et al., 2007, J. Immunol. 178, 3272-3280) and, as a

consequence, exhibit dysregulated calcium signaling (Mackay, M. et al., 2006, J. Exp. Med. 203, 2157-2164). The pivotal role of FcγRIIb in regulating B cells, supported by mouse models and clinical evidence, makes it an attractive therapeutic target for controlling autoimmune and inflammatory disorders (Pritchard, N. R. & Smith, K. G., 2003, Immunology 108, 263-273; Ravetch, J. V. & Lanier, L. L., 2000, Science 290, 84-89; Stefanescu, R. N. et al., 2004, J. Clin. Immunol. 24, 315-326).

[0153] Described herein are antibodies that mimic the inhibitory effects of coengagement of cognate BCR with FcγRIIb on B cells. For example, describe herein are variant anti-CD19 antibodies engineered such that the Fc domain binds to FcγRIIb with up to ~430-fold greater affinity. Relative to native IgG1, the FcγRIIb binding-enhanced (IIbE) variants strongly inhibit BCR-induced calcium mobilization and viability in primary human B cells. Inhibitory effects involved phosphorylation of SH2-containing inositol polyphosphate 5-phosphatase (SHIP), which is known to be involved in FcγRIIb-induced negative feedback of B cell activation. Coengagement of BCR and FcγRIIb by IIbE variants also overcame the anti-apoptotic effects of BCR activation. The use of a single antibody to suppress B cell functions by coengagement of cognate BCR and FcγRIIb may represent a novel approach in the treatment of B cell-mediated diseases. Nonlimiting examples of B cell-mediated diseases include hematological malignancies, autoimmunity, allergic responses, etc.

[0154] In order that the invention may be more completely understood, several definitions are set forth below. Such definitions are meant to encompass grammatical equivalents.

[0155] By "ADCC" or "antibody dependent cell-mediated cytotoxicity" as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

[0156] By "ADCP" or antibody dependent cell-mediated phagocytosis as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause phagocytosis of the target cell.

[0157] By "modification" herein is meant an alteration in the physical, chemical, or sequence properties of a protein, polypeptide, antibody, or immunoglobulin. Modifications described herein include amino acid modifications and glycoform modifications.

[0158] By "amino acid modification" herein is meant an amino acid substitution, insertion, and/or deletion in a polypeptide sequence. The preferred amino acid modification herein is a substitution. By "amino acid substitution" or "substitution" herein is meant the replacement of an amino acid at a particular position in a parent polypeptide sequence with another amino acid. For example, the substitution I332E refers to a variant polypeptide, in this case an Fc variant, in which the isoleucine at position 332 is replaced with a glutamic acid. In some embodiments, the WT identity need not be defined. For example, the substitution 332E refers to a variant polypeptide in which position 332 is mutated to glutamic acid.

[0159] By "glycoform modification" or "modified glycoform" or "engineered glycoform" as used herein is meant a carbohydrate composition that is covalently attached to a protein, for example an antibody, wherein said carbohydrate composition differs chemically from that of a parent protein. Modified glycoform typically refers to the different carbohydrate or oligosaccharide; thus for example an Fc variant may comprise a modified glycoform. Alternatively, modified glycoform may refer to the Fc variant that comprises the different carbohydrate or oligosaccharide.

[0160] By "antibody" herein is meant a protein consisting of one or more polypeptides substantially encoded by all or part of the recognized immunoglobulin genes. The recognized immunoglobulin genes, for example in humans, include the kappa (κ), lambda (λ), and heavy chain genetic loci, which together comprise the myriad variable region genes, and the constant region genes mu (μ), delta (δ), gamma (γ), sigma (σ), and alpha (α) which encode the IgM, IgD, IgG, IgE, and IgA isotypes respectively. Antibody herein is meant to include full length antibodies and antibody fragments, and may refer to a natural antibody from any organism, an engineered antibody, or an antibody generated recombinantly for experimental, therapeutic, or other purposes as further defined below. The term "antibody" includes antibody fragments, as are known in the art, such as Fab, Fab', $F(ab')_2$, Fv, scFv, or other antigen-binding subsequences of antibodies, either produced by the modification of whole antibodies or those synthesized de novo using recombinant DNA technologies. Particularly preferred are full length antibodies that comprise Fc variants as described herein. The term "antibody" comprises monoclonal and polyclonal antibodies. Antibodies can be antagonists, agonists, neutralizing, inhibitory, or stimulatory. The antibodies of the present invention may be nonhuman, chimeric, humanized, or fully human, as described below in more detail.

[0161] Specifically included within the definition of "antibody" are aglycosylated antibodies. By "aglycosylated antibody" as used herein is meant an antibody that lacks carbohydrate attached at position 297 of the Fc region, wherein numbering is according to the EU system as in Kabat. The aglycosylated antibody may be a deglycosylated antibody, that is an antibody for which the Fc carbohydrate has been removed, for example chemically or enzymatically. Alternatively, the aglycosylated antibody may be a nonglycosylated or unglycosylated antibody, that is an antibody that was expressed without Fc carbohydrate, for example by mutation of one or residues that encode the glycosylation pattern or by expression in an organism that does not attach carbohydrates to proteins, for example bacteria.

[0162] Specifically included within the definition of "antibody" are full-length antibodies that contain an Fc variant portion.

[0163] By "full length antibody" herein is meant the structure that constitutes the natural biological form of an antibody, including variable and constant regions. For example, in most mammals, including humans and mice, the full length antibody of the IgG class is a tetramer and consists of two identical pairs of two immunoglobulin chains, each pair having one light and one heavy chain, each light chain comprising immunoglobulin domains V_L and C_L, and each heavy chain comprising immunoglobulin domains V_H, Cγ1 (C_H1), Cγ2 (C_H2), and Cγ3 (C_H3). In some mammals, for example in camels and llamas, IgG antibodies may consist of only two heavy chains, each heavy chain comprising a variable domain attached to the Fc region. By "IgG" as used herein is meant a polypeptide belonging to the class of antibodies that are substantially encoded by a recognized immunoglobulin gamma

gene. In humans this class comprises IgG1, IgG2, IgG3, and IgG4. In mice this class comprises IgG1, IgG2a, IgG2b, IgG3.

[0164] By "amino acid" and "amino acid identity" as used herein is meant one of the 20 naturally occurring amino acids or any non-natural analogues that may be present at a specific, defined position. By "protein" herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides. The protein may be made up of naturally occurring amino acids and peptide bonds, or synthetic peptidomimetic structures, i.e. "analogs", such as peptoids (see Simon et al., 1992, *Proc Natl Acad Sci USA* 89(20):9367, incorporated by reference) particularly when LC peptides are to be administered to a patient. Thus "amino acid", or "peptide residue", as used herein means both naturally occurring and synthetic amino acids. For example, homophenylalanine, citrulline and noreleucine are considered amino acids for the purposes of the invention. "Amino acid" also includes imino acid residues such as proline and hydroxyproline. The side chain may be in either the (R) or the (S) configuration. In the preferred embodiment, the amino acids are in the (S) or L-configuration. If non-naturally occurring side chains are used, non-amino acid substituents may be used, for example to prevent or retard in vivo degradation.

[0165] By "$CD32b^+$ cell" or "$Fc\gamma RIIb^+$ cell" as used herein is meant any cell or cell type that expresses CD32b (FcγRIIb). CD32b+ cells include but are not limited to B cells, plasma cells, dendritic cells, macrophages, neutrophils, mast cells, basophils, or eosinophils.

[0166] By "CDC" or "complement dependent cytotoxicity" as used herein is meant the reaction wherein one or more complement protein components recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

[0167] By "constant region" of an antibody as defined herein is meant the region of the antibody that is encoded by one of the light or heavy chain immunoglobulin constant region genes. By "constant light chain" or "light chain constant region" as used herein is meant the region of an antibody encoded by the kappa (Cκ) or lambda (Cλ) light chains. The constant light chain typically comprises a single domain, and as defined herein refers to positions 108-214 of Cκ or Cλ, wherein numbering is according to the EU index. By "constant heavy chain" or "heavy chain constant region" as used herein is meant the region of an antibody encoded by the mu, delta, gamma, alpha, or epsilon genes to define the antibody's isotype as IgM, IgD, IgG, IgA, or IgE, respectively. For full length IgG antibodies, the constant heavy chain, as defined herein, refers to the N-terminus of the CH1 domain to the C-terminus of the CH3 domain, thus comprising positions 118-447, wherein numbering is according to the EU index.

[0168] By "effector function" as used herein is meant a biochemical event that results from the interaction of an antibody Fc region with an Fc receptor or ligand. Effector functions include but are not limited to ADCC, ADCP, and CDC. Further, effector functions include FcγRIIb-mediated effector functions, such as inhibitory functions (e.g., downregulating, reducing, inhibiting etc., B cell responses, e.g., a humoral immune response).

[0169] By "effector cell" as used herein is meant a cell of the immune system that expresses one or more Fc receptors and mediates one or more effector functions. Effector cells include but are not limited to monocytes, macrophages, neutrophils, dendritic cells, eosinophils, mast cells, platelets, B cells, large granular lymphocytes, Langerhans' cells, natural killer (NK) cells, and γγ T cells, and may be from any organism including but not limited to humans, mice, rats, rabbits, and monkeys. By "library" herein is meant a set of Fc variants in any form, including but not limited to a list of nucleic acid or amino acid sequences, a list of nucleic acid or amino acid substitutions at variable positions, a physical library comprising nucleic acids that encode the library sequences, or a physical library comprising the Fc variant proteins, either in purified or unpurified form.

[0170] By "Fab" or "Fab region" as used herein is meant the polypeptides that comprise the V_H, CH1, V_H, and C_L immunoglobulin domains. Fab may refer to this region in isolation, or this region in the context of a full length antibody or antibody fragment.

[0171] By "Fc" or "Fc region", as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain. Thus Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, as illustrated in FIG. **1**, Fc comprises immunoglobulin domains Cgamma2 and Cgamma3 (Cγ2 and Cγ3) and the hinge between Cgamma1 (Cγ1) and Cgamma2 (Cγ2). Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to comprise residues C226 or P230 to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat. Fc may refer to this region in isolation, or this region in the context of an Fc polypeptide, as described below.

[0172] By "Fc polypeptide" as used herein is meant a polypeptide that comprises all or part of an Fc region. Fc polypeptides include antibodies, Fc fusions, isolated Fcs, and Fc fragments.

[0173] By "Fc fusion" as used herein is meant a protein wherein one or more polypeptides or small molecules is operably linked to an Fc region or a derivative thereof. Fc fusion is herein meant to be synonymous with the terms "immunoadhesin", "Ig fusion", "Ig chimera", and "receptor globulin" (sometimes with dashes) as used in the prior art (Chamow et al., 1996, *Trends Biotechnol* 14:52-60; Ashkenazi et al., 1997, *Curr Opin Immunol* 9:195-200. incorporated by reference). An Fc fusion combines the Fc region of an immunoglobulin with a fusion partner, which in general can be any protein or small molecule. The role of the non-Fc part of an Fc fusion, i.e. the fusion partner, may be to mediate target binding, and thus it is functionally analogous to the variable regions of an antibody. Virtually any protein or small molecule may be linked to Fc to generate an Fc fusion. Protein fusion partners may include, but are not limited to, the variable region of any antibody, the target-binding region of a receptor, an adhesion molecule, a ligand, an enzyme, a cytokine, a chemokine, or some other protein or protein domain. Small molecule fusion partners may include any agent that directs the Fc fusion to a target antigen. Such target antigen may be any molecule, e.g., an extracellular receptor, that is implicated in disease. Fc fusions of embodiments described herein may target virtually antigen that is expressed on $CD32b^+$ cells.

[0174] By "Fc gamma receptor" or "FcγR" as used herein is meant any member of the family of proteins that bind the IgG antibody Fc region and are substantially encoded by the FcγR genes. In humans this family includes but is not limited to FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and Fcγ-

RIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIIb-NA1 and FcγRIIIb-NA2), as well as any undiscovered human FcγRs or FcγR isoforms or allotypes. An FcγR may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. Mouse FcγRs include but are not limited to FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16), and FcγRIII-2 (CD16-2), as well as any undiscovered mouse FcγRs or FcγR isoforms or allotypes.

[0175] By "Fc ligand" or "effector ligand" as used herein is meant a molecule, preferably a polypeptide, from any organism that binds to the Fc region of an antibody to form an Fc/Fc ligand complex. Binding of an Fc ligand to Fc preferably elicits or more effector functions. Fc ligands include but are not limited to Fc receptors, FcγRs, FcαRs, FcεRs, FcRn, C1q, C3, mannan binding lectin, mannose receptor, staphylococcal protein A, streptococcal protein G, and viral FcγR. Fc ligands also include Fc receptor homologs (FcRH), which are a family of Fc receptors that are homologous to the FcγRs (Davis et al., 2002, *Immunological Reviews* 190:123-136, incorporated by reference). Fc ligands may include undiscovered molecules that bind Fc.

[0176] By "IgG" as used herein is meant a polypeptide belonging to the class of antibodies that are substantially encoded by a recognized immunoglobulin gamma gene. In humans this class comprises IgG1, IgG2, IgG3, and IgG4. In mice this class comprises IgG1, IgG2a, IgG2b, IgG3. By "immunoglobulin (Ig)" herein is meant a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. Immunoglobulins include but are not limited to antibodies, antibody fragments, and individual immunoglobulin domains. Immunoglobulins may have a number of structural forms, including but not limited to full length antibodies, antibody fragments, and individual immunoglobulin domains. By "immunoglobulin (Ig) domain" herein is meant a region of an immunoglobulin that exists as a distinct structural entity as ascertained by one skilled in the art of protein structure. Ig domains typically have a characteristic β-sandwich folding topology. The known Ig domains in the IgG class of antibodies are V_H, Cγ1, Cγ2, Cγ3, V_L, and C_L.

[0177] By "parent polypeptide," "parent protein," "parent immunoglobulin" or "precursor polypeptide" (including Fc parent or precursors) as used herein is meant a polypeptide, protein, or immunoglobulin that is subsequently modified to generate a variant, e.g., any polypeptide, protein or immunoglobulin which serves as a template and/or basis for at least one amino acid modification described herein. Said parent polypeptide may be a naturally occurring polypeptide, or a variant or engineered version of a naturally occurring polypeptide. Parent polypeptide may refer to the polypeptide itself, compositions that comprise the parent polypeptide, or the amino acid sequence that encodes it. Accordingly, by "parent Fc Polypeptide" as used herein is meant a Fc polypeptide that is modified to generate a variant, and by "parent antibody" as used herein is meant an antibody that is modified to generate a variant antibody (e.g., a parent antibody may include, but is not limited to, a protein comprising the constant region of a naturally occurring Ig).

[0178] As outlined above, certain positions of the Fc molecule can be altered. By "position" as used herein is meant a location in the sequence of a protein. Positions may be numbered sequentially, or according to an established format, for example the EU index as in Kabat. For example, position 297 is a position in the human antibody IgG1. Corresponding positions are determined as outlined above, generally through alignment with other parent sequences.

[0179] By "residue" as used herein is meant a position in a protein and its associated amino acid identity. For example, Asparagine 297 (also referred to as Asn297, also referred to as N297) is a residue in the human antibody IgG1.

[0180] By "target antigen" as used herein is meant the molecule that is bound by the variable region of a given antibody. A target antigen may be a protein, carbohydrate, lipid, or other chemical compound.

[0181] By "target cell" as used herein is meant a cell that expresses a target antigen.

[0182] By "variable region" as used herein is meant the region of an immunoglobulin that comprises one or more Ig domains substantially encoded by any of the Vκ, Vλ, and/or V_H genes that make up the kappa, lambda, and heavy chain immunoglobulin genetic loci respectively.

[0183] By "variant polypeptide" as used herein is meant a polypeptide sequence that differs from that of a parent polypeptide sequence by virtue of at least one amino acid modification. The parent polypeptide may be a naturally occurring or wild-type (WT) polypeptide, or may be a modified version of a WT polypeptide. Variant polypeptide may refer to the polypeptide itself, a composition comprising the polypeptide, or the amino sequence that encodes it. Preferably, the variant polypeptide has at least one amino acid modification compared to the parent polypeptide, e.g. from about one to about ten amino acid modifications, and preferably from about one to about five amino acid modifications compared to the parent. The variant polypeptide sequence herein will preferably possess at least about 80% homology with a parent polypeptide sequence, and most preferably at least about 90% homology, more preferably at least about 95% homology. Accordingly, by "Fc variant" as used herein is meant an Fc sequence that differs from that of a parent Fc sequence by virtue of at least one amino acid modification. An Fc variant may only encompass an Fc region, or may exist in the context of an antibody, Fc fusion, isolated Fc, Fc fragment, or other polypeptide that is substantially encoded by Fc. Fc variant may refer to the Fc polypeptide itself, compositions comprising the Fc variant polypeptide, or the amino acid sequence that encodes it. In some embodiments, variant polypeptides disclosed herein (e.g., variant immunoglobulins) may have at least one amino acid modification compared to the parent polypeptide, e.g. from about one to about ten amino acid modifications, from about one to about five amino acid modifications, etc. compared to the parent. The variant polypeptide sequence herein may possess at least about 80% homology with a parent polypeptide sequence, e.g., at least about 90% homology, 95% homology, etc. Accordingly, by "Fc variant" or "variant Fc" as used herein is meant an Fc sequence that differs from that of a parent Fc sequence by virtue of at least one amino acid modification. An Fc variant may only encompass an Fc region, or may exist in the context of an antibody, Fc fusion, isolated Fc, Fc fragment, or other polypeptide that is substantially encoded by Fc. Fc variant may refer to the Fc polypeptide itself, compositions comprising the Fc variant polypeptide, or the amino acid sequence that encodes it. By "Fc polypeptide variant" or "variant Fc polypeptide" as used herein is meant an Fc polypeptide that differs from a parent Fc polypeptide by virtue of at least one

amino acid modification. By "protein variant" or "variant protein" as used herein is meant a protein that differs from a parent protein by virtue of at least one amino acid modification. By "antibody variant" or "variant antibody" as used herein is meant an antibody that differs from a parent antibody by virtue of at least one amino acid modification. By "IgG variant" or "variant IgG" as used herein is meant an antibody that differs from a parent IgG by virtue of at least one amino acid modification. By "immunoglobulin variant" or "variant immunoglobulin" as used herein is meant an immunoglobulin sequence that differs from that of a parent immunoglobulin sequence by virtue of at least one amino acid modification.

[0184] By "wild type" or "WT" herein is meant an amino acid sequence or a nucleotide sequence that is found in nature, including allelic variations. A WT protein, polypeptide, antibody, immunoglobulin, IgG, etc. has an amino acid sequence or a nucleotide sequence that has not been intentionally modified.

[0185] The Fc variants of the present invention are defined according to the amino acid modifications that compose them. Thus, for example, I332E is an Fc variant with the substitution I332E relative to the parent Fc polypeptide. Likewise, S239D/A330L/I332E (also referred to as 239D/330L/332E) defines an Fc variant with the substitutions S239D, A330L, and I332E (239D, 330L, and 332E) relative to the parent Fc polypeptide. It is noted that the order in which substitutions are provided is arbitrary, that is to say that, for example, S239D/A330L/I332E is the same Fc variant as S239D/I332E/A330L, and so on. For all positions discussed in the present invention, numbering is according to the EU index or EU numbering scheme (Kabat et al., 1991, *Sequences of Proteins of Immunological Interest,* 5th Ed., United States Public Health Service, National Institutes of Health, Bethesda, incorporated by reference). The EU index or EU index as in Kabat refers to the numbering of the EU antibody (Edelman et al., 1969, Proc Natl Acad Sci USA 63:78-85, incorporated by reference).

[0186] The present invention is directed to optimized Fc variants useful in a variety of contexts. As outlined above, current antibody therapies suffer from a variety of problems. The present invention provides a promising means for enhancing the anti-tumor potency of antibodies is via enhancement of their ability to mediate cytotoxic effector functions such as ADCC, ADCP, and CDC. The present invention shows that antibodies with an Fc region optimized for binding to certain FcγRs may better mediate effector functions and thereby destroy cancer cells more effectively in patients. The balance between activating and inhibiting receptors is an important consideration, and optimal effector function may result from an Fc with enhanced affinity for activation receptors, for example FcγRI, FcγRIIa/c, and FcγRIIIa, yet reduced affinity for the inhibitory receptor FcγRIIb. Furthermore, because FcγRs can mediate antigen uptake and processing by antigen presenting cells, enhanced Fc/FcγR affinity may also improve the capacity of antibody therapeutics to elicit an adaptive immune response. For example, several mutations disclosed in this application, including S298A, E333A, and K334A, show enhanced binding to the activating receptor FcγRIIIa and reduced binding to the inhibitory receptor FcγRIIb. These mutations maybe combined to obtain double and triple mutation variants that show additive improvements in binding. A particular variant is a S298A/E333A/K334A triple mutant with approximately a 1.7-fold increase in binding to F158 FcγRIIIa, a 5-fold decrease in binding to FcγRIIb, and a 2.1-fold enhancement in ADCC.

[0187] Although there is a need for greater effector function, for some antibody therapeutics reduced or eliminated effector function may be desired. This is often the case for therapeutic antibodies whose mechanism of action involves blocking or antagonism but not killing of the cells bearing target antigen. In these cases depletion of target cells is undesirable and can be considered a side effect. For example, the ability of anti-CD4 antibodies to block CD4 receptors on T cells makes them effective anti-inflammatories, yet their ability to recruit FcγR receptors also directs immune attack against the target cells, resulting in T cell depletion (Reddy et al., 2000, *J Immunol* 164:1925-1933, incorporated by reference). Effector function can also be a problem for radiolabeled antibodies, referred to as radioconjugates, and antibodies conjugated to toxins, referred to as immunotoxins. These drugs can be used to destroy cancer cells, but the recruitment of immune cells via Fc interaction with FcγRs brings healthy immune cells in proximity to the deadly payload (radiation or toxin), resulting in depletion of normal lymphoid tissue along with targeted cancer cells (Hutchins et al., 1995, *Proc Natl Acad Sci USA* 92:11980-11984; White et al., 2001, Annu Rev Med 52:125-145, incorporated by reference). This problem can potentially be circumvented by using IgG isotypes that poorly recruit complement or effector cells, for example IgG2 and IgG4. An alternate solution is to develop Fc variants that reduce or ablate binding (Alegre et al., 1994, *Transplantation* 57:1537-1543; Hutchins et al., 1995, *Proc Natl Acad Sci USA* 92:11980-11984; Armour et al., 1999, *Eur J Immunol* 29:2613-2624; Reddy et al., 2000, *J Immunol* 164:1925-1933; Xu et al., 2000, *Cell Immunol* 200:16-26; Shields et al., 2001, *J Biol Chem* 276:6591-6604) (U.S. Pat. No. 6,194,551; U.S. Pat. No. 5,885,573; PCT WO 99/58572), all incorporated by reference. A critical consideration for the reduction or elimination of effector function is that other important antibody properties not be perturbed. Fc variants should be engineered that not only ablate binding to FcγRs and/or C1q, but also maintain antibody stability, solubility, and structural integrity, as well as ability to interact with other important Fc ligands such as FcRn and proteins A and G.

[0188] In addition, the invention utilizes engineered glycoforms that can enhance Fc/FcγR affinity and effector function. An aglycosylated Fc with favorable solution properties and the capacity to mediate effector functions would be significantly enabling for the alternate production methods described above. By overcoming the structural and functional shortcomings of aglycosylated Fc, antibodies can be produced in bacteria and transgenic plants and animals with reduced risk of immunogenicity, and with effector function for clinical applications in which cytotoxicity is desired such as cancer. The present invention describes the utilization of protein engineering methods to develop stable, soluble Fc variants with effector function. Currently, such Fc variants do not exist in the art.

Fc Variants of the Present Invention

[0189] The Fc variants of the present invention may find use in a variety of Fc polypeptides. An Fc polypeptide that comprises an Fc variant of the present invention is herein referred to as an "Fc polypeptide of the present invention". Fc polypeptides of the present invention include polypeptides that comprise the Fc variants of the present invention in the

context of a larger polypeptide, such as an antibody or Fc fusion. That is, Fc polypeptides of the present invention include antibodies and Fc fusions that comprise Fc variants of the present invention. By "antibody of the present invention" as used herein is meant an antibody that comprises an Fc variant of the present invention. By "Fc fusion of the present invention" as used herein refers to an Fc fusion that comprises an Fc variant of the present invention. Fc polypeptides of the present invention also include polypeptides that comprise little or no additional polypeptide sequence other than the Fc region, referred to as an isolated Fc. By "isolated Fc of the present invention" used herein is meant an Fc polypeptide that comprises an Fc variant of the present invention, and comprises little or no additional polypeptide sequence other than the Fc region. Fc polypeptides of the present invention also include fragments of the Fc region. By "Fc fraqment of the present invention" as used herein is meant an Fc fragment that comprises an Fc variant of the present invention. As described below, any of the aforementioned Fc polypeptides of the present invention may be fused to one or more fusion partners or conjugate partners to provide desired functional properties.

[0190] Fc variants may be constructed in a parent Fc polypeptide irrespective of its context. That is to say that, the sole criteria for a parent Fc polypeptide is that it comprise an Fc region. The parent Fc polypeptides described herein may be derived from a wide range of sources, and may be substantially encoded by one or more Fc genes from any organism, including but not limited to humans, rodents including but not limited to mice and rats, lagomorpha such as rabbits and hares, camelidae such as camels, llamas, and dromedaries, and non-human primates, including but not limited to Prosimians, Platyrrhini (New World monkeys), Cercopithecoidea (Old World monkeys), and Hominoidea include the Gibbons, Lesser and Great Apes, with humans most preferred. The parent Fc polypeptides of the present invention may be substantially encoded by immunoglobulin genes belonging to any of the antibody classes, including but not limited to sequences belonging to the IgG (including human subclasses IgG1, IgG2, IgG3, or IgG4), IgA (including human subclasses IgA1 and IgA2), IgD, IgE, IgG, or IgM classes of antibodies. Most preferably the parent Fc polypeptides of the present invention comprise sequences belonging to the human IgG class of antibodies. For example, the parent Fc polypeptide may be a parent antibody, for example a human IgG1 antibody, a human IgA antibody, or a mouse IgG2a or IgG2b antibody. Said parent antibody may be nonhuman, chimeric, humanized, or fully human as described in detail below. The parent Fc polypeptide may be modified or engineered in some way, for example a parent antibody may be affinity matured, or may possess engineered glycoforms, all as described more fully below. Alternatively, the parent Fc polypeptide may be an Fc fusion, for example an Fc fusion wherein the fusion partner targets a cell surface receptor. Alternatively, the parent Fc polypeptide may be an isolated Fc region, comprising little or no other polypeptide sequence outside the Fc region. The parent Fc polypeptide may be a naturally existing Fc region, or may be an existing engineered variant of an Fc polypeptide. What is important is that the parent Fc polypeptide comprise an Fc region, which can then be mutated to generate an Fc variant.

[0191] The Fc variants of the present invention may be an antibody, referred to herein as an "antibody of the present invention". Antibodies of the present invention may comprise immunoglobulin sequences that are substantially encoded by immunoglobulin genes belonging to any of the antibody classes, including but not limited to IgG (including human subclasses IgG1, IgG2, IgG3, or IgG4), IgA (including human subclasses IgA1 and IgA2), IgD, IgE, IgG, and IgM classes of antibodies. Most preferably the antibodies of the present invention comprise sequences belonging to the human IgG class of antibodies. Antibodies of the present invention may be nonhuman, chimeric, humanized, or fully human. As will be appreciated by one skilled in the art, these different types of antibodies reflect the degree of "humanness" or potential level of immunogenicity in a human. For a description of these concepts, see Clark et al., 2000 and references cited therein (Clark, 2000, *Immunol Today* 21:397-402, incorporated by reference). Chimeric antibodies comprise the variable region of a nonhuman antibody, for example V_H and V_L domains of mouse or rat origin, operably linked to the constant region of a human antibody (see for example U.S. Pat. No. 4,816,567, incorporated by reference). Said nonhuman variable region may be derived from any organism as described above, preferably mammals and most preferably rodents or primates. In one embodiment, the antibody of the present invention comprises monkey variable domains, for example as described in Newman et al., 1992, Biotechnology 10:1455-1460, U.S. Pat. No. 5,658,570, and U.S. Pat. No. 5,750,105, incorporated by reference. In a preferred embodiment, the variable region is derived from a nonhuman source, but its immunogenicity has been reduced using protein engineering. In a preferred embodiment, the antibodies of the present invention are humanized (Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), incorporated by reference). By "humanized" antibody as used herein is meant an antibody comprising a human framework region (FR) and one or more complementarity determining regions (CDR's) from a non-human (usually mouse or rat) antibody. The non-human antibody providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Humanization relies principally on the grafting of donor CDRs onto acceptor (human) V_L and V_H frameworks (Winter U.S. Pat. No. 5,225,539, incorporated by reference). This strategy is referred to as "CDR grafting". "Backmutation" of selected acceptor framework residues to the corresponding donor residues is often required to regain affinity that is lost in the initial grafted construct (U.S. Pat. No. 5,530,101; U.S. Pat. No. 5,585,089; U.S. Pat. No. 5,693,761; U.S. Pat. No. 5,693,762; U.S. Pat. No. 6,180,370; U.S. Pat. No. 5,859,205; U.S. Pat. No. 5,821,337; U.S. Pat. No. 6,054,297; U.S. Pat. No. 6,407,213, incorporated by reference). A large number of other methods for humanization are known in the art (Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), incorporated by reference), and any of such methods may find use in the present invention for modifying Fc variants for reduced immunogenicity. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region. In a most preferred embodiment, the immunogenicity of an Fc variant of the present invention is reduced using a method described in U.S. Ser. No. 11/004,590, filed Dec. 3, 2004, entitled "Methods of Generating Variant Proteins with Increased Host String Content and Compositions Thereof," incorporated by

reference. In an alternate embodiment, the antibodies of the present invention may be fully human, that is the sequences of the antibodies are completely or substantially human. A number of methods are known in the art for generating fully human antibodies, including the use of transgenic mice (Bruggemann et al., 1997, *Curr Opin Biotechnol* 8:455-458, incorporated by reference) or human antibody libraries coupled with selection methods (Griffiths et al., 1998, *Curr Opin Biotechnol* 9:102-108, incorporated by reference).

[0192] The Fc variants of the present invention may be an Fc fusion, referred to herein as an "Fc fusion of the present invention". Fc fusions of the present invention comprise an Fc polypeptide operably linked to one or more fusion partners. The role of the fusion partner typically, but not always, is to mediate binding of the Fc fusion to a target antigen. (Chamow et al., 1996, *Trends Biotechnol* 14:52-60; Ashkenazi et al., 1997, *Curr Opin Immunol* 9:195-200, incorporated by reference). For example, the approved drug alefacept (marketed as AMEVIVE®) is an immunosuppressive Fc fusion that consists of the extracellular CD2-binding portion of the human leukocyte function antigen-3 (LFA-3) linked to the Fc region of human IgG1. The approved drug etanercept (marketed as ENBREL®) is an Fc fusion comprising the extracellular ligand-binding portion of human tumor necrosis factor receptor (TNFR) linked to human IgG1Fc. Virtually any protein, polypeptide, peptide, or small molecule may be linked to Fc to generate an Fc fusion. Fusion partners include but are not limited to receptors and extracellular receptor domains, adhesion molecules, ligands, enzymes, cytokines, chemokines, or some other protein or protein domain. The fusion partner may also play a role as a chemoattractant. Undiscovered ligands or receptors may serve as fusion partners for the Fc variants of the present invention. Small molecules may serve as fusion partners, and may include any therapeutic agent that directs the Fc fusion to a therapeutic target. Such targets may be any molecule, preferrably an extracellular receptor, that is implicated in disease. Two families of surface receptors that are targets of a number of approved small molecule drugs are G-Protein Coupled Receptors (GPCRs), and ion channels, including K+, Na+, Ca+ channels. Nearly 70% of all drugs currently marketed worldwide target GPCRs. Thus the Fc variants of the present invention may be fused to a small molecule that targets, for example, one or more GABA receptors, purinergic receptors, adrenergic receptors, histaminergic receptors, opiod receptors, chemokine receptors, glutamate receptors, nicotinic receptors, the 5HT (serotonin) receptor, and estrogen receptors. A fusion partner may be a small-molecule mimetic of a protein that targets a therapeutically useful target. Specific examples of particular drugs that may serve as Fc fusion partners can be found in L. S. Goodman et al., Eds., *Goodman and Gilman's The Pharmacological Basis of Therapeutics* (McGraw-Hill, New York, ed. 9, 1996, incorporated by reference). Fusion partners include not only small molecules and proteins that bind known targets for existing drugs, but orphan receptors that do not yet exist as drug targets. The completion of the genome and proteome projects are proving to be a driving force in drug discovery, and these projects have yielded a trove of orphan receptors. There is enormous potential to validate these new molecules as drug targets, and develop protein and small molecule therapeutics that target them. Such protein and small molecule therapeutics are contemplated as Fc fusion partners that employ the Fc variants of the present invention. Fc fusions of the invention may comprise immunoglobulin sequences that are substantially encoded by immunoglobulin genes belonging to any of the antibody classes, including but not limited to IgG (including human subclasses IgG1, IgG2, IgG3, or IgG4), IgA (including human subclasses IgA1 and IgA2), IgD, IgE, IgG, and IgM classes of antibodies. Most preferably the Fc fusions of the present invention comprise sequences belonging to the human IgG class of antibodies. A variety of linkers, defined and described below, may be used to covalently link Fc to a fusion partner to generate an Fc fusion.

[0193] The Fc variants of the present invention may find use in an isolated Fc, that is an Fc polypeptide that comprises little or no additional polypeptide sequence other than the Fc region and that comprises an Fc variant of the present invention. Isolated Fc of the present invention are meant as molecules wherein the desired function of the molecule, for example the desired therapeutic function, resides solely in the Fc region. Thus the therapeutic target of an isolated Fc of the present invention is likely to involve one or more Fc ligands. An isolated Fc that comprises the Fc variant may require no additional covalent polypeptide sequence to achieve its desired outcome. In a preferred embodiment, said isolated Fc comprises from 90-100% of the Fc region, with little or no "extra" sequence. Thus, for example, an isolated Fc of the present invention may comprise residues C226 or P230 to the carboxyl-terminus of human IgG1, wherein the numbering is according to the EU index as in Kabat. In one embodiment, the isolated Fc of the present invention may contain no extra sequence outside the Fc region. However it is also contemplated that isolated Fc's may not also comprise additional polypeptide sequences. For example, an isolated Fc may, in addition to comprising an Fc variant Fc region, comprise additional polypeptide sequence tags that enable expression, purification, and the like.

[0194] The Fc variants of the present invention may find use in a fragment of the Fc region, that is an Fc polypeptide that comprises an Fc fragment that comprises an Fc variant of the present invention. Clearly a requirement of an Fc fragment of the present invention is that it contains the position(s) at which the amino acid modifications of the Fc variant are made. An Fc fragment of the present invention may comprise from 1-90% of the Fc region, with 10-90% being preferred, and 30-90% being most preferred. Thus for example, an Fc fragment of the present invention may comprise an Fc variant IgG1 Cγ2 domain, an Fc variant IgG1 Cγ2 domain and hinge region, an Fc variant IgG1 Cγ3 domain, and so forth. In one embodiment, an Fc fragment of the present invention additionally comprises a fusion partner, effectively making it an Fc fragment fusion. As with isolated Fcs, Fc fragments may or may not contain extra polypeptide sequence.

[0195] Fc variants of the present invention may be substantially encoded by genes from any organism, preferably mammals, including but not limited to humans, rodents including but not limited to mice and rats, lagomorpha including but not limited to rabbits and hares, camelidae including but not limited to camels, llamas, and dromedaries, and non-human primates, including but not limited to Prosimians, Platyrrhini (New World monkeys), Cercopithecoidea (Old World monkeys), and Hominoidea including the Gibbons and Lesser and Great Apes. In a most preferred embodiment, the Fc variants of the present invention are substantially human. The Fc variants of the present invention may be substantially encoded by immunoglobulin genes belonging to any of the antibody classes. In a most preferred embodiment, the Fc

variants of the present invention comprise sequences belonging to the IgG class of antibodies, including human subclasses IgG1, IgG2, IgG3, and IgG4. In an alternate embodiment, the Fc variants of the present invention comprise sequences belonging to the IgA (including human subclasses IgA1 and IgA2), IgD, IgE, IgG, or IgM classes of antibodies. The Fc variants of the present invention may comprise more than one protein chain. That is, the present invention may find use in an Fc variant that is a monomer or an oligomer, including a homo- or hetero-oligomer.

[0196] In the most preferred embodiment, the Fc polypeptides of the invention are based on human IgG sequences, and thus human IgG sequences are used as the "base" sequences against which other sequences are compared, including but not limited to sequences from other organisms, for example rodent and primate sequences, as well as sequences from other immunoglobulin classes such as IgA, IgE, IgGD, IgGM, and the like. It is contemplated that, although the Fc variants of the present invention are engineered in the context of one parent Fc variant, the variants may be engineered in or "transferred" to the context of another, second parent Fc variant. This is done by determining the "equivalent" or "corresponding" residues and substitutions between the first and second Fc variants, typically based on sequence or structural homology between the sequences of the two Fc variants. In order to establish homology, the amino acid sequence of a first Fc variant outlined herein is directly compared to the sequence of a second Fc variant. After aligning the sequences, using one or more of the homology alignment programs known in the art (for example using conserved residues as between species), allowing for necessary insertions and deletions in order to maintain alignment (i.e., avoiding the elimination of conserved residues through arbitrary deletion and insertion), the residues equivalent to particular amino acids in the primary sequence of the first Fc variant are defined. Alignment of conserved residues preferably should conserve 100% of such residues. However, alignment of greater than 75% or as little as 50% of conserved residues is also adequate to define equivalent residues. Equivalent residues may also be defined by determining structural homology between a first and second Fc variant that is at the level of tertiary structure for Fc variants whose structures have been determined. In this case, equivalent residues are defined as those for which the atomic coordinates of two or more of the main chain atoms of a particular amino acid residue of the parent or precursor (N on N, CA on CA, C on C and O on o) are within 0.13 nm and preferably 0.1 nm after alignment. Alignment is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the proteins. Regardless of how equivalent or corresponding residues are determined, and regardless of the identity of the parent Fc variant in which the Fc variants are made, what is meant to be conveyed is that the Fc variants discovered by the present invention may be engineered into any second parent Fc variant that has significant sequence or structural homology with said Fc variant. Thus for example, if a variant antibody is generated wherein the parent antibody is human IgG1, by using the methods described above or other methods for determining equivalent residues, said variant antibody may be engineered in a human IgG2 parent antibody, a human IgA parent antibody, a mouse IgG2a or IgG2b parent antibody, and the like. Again, as described above, the context of the parent Fc variant does not affect the ability to transfer the Fc variants of the present invention to other parent Fc variants. For example, the variant antibodies that are engineered in a human IgG1 antibody that targets one epitope may be transferred into a human IgG2 antibody that targets a different epitope, into an Fc fusion that comprises a human IgG1 Fc region that targets yet a different epitope, and so forth.

[0197] The Fc variants of the present invention may find use in a wide range of products. In one embodiment the Fc variant of the invention is a therapeutic, a diagnostic, or a research reagent, preferably a therapeutic. Alternatively, the Fc variant of the present invention may be used for agricultural or industrial uses. An antibody of the present invention may find use in an antibody composition that is monoclonal or polyclonal. The Fc variants of the present invention may be agonists, antagonists, neutralizing, inhibitory, or stimulatory. In a preferred embodiment, the Fc variants of the present invention are used to kill target cells that bear the target antigen, for example cancer cells. In an alternate embodiment, the Fc variants of the present invention are used to block, antagonize, or agonize the target antigen. In an alternately preferred embodiment, the Fc variants of the present invention are used to block, antagonize, or agonize the target antigen and kill the target cells that bear the target antigen.

Targets

[0198] Virtually any antigen may be targeted by the Fc variants of the present invention, including but not limited to proteins, subunits, domains, motifs, and/or epitopes belonging to the following list of targets: 17-IA, 4-1BB, 4Dc, 6-keto-PGF1a, 8-iso-PGF2a, 8-oxo-dG, A1 Adenosine Receptor, A33, ACE, ACE-2, Activin, Activin A, Activin AB, Activin B, Activin C, Activin RIA, Activin RIA ALK-2, Activin RIB ALK-4, Activin RIIA, Activin RIIB, ADAM, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAM8, ADAM9, ADAMTS, ADAMTS4, ADAMTS5, Addressins, aFGF, ALCAM, ALK, ALK-1, ALK-7, alpha-1-antitrypsin, alpha-V/beta-1 antagonist, ANG, Ang, APAF-1, APE, APJ, APP, APRIL, AR, ARC, ART, Artemin, anti-id, ASPARTIC, Atrial natriuretic factor, av/b3 integrin, Axl, b2M, B7-1, B7-2, B7-H, B-lymphocyte Stimulator (B1yS), BACE, BACE-1, Bad, BAFF, BAFF-R, Bag-1, BAK, Bax, BCA-1, BCAM, Bcl, BCMA, BDNF, b-ECGF, bFGF, BID, Bik, BIM, BLC, BL-CAM, BLK, BMP, BMP-2 BMP-2a, BMP-3 Osteogenin, BMP-4 BMP-2b, BMP-5, BMP-6 Vgr-1, BMP-7 (OP-1), BMP-8 (BMP-8a, OP-2), BMPR, BMPR-IA (ALK-3), BMPR-IB (ALK-6), BRK-2, RPK-1, BMPR-11 (BRK-3), BMPs, b-NGF, BOK, Bombesin, Bone-derived neurotrophic factor, BPDE, BPDE-DNA, BTC, complement factor 3 (C3), C3a, C4, C5, C5a, C10, CA125, CAD-8, Calcitonin, cAMP, carcinoembryonic antigen (CEA), carcinoma-associated antigen, Cathepsin A, Cathepsin B, Cathepsin C/DPPI, Cathepsin D, Cathepsin E, Cathepsin H, Cathepsin L, Cathepsin O, Cathepsin S, Cathepsin V, Cathepsin X/Z/P, CBL, CCI, CCK2, CCL, CCL1, CCL11, CCL12, CCL13, CCL14, CCL15, CCL16, CCL17, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCR, CCR1, CCR10, CCR10, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CD1, CD2, CD3, CD3E, CD4, CD5, CD6, CD7, CD8, CD10, CD11a, CD11b, CD11c, CD13, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD27L, CD28, CD29, CD30, CD30L, CD32, CD33 (p67 proteins), CD34, CD38, CD40, CD40L, CD44, CD45, CD46, CD49a, CD52, CD54, CD55,

CD56, CD61, CD64, CD66e, CD74, CD80 (B7-1), CD89, CD95, CD123, CD137, CD138, CD140a, CD146, CD147, CD148, CD152, CD164, CEACAM5, CFTR, cGMP, CINC, *Clostridium botulinum toxin, Clostridium perfringens* toxin, CKb8-1, CLC, CMV, CMV UL, CNTF, CNTN-1, COX, C-Ret, CRG-2, CT-1, CTACK, CTGF, CTLA-4, CX3CL1, CX3CR1, CXCL, CXCL1, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CXCR, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, cytokeratin tumor-associated antigen, DAN, DCC, DcR3, DC-SIGN, Decay accelerating factor, des(1-3)-IGF-I (brain IGF-1), Dhh, digoxin, DNAM-1, Dnase, Dpp, DPPIV/CD26, Dtk, ECAD, EDA, EDA-A1, EDA-A2, EDAR, EGF, EGFR (ErbB-1), EMA, EMMPRIN, ENA, endothelin receptor, Enkephalinase, eNOS, Eot, eotaxinl, EpCAM, Ephrin B2/EphB4, EPO, ERCC, E-selectin, ET-1, Factor IIa, Factor VII, Factor VIIIc, Factor IX, fibroblast activation protein (FAP), Fas, FcR1, FEN-1, Ferritin, FGF, FGF-19, FGF-2, FGF3, FGF-8, FGFR, FGFR-3, Fibrin, FL, FLIP, Flt-3, Flt-4, Follicle stimulating hormone, Fractalkine, FZD1, FZD2, FZD3, FZD4, FZD5, FZD6, FZD7, FZD8, FZD9, FZD10, G250, Gas 6, GCP-2, GCSF, GD2, GD3, GDF, GDF-1, GDF-3 (Vgr-2), GDF-5 (BMP-14, CDMP-1), GDF-6 (BMP-13, CDMP-2), GDF-7 (BMP-12, CDMP-3), GDF-8 (Myostatin), GDF-9, GDF-15 (MIC-1), GDNF, GDNF, GFAP, GFRa-1, GFR-alpha1, GFR-alpha2, GFR-alpha3, GITR, Glucagon, Glut 4, glycoprotein IIb/IIa (GP IIb/IIIa), GM-CSF, gp130, gp72, GRO, Growth hormone releasing factor, Hapten (NP-cap or NIP-cap), HB-EGF, HCC, HCMV gB envelope glycoprotein, HCMV) gH envelope glycoprotein, HCMV UL, Hemopoietic growth factor (HGF), Hep B gp120, heparanase, Her2, Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), herpes simplex virus (HSV) gB glycoprotein, HSV gD glycoprotein, HGFA, High molecular weight melanoma-associated antigen (HMW-MAA), HIV gp120, HIV IIIB gp120 V3 loop, HLA, HLA-DR, HM1.24, HMFG PEM, HRG, Hrk, human cardiac myosin, human cytomegalovirus (HCMV), human growth hormone (HGH), HVEM, 1-309, IAP, ICAM, ICAM-1, ICAM-3, ICE, ICOS, IFNg, Ig, IgA receptor, IgE, IGF, IGF binding proteins, IGF-1R, IGFBP, IGF-I, IGF-II, IL, IL-1, IL-1R, IL-2, IL-2R, IL-4, IL-4R, IL-5, IL-5R, IL-6, IL-6R, IL-8, IL-9, IL-10, IL-12, IL-13, IL-15, IL-18, IL-18R, IL-23, interferon (INF)-alpha, INF-beta, INF-gamma, Inhibin, iNOS, Insulin A-chain, Insulin B-chain, Insulin-like growth factor 1, integrin alpha2, integrin alpha3, integrin alpha4, integrin alpha4/beta1, integrin alpha4/beta7, integrin alpha5 (alphaV), integrin alpha5/beta1, integrin alpha5/beta3, integrin alpha6, integrin beta1, integrin beta2, interferon gamma, IP-10, I-TAC, JE, Kallikrein 2, Kallikrein 5, Kallikrein 6, Kallikrein 11, Kallikrein 12, Kallikrein 14, Kallikrein 15, Kallikrein L1, Kallikrein L2, Kallikrein L3, Kallikrein L4, KC, KDR, Keratinocyte Growth Factor (KGF), laminin 5, LAMP, LAP, LAP (TGF-1), Latent TGF-1, Latent TGF-1 bp1, LBP, LDGF, LECT2, Lefty, Lewis-Y antigen, Lewis-Y related antigen, LFA-1, LFA-3, Lfo, LIF, LIGHT, lipoproteins, LIX, LKN, Lptn, L-Selectin, LT-a, LT-b, LTB4, LTBP-1, Lung surfactant, Luteinizing hormone, Lymphotoxin Beta Receptor, Mac-1, MAdCAM, MAG, MAP2, MARC, MCAM, MCAM, MCK-2, MCP, M-CSF, MDC, Mer, METALLOPROTEASES, MGDF receptor, MGMT, MHC (HLA-DR), MIF, MIG, MIP, MIP-1-alpha, MK, MMAC1, MMP, MMP-1, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-2, MMP-24, MMP-3, MMP-7, MMP-8, MMP-9, MPIF, Mpo, MSK, MSP, mucin (Muc1), MUC18, Muellerian-inhibitin substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, NCAM, NCAM, Neprilysin, Neurotrophin-3, -4, or -6, Neurturin, Neuronal growth factor (NGF), NGFR, NGF-beta, nNOS, NO, NOS, Npn, NRG-3, NT, NTN, OB, OGG1, OPG, OPN, OSM, OX40L, OX40R, p150, p95, PADPr, Parathyroid hormone, PARC, PARP, PBR, PBSF, PCAD, P-Cadherin, PCNA, PDGF, PDGF, PDK-1, PECAM, PEM, PF4, PGE, PGF, PGI2, PGJ2, PIN, PLA2, placental alkaline phosphatase (PLAP), PIGF, PLP, PP14, Proinsulin, Prorelaxin, Protein C, PS, PSA, PSCA, prostate specific membrane antigen (PSMA), PTEN, PTHrp, Ptk, PTN, R51, RANK, RANKL, RANTES, RANTES, Relaxin A-chain, Relaxin B-chain, renin, respiratory syncytial virus (RSV) F, RSV Fgp, Ret, Rheumatoid factors, RLIP76, RPA2, RSK, S100, SCF/KL, SDF-1, SERINE, Serum albumin, sFRP-3, Shh, SIGIRR, SK-1, SLAM, SLPI, SMAC, SMDF, SMOH, SOD, SPARC, Stat, STEAP, STEAP-II, TACE, TACI, TAG-72 (tumor-associated glycoprotein-72), TARC, TCA-3, T-cell receptors (e.g., T-cell receptor alpha/beta), TdT, TECK, TEM1, TEM5, TEM7, TEM8, TERT, testicular PLAP-like alkaline phosphatase, TfR, TGF, TGF-alpha, TGF-beta, TGF-beta Pan Specific, TGF-beta RI (ALK-5), TGF-beta RII, TGF-beta RIIb, TGF-beta RIII, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta4, TGF-beta5, Thrombin, Thymus Ck-1, Thyroid stimulating hormone, Tie, TIMP, TIQ, Tissue Factor, TMEFF2, Tmpo, TMPRSS2, TNF, TNF-alpha, TNF-alpha beta, TNF-beta2, TNFα, TNF-RI, TNF-RII, TNFRSF10A (TRAIL R1 Apo-2, DR4), TNFRSF10B (TRAIL R2 DR5, KILLER, TRICK-2A, TRICK-B), TNFRSF10C (TRAIL R3 DcR1, LIT, TRID), TNFRSF10D (TRAIL R4 DcR2, TRUNDD), TNFRSF11A (RANK ODF R, TRANCE R), TNFRSF11B (OPG OCIF, TR1), TNFRSF12 (TWEAK R FN14), TNFRSF13B (TACI), TNFRSF13C (BAFF R), TNFRSF14 (HVEM ATAR, HveA, LIGHT R, TR2), TNFRSF16 (NGFR p75NTR), TNFRSF17 (BCMA), TNFRSF18 (GITR AITR), TNFRSF19 (TROY TAJ, TRADE), TNFRSF19L (RELT), TNFRSF1A (TNF RI CD120a, p55-60), TNFRSF1B (TNF RII CD120b, p75-80), TNFRSF26 (TNFRH3), TNFRSF3 (LTbR TNF RIII, TNFC R), TNFRSF4 (OX40 ACT35, TXGP1 R), TNFRSF5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-1BB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2 TNFRH2), TNFRST23 (DcTRAIL R1 TNFRH1), TNFRSF25 (DR3 Apo-3, LARD, TR-3, TRAMP, WSL-1), TNFSF10 (TRAIL Apo-2 Ligand, TL2), TNFSF11 (TRANCE/RANK Ligand ODF, OPG Ligand), TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TL1A/VEGI), TNFSF18 (GITR Ligand AITR Ligand, TL6), TNFSF1A (TNF-a Conectin, DIF, TNFSF2), TNFSF1B (TNF-b LTa, TNFSF1), TNFSF3 (LTb TNFC, p33), TNFSF4 (OX40 Ligand gp34, TXGP1), TNFSF5 (CD40 Ligand CD154, gp39, HIGM1, IMD3, TRAP), TNFSF6 (Fas Ligand Apo-1 Ligand, APT1 Ligand), TNFSF7 (CD27 Ligand CD70), TNFSF8 (CD30 Ligand CD153), TNFSF9 (4-1BB Ligand CD137 Ligand), TP-1, t-PA, Tpo, TRAIL, TRAIL R, TRAIL-R1, TRAIL-R2, TRANCE, transferring receptor, TRF, Trk, TROP-2, TSG, TSLP, tumor-associated antigen CA 125, tumor-associated antigen expressing Lewis Y related carbohydrate, TWEAK,

TXB2, Ung, uPAR, uPAR-1, Urokinase, VCAM, VCAM-1, VECAD, VE-Cadherin, VE-cadherin-2, VEFGR-1 (flt-1), VEGF, VEGFR, VEGFR-3 (flt-4), VEGI, VIM, Viral antigens, VLA, VLA-1, VLA-4, VNR integrin, von Willebrands factor, WIF-1, WNT1, WNT2, WNT2B/13, WNT3, WNT3A, WNT4, WNT5A, WNT5B, WNT6, WNT7A, WNT7B, WNT8A, WNT8B, WNT9A, WNT9A, WNT9B, WNT10A, WNT10B, WNT11, WNT16, XCL1, XCL2, XCR1, XCR1, XEDAR, XIAP, XPD, and receptors for hormones and growth factors.

[0199] In one embodiment, to inhibit CD32b+ cells, antigens may include those that are expressed on CD32b+ cells, e.g., B cell proteins, e.g., one or more proteins of the B cell receptor complex. Target antigens include, but are not limited to CD19, CD20, CD21 (CR2), CD22, CD23/FcεRII, FcεRI, (α, β, and γ subunits), CD24/BBA-1/HSA, CD27, CD35 (CR1), CD38, CD40, CD45RA, CD52/CAMPATH-1/HE5, CD72, CD79a (Iga), CD79b (Igp), IgM (μ), CD80, CD81, CD86, Leu13, HLA-DR, -DP, -DQ, CD138, CD317/HM1. 24, CD11a, CD11b, CD11c, CD14, CD68, CD163, CD172a, CD200R, and CD206. In one embodiment, the immunoglobulins disclosed herein are also specific for a target antigen selected from the group consisting of: IgM (μ), CD19, CD20, CD21, CD22, CD23, CD24, CD35, CD40, CD45RA, CD72, CD79a, CD79b, CD80, CD81, CD86, and HLA-DR. In one embodiment, immunoglobulins disclosed herein are also specific for a target antigen selected from the group consisting of: IgM (μ), CD79a, CD79b, CD19, CD21, CD22, CD72, CD81, and Leu13. In one embodiment, immunoglobulins disclosed herein are also specific for a target antigen selected from the group consisting of: μ, CD19, CD79a, CD79b, CD81, and HLA-DR. In another embodiment, immunoglobulins disclosed herein are also specific for a target antigen selected from the group consisting of: CD22, CD40, and CD72.

[0200] One skilled in the art will appreciate that the aforementioned list of targets refers not only to specific proteins and biomolecules, but the biochemical pathway or pathways that comprise them. For example, reference to CTLA-4 as a target antigen implies that the ligands and receptors that make up the T cell co-stimulatory pathway, including CTLA-4, B7-1, B7-2, CD28, and any other undiscovered ligands or receptors that bind these proteins, are also targets. Thus target as used herein refers not only to a specific biomolecule, but the set of proteins that interact with said target and the members of the biochemical pathway to which said target belongs. One skilled in the art will further appreciate that any of the aforementioned target antigens, the ligands or receptors that bind them, or other members of their corresponding biochemical pathway, may be operably linked to the Fc variants of the present invention in order to generate an Fc fusion. Thus for example, an Fc fusion that targets EGFR could be constructed by operably linking an Fc variant to EGF, TGF-β, or any other ligand, discovered or undiscovered, that binds EGFR. Accordingly, an Fc variant of the present invention could be operably linked to EGFR in order to generate an Fc fusion that binds EGF, TGF-β, or any other ligand, discovered or undiscovered, that binds EGFR. Thus virtually any polypeptide, whether a ligand, receptor, or some other protein or protein domain, including but not limited to the aforementioned targets and the proteins that compose their corresponding biochemical pathways, may be operably linked to the Fc variants of the present invention to develop an Fc fusion.

[0201] Choosing the right target antigen for antibody therapy is a complex process and encompasses many variables. For anti-cancer treatment it is desirable to have a target whose expression is restricted to the cancerous cells. Some targets that have proven especially amenable to antibody therapy are those with signaling functions. Other therapeutic antibodies exert their effects by blocking signaling of the receptor by inhibiting the binding between a receptor and it's cognate ligand. Another mechanism of action of therapeutic antibodies is to cause receptor down regulation. Although many therapeutically effective antibodies work in part by signaling through their target antigen, this is not always the case. For example, some target classes such as cell surface glycoforms do not generate any biological signal. However, altered glycoforms are often associated with disease states such as cancer. Another significant target type are those that internalize either as a normal function or in response to antibody binding. In the case of targets that are soluble rather than cell surface bound the recruitment of effector functions would not result in any cell death.

[0202] Some targets that have proven especially amenable to antibody therapy are those with signalling functions. For example, antibody cross-linking of the Her2/neu antigen may generate an apoptotic signal that results in cancer cell death. In some cases such as the CD30 antigen, this clustering with free antibody may be insufficient to cause apoptosis in vitro. For in vitro assays sufficient clustering can be mediated by crosslinking the antibody or by immobilizing it at high density to a surface such as the well of a microtiter plate. However, in vivo this effect may be mediated by binding of the antibody to the Fc ligands, for example FcγRs expressed on a nearby cell. Antibody Fc variants that bind more tightly to Fc ligands may thus more effectively cluster the signaling target and lead to enhanced induction of apoptosis. Such a mechanism could be tested experimentally by adding antibody with and without enhanced Fc ligand binding to cells expressing the desired target that signals, and/or adding an Fc receptor and a corresponding antibody that will cluster the Fc receptor. Alternative means for clustering Fc receptor include immobilization on beads, and over-expression in a non-effector cell line. After allowing apoptosis to occur, measurement of the relative apoptosis of target expressing cells would enable a quantitative determination of the effect.

[0203] Antibodies that cause cell death through their interaction with targets may have an additional benefit. The signals released by such dying cells attract macrophages and other cells of the immune system. These cells can then takeup the dead or dying cells in an antibody mediated manner. This has been shown to result in cross-presentation of antigen and the potential for a host immune response against the target cells. Such auto-antibodies in response to antibody therapy have been reported for the antigen targets Her2 and CD20. For this reason it may be advantageous to have Fc variants with altered receptor specificities to specifically stimulate cross-presentation and an immune response rather than the undesired effect of tolerance induction.

[0204] Other therapeutic antibodies exert their effects by inhibiting interaction between a receptor and it's cognate ligand, ultimately blocking signaling of the receptor. Such antibodies are used to treat many disease states. In this case it may be advantageous to utilize antibodies that do not recruit any host immune functions. A secondary effect of such an antibody may be actually inducing signalling itself through receptor clustering. In this case the desired therapeutic effect of blocking signaling would be abrogated by antibody mediated signaling. As discussed above, this clustering may be

enhanced by antibody interaction with cells containing an Fc receptor. In this case, use of an Fc variant that binds less tightly or not at all to the Fc receptor would be preferable. Such an antibody would not mediate signaling, and its mechanism of action would thereby be restricted to blockage of receptor/ligand interactions. Signaling receptors for which this would be most appropriate would likely be monomeric receptors which can only be dimerized but not substantially clustered by a primary antibody. Mulitimeric receptors may be significantly clustered by the primary antibody and may not require additional clustering by Fc receptor binding.

[0205] Another potential mechanism of action of therapeutic antibodies is receptor downregulation. Such may be the case, for example, with the insulin-like growth factor receptor. Cell growth depends on continued signaling through the receptor, whereas in its absence cells cease to grow. One effect of antibodies directed against this receptor is to downregulate its expression and thereby ablate signaling. Cell recovery from cytotoxic therapy requires stimulation of this receptor. Downregulation of this receptor prevents these cells from recovery and renders the cytotoxic therapy substantially more effective. For antibodies for which this is the primary mechanism of action, decreased Fc receptor binding may prevent the sequestration of antibody by nontarget binding to Fc receptors.

[0206] Although many therapeutically effective antibodies work in part by signaling through their target antigen, this is not always the case. For example, some target classes such as cell surface glycoforms do not generate any biological signal. However, altered glycoforms are often associated with disease states such as cancer. In other cases, interaction of antibodies with different epitopes of the same target antigen may confer different signaling effects. In such cases where this is little or no elicited signaling by binding of antibody or Fc fusion to target antigen, Fc polypeptides of the present invention may find utility in providing novel mechanisms of efficacy for otherwise non-efficacious molecules.

[0207] One approach that has been taken in generating therapeutic antibodies to such nonsignaling targets is to couple the antibody to a cytotoxic agent such as a radioisotope, toxin, or an enzyme that will process a substrate to produce a cytotoxic agent in the vicinity of the tumor. As an alternative to a cytotoxic moiety, Fc variants of the present invention may provide increased recruitment of immune functions that are inherently less toxic to the host while still effective at destroying target cancer cells. Such Fc variants may, for example, be more efficient at recruiting NK cells or at activating phagocytosis or initiating CDC. Alternatively, if a cytotoxic agent is utilized, it may be advantageous to use an Fc variant that provides reduced or altered Fc ligand binding. This may reduce or ablate the cytotoxic effects of the agent on immune cells that express Fc receptors, thereby reducing toxicity to the patient. Furthermore, reduction of Fc ligand binding may help to minimize the generation of an immune response to the toxic agent or enzyme. As mentioned above, cell death may result in recruitment of host immune cells; antibody mediated cross-presentation in such a case may be increased with immune response rather than immune tolerance if in addition to a cytotoxic moiety the therapeutic antibody has increased Fc receptor binding affinity or altered receptor specificity.

[0208] Another significant target type are those targets that internalize, either as a normal part of their biological function or in response to antibody binding. For such targets, many efforts have been made to couple cytotoxic agents such as RNase, ricin and calicheamicin, which can only exert their effect after internalization. For such reagents, Fc ligand binding may reduce efficacy due to nonproductive sequestration of the therapeutic by Fc ligands. In this case it may be advantageous to utilize Fc variants that provide decreased Fc ligand affinity. Conversely, antibody pre-association with Fc ligands prior to their binding to target antigen presented on cells may serve to inhibit internalization of the target. In this case, increased Fc ligand affinity may serve to improve pre-association and thereby recruitment of effector cells and the host immune response.

[0209] In the case of targets that are soluble rather than cell surface bound, recruitment of effector functions would not result directly in cell death. However, there may be utility in stimulating the generation of host antibodies to the target. For some disease states, successful treatment may require administration of the therapeutic antibody for extremely long periods of time. Such therapy may be prohibitively costly or cumbersome. In these cases, stimulation of the host immune response and the generation of antibodies may result in improved efficacy of the therapeutic. This may be applicable as an adjuvant to vaccine therapy. Antibody Fc variants that mediate such an effect may have increased affinity for Fc ligands or altered Fc ligand specificity.

[0210] A number of antibodies and Fc fusions that are approved for use, in clinical trials, or in development may benefit from the Fc variants of the present invention. These antibodies and Fc fusions are herein referred to as "clinical products and candidates". Thus in a preferred embodiment, the Fc polypeptides of the present invention may find use in a range of clinical products and candidates. For example, a number of antibodies that target CD20 may benefit from the Fc polypeptides of the present invention. For example the Fc polypeptides of the present invention may find use in an antibody that is substantially similar to rituximab (Rituxan®, IDEC/Genentech/Roche) (see for example U.S. Pat. No. 5,736,137), a chimeric anti-CD20 antibody approved to treat Non-Hodgkin's lymphoma; HuMax-CD20, an anti-CD20 currently being developed by Genmab, an anti-CD20 antibody described in U.S. Pat. No. 5,500,362, AME-133 (Applied Molecular Evolution), hA20 (Immunomedics, Inc.), HumaLYM (Intracel), and PRO70769 (PCT/US2003/040426, entitled "Immunoglobulin Variants and Uses Thereof"). A number of antibodies that target members of the family of epidermal growth factor receptors, including EGFR (ErbB-1), Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), may benefit from the Fc polypeptides of the present invention. For example the Fc polypeptides of the present invention may find use in an antibody that is substantially similar to trastuzumab (Herceptin®, Genentech) (see for example U.S. Pat. No. 5,677,171), a humanized anti-Her2/neu antibody approved to treat breast cancer; pertuzumab (rhuMab-2C4, Omnitarg™), currently being developed by Genentech; an anti-Her2 antibody described in U.S. Pat. No. 4,753,894; cetuximab (Erbitux®), Imclone) (U.S. Pat. No. 4,943,533; PCT WO 96/40210), a chimeric anti-EGFR antibody in clinical trials for a variety of cancers; ABX-EGF (U.S. Pat. No. 6,235,883), currently being developed by Abgenix-Immunex-Amgen; HuMax-EGFr (U.S. Ser. No. 10/172,317), currently being developed by Genmab; 425, EMD55900, EMD62000, and EMD72000 (Merck KGaA) (U.S. Pat. No. 5,558,864; Murthy et al. 1987, *Arch Biochem Biophys.* 252 (2):549-60; Rodeck et al., 1987, *J Cell Biochem.* 35(4):315-

20; Kettleborough et al., 1991, *Protein Eng.* 4(7):773-83); ICR62 (Institute of Cancer Research) (PCT WO 95/20045; Modjtahedi et al., 1993, *J. Cell Biophys.* 1993, 22(1-3):129-46; Modjtahedi et al., 1993, *Br J. Cancer.* 1993, 67(2):247-53; Modjtahedi et al, 1996, *Br J Cancer,* 73(2):228-35; Modjtahedi et al, 2003, *Int J Cancer,* 105(2):273-80); TheraCIM hR3 (YM Biosciences, Canada and Centro de Immunologia Molecular, Cuba (U.S. Pat. No. 5,891,996; U.S. Pat. No. 6,506,883; Mateo et al, 1997, *Immunotechnology,* 3(1):71-81); mAb-806 (Ludwig Institute for Cancer Research, Memorial Sloan-Kettering) (Jungbluth et al. 2003, *Proc Natl Acad Sci USA.* 100(2):639-44); KSB-102 (KS Biomedix); MR1-1 (IVAX, National Cancer Institute) (PCT WO 0162931A2); and SC100 (Scancell) (PCT WO 01/88138). In another preferred embodiment, the Fc polypeptides of the present invention may find use in alemtuzumab (Campath®, Millenium), a humanized monoclonal antibody currently approved for treatment of B-cell chronic lymphocytic leukemia. The Fc polypeptides of the present invention may find use in a variety of antibodies or Fc fusions that are substantially similar to other clinical products and candidates, including but not limited to muromonab-CD3 (Orthoclone OKT3®), an anti-CD3 antibody developed by Ortho Biotech/Johnson & Johnson, ibritumomab tiuxetan (Zevalin®), an anti-CD20 antibody developed by IDEC/Schering AG, gemtuzumab ozogamicin (Mylotarg®), an anti-CD33 (p67 protein) antibody developed by Celltech/Wyeth, alefacept (Amevive®), an anti-LFA-3 Fc fusion developed by Biogen), abciximab (ReoPro®), developed by Centocor/Lilly, basiliximab (Simulect®), developed by Novartis, palivizumab (Synagis®), developed by MedImmune, infliximab (Remicade®), an anti-TNFalpha antibody developed by Centocor, adalimumab (Humira®), an anti-TNFalpha antibody developed by Abbott, Humicade™, an anti-TNFalpha antibody developed by Celltech, etanercept (Enbrel®), an anti-TNFalpha Fc fusion developed by Immunex/Amgen, ABX-CBL, an anti-CD147 antibody being developed by Abgenix, ABX-IL8, an anti-IL8 antibody being developed by Abgenix, ABX-MA1, an anti-MUC18 antibody being developed by Abgenix, Pemtumomab (R1549, ^{90}Y-muHMFG1), an anti-MUC1 In development by Antisoma, Therex (R1550), an anti-MUC1 antibody being developed by Antisoma, AngioMab (AS1405), being developed by Antisoma, HuBC-1, being developed by Antisoma, Thioplatin (AS1407) being developed by Antisoma, Antegren® (natalizumab), an anti-alpha-4-beta-1 (VLA-4) and alpha-4-beta-7 antibody being developed by Biogen, VLA-1 mAb, an anti-VLA-1 integrin antibody being developed by Biogen, LTBR mAb, an anti-lymphotoxin beta receptor (LTBR) antibody being developed by Biogen, CAT-152, an anti-TGF-β2 antibody being developed by Cambridge Antibody Technology, J695, an anti-IL-12 antibody being developed by Cambridge Antibody Technology and Abbott, CAT-192, an anti-TGFβ1 antibody being developed by Cambridge Antibody Technology and Genzyme, CAT-213, an anti-Eotaxin1 antibody being developed by Cambridge Antibody Technology, LymphoStat-B™ an anti-Blys antibody being developed by Cambridge Antibody Technology and Human Genome Sciences Inc., TRAIL-R1 mAb, an anti-TRAIL-R1 antibody being developed by Cambridge Antibody Technology and Human Genome Sciences, Inc., Avastin™ (bevacizumab, rhuMAb-VEGF), an anti-VEGF antibody being developed by Genentech, an anti-HER receptor family antibody being developed by Genentech, Anti-Tissue Factor (ATF), an anti-Tissue Factor antibody being developed by Genentech, Xolair™ (Omalizumab), an anti-IgE antibody being developed by Genentech, Raptiva™ (Efalizumab), an anti-CD11a antibody being developed by Genentech and Xoma, MLN-02 Antibody (formerly LDP-02), being developed by Genentech and Millenium Pharmaceuticals, HuMax CD4, an anti-CD4 antibody being developed by Genmab, HuMax-ILL5, an anti-iLl5 antibody being developed by Genmab and Amgen, HuMax-Inflam, being developed by Genmab and Medarex, HuMax-Cancer, an anti-Heparanase I antibody being developed by Genmab and Medarex and Oxford GcoSciences, HuMax-Lymphoma, being developed by Genmab and Amgen, HuMax-TAC, being developed by Genmab, IDEC-131, and anti-CD40L antibody being developed by IDEC Pharmaceuticals, IDEC-151 (Clenoliximab), an anti-CD4 antibody being developed by IDEC Pharmaceuticals, IDEC-114, an anti-CD80 antibody being developed by IDEC Pharmaceuticals, IDEC-152, an anti-CD23 being developed by IDEC Pharmaceuticals, anti-macrophage migration factor (MIF) antibodies being developed by IDEC Pharmaceuticals, BEC2, an anti-idiotypic antibody being developed by Imclone, IMC-1C11, an anti-KDR antibody being developed by Imclone, DC101, an anti-flk-1 antibody being developed by Imclone, anti-VE cadherin antibodies being developed by Imclone, CEA-Cide™ (labetuzumab), an anti-carcinoembryonic antigen (CEA) antibody being developed by Immunomedics, Lympho-Cide™ (Epratuzumab), an anti-CD22 antibody being developed by Immunomedics, AFP-Cide, being developed by Immunomedics, MyelomaCide, being developed by Immunomedics, LkoCide, being developed by Immunomedics, ProstaCide, being developed by Immunomedics, MDX-010, an anti-CTLA4 antibody being developed by Medarex, MDX-060, an anti-CD30 antibody being developed by Medarex, MDX-070 being developed by Medarex, MDX-018 being developed by Medarex, Osidem™ (IDM-1), and anti-Her2 antibody being developed by Medarex and Immuno-Designed Molecules, HuMax™-CD4, an anti-CD4 antibody being developed by Medarex and Genmab, HuMax-IL15, an anti-IL15 antibody being developed by Medarex and Genmab, CNTO 148, an anti-TNFα antibody being developed by Medarex and Centocor/J&J, CNTO 1275, an anti-cytokine antibody being developed by Centocor/J&J, MOR101 and MOR102, anti-intercellular adhesion molecule-1 (ICAM-1) (CD54) antibodies being developed by MorphoSys, MOR201, an anti-fibroblast growth factor receptor 3 (FGFR-3) antibody being developed by MorphoSys, Nuvion® (visilizumab), an anti-CD3 antibody being developed by Protein Design Labs, HuZAF™, an anti-gamma interferon antibody being developed by Protein Design Labs, Anti-α5β1 Integrin, being developed by Protein Design Labs, anti-IL-12, being developed by Protein Design Labs, ING-1, an anti-Ep-CAM antibody being developed by Xoma, and MLN01, an anti-Beta2 integrin antibody being developed by Xoma, all references incorporated by reference.

[0211] Application of the Fc polypeptides to the aforementioned antibody and Fc fusion clinical products and candidates is not meant to be constrained to their precise composition. The Fc polypeptides of the present invention may be incorporated into the aforementioned clinical candidates and products, or into antibodies and Fc fusions that are substantially similar to them. The Fc polypeptides of the present invention may be incorporated into versions of the aforementioned clinical candidates and products that are humanized, affinity matured, engineered, or modified in some other way.

Furthermore, the entire polypeptide of the aforementioned clinical products and candidates need not be used to construct a new antibody or Fc fusion that incorporates the Fc polypeptides of the present invention; for example only the variable region of a clinical product or candidate antibody, a substantially similar variable region, or a humanized, affinity matured, engineered, or modified version of the variable region may be used. In another embodiment, the Fc polypeptides of the present invention may find use in an antibody or Fc fusion that binds to the same epitope, antigen, ligand, or receptor as one of the aforementioned clinical products and candidates.

[0212] In one embodiment, the Fc polypeptides of the present invention are used for the treatment of autoimmune, inflammatory, or transplant indications. Target antigens and clinical products and candidates that are relevant for such diseases include but are not limited to anti-α4β7 integrin antibodies such as LDP-02, anti-beta2 integrin antibodies such as LDP-01, anti-complement (C5) antibodies such as 5G1.1, anti-CD2 antibodies such as BTI-322, MEDI-507, anti-CD3 antibodies such as OKT3, SMART anti-CD3, anti-CD4 antibodies such as IDEC-151, MDX-CD4, OKT4A, anti-CD11a antibodies, anti-CD14 antibodies such as IC14, anti-CD18 antibodies, anti-CD23 antibodies such as IDEC 152, anti-CD25 antibodies such as Zenapax, anti-CD40L antibodies such as 5c8, Antova, IDEC-131, anti-CD64 antibodies such as MDX-33, anti-CD80 antibodies such as IDEC-114, anti-CD147 antibodies such as ABX-CBL, anti-E-selectin antibodies such as CDP850, anti-gpIIb/IIIa antibodies such as ReoPro/Abcixima, anti-ICAM-3 antibodies such as ICM3, anti-ICE antibodies such as VX-740, anti-FcR1 antibodies such as MDX-33, anti-IgE antibodies such as rhuMab-E25, anti-IL-4 antibodies such as SB-240683, anti-IL-5 antibodies such as SB-240563, SCH55700, anti-IL-8 antibodies such as ABX-IL8, anti-interferon gamma antibodies, anti-TNF (TNF, TNFα, TNFα, TNF-alpha) antibodies such as CDP571, CDP870, D2E7, Infliximab, MAK-195F, and anti-VLA-4 antibodies such as Antegren.

[0213] Fc variants of the present invention may be utilized in TNF inhibitor molecules to provide enhanced properties. It has been shown that the effector function associated with FcγRIIIa may negatively impact the effectiveness of certain TNF inhibitor molecules used in the treatment of rheumatoid arthritis or psoriatic arthritis patients that have a high-affinity polymorphism (158 F:V discussed herein elsewhere) and vice-versa (Z. Tutuncu et al., 2004, "FcR Polymorphisms and Treatment Outcomes in Patients with Inflammatory Arthritis Treated with TNF Blocking Agents", oral presentation on Oct. 18, 2004 at the 2004 ACR Meeting, San Antonio, Tex.; abstract published in Arthritis & Rheumatism, September 2004, incorporated by reference). In general for autoimmune conditions such as rheumatoid arthritis or psoriatic arthritis, combining a TNF inhibitor with an Fc variant that provides reduced binding to one or more FcγRs as compared to the parent enhances the effectiveness of therapy. Ideally, reduced or even ablated binding to one or more FcγRs, for example FcγRIIIa, with a TNF inhibitor molecule would produce the best results.

[0214] Useful TNF inhibitor molecules include any molecule that inhibits the action of TNF-alpha in a mammal. Suitable examples include the Fc fusion Enbrel® (etanercept) and the antibodies Humira® (adalimumab) and Remicade®E) (infliximab). Monoclonal antibodies (such as Remicade and Humira) engineered using the Fc variants of the present invention to reduce Fc binding, may translate to better efficacy. Effector function of Humira, Remicade, and Enbrel was not considered in the development of these drugs, let alone modulation of effector function. By using an Fc variant of the present invention that reduces binding to one or more FcγRs in the context of an antibody or Fc fusion that acts on autoimmune conditions, efficacy may be enhanced as compared to the currently commercialized products. Useful TNF inhibitor molecules preferably include Dominant Negative TNF molecules (as defined in U.S. Ser. No. 09/798,789, filed Mar. 2, 2000; 09/981,289, filed Oct. 15, 2001; 10/262,630, filed Sep. 30, 2002; and 10/963,994, filed Oct. 12, 2004, all incorporated by reference). The Dominant Negative TNF molecules (DN-TNF) have no intrinsic effector activity, and act to "save" transmembrane TNF (tmTNF) (i.e., if the killing of cells that contain tmTNF has a negative effect on disease outcome for rheumatoid or psoriatic arthritis). A DN-TNF molecule associated with an Fc variant that reduces or ablates FcγR binding to the receptor is preferred.

[0215] In one embodiment, the Fc polypeptides of the present invention function therapeutically, in whole or in part, through ADCC activity. Target antigens and clinical products and candidates that are relevant for such application may include but are not limited to: anti-CD20 antibodies such as Bexocar, RituxanO, Zevalin®, and PRO70769, anti-CD33 antibodies such as Smart M195, anti-CD22 antibodies such as Lymphocide™, anti-CD30 antibodies such as AC-10 and SGN-30, anti-EGFR antibodies such as ABX-EGF, Cetuximab, IMC-C225, Merck Mab 425, anti-EpCAM antibodies such as Crucell's anti-EpCAM, anti-HER2 antibodies such as Herceptin and MDX-210, and anti-CEA antibodies such as cantumab and Pentacea.

[0216] In one embodiment, the Fc polypeptides of the present invention function therapeutically, in whole or in part, through CDC activity. Target antigens and clinical products and candidates that are relevant for such application may include but are not limited to: anti-CEA antibodies such as cantumab and Pentacea, anti-CD20 antibodies such as Bexocar, Rituxan®, Zevalin®, and PRO70769, anti-EpCAM antibodies such as Crucell's anti-EpCAM and Edrecolomab, and anti-CD52 antibodies such as Campath® (alemtuzumab).

[0217] In one embodiment, the Fc polypeptides of the present invention are directed against antigens expressed in the hematological lineage. Target antigens and clinical products and candidates that are relevant for such application may include but are not limited to: anti-CD33 antibodies such as Smart M195, anti-CD40L antibodies such as Antova™, IDEC-131, anti-CD44 antibodies such as Bivatuzumab, anti-CD52 antibodies such as Campath® (alemtuzumab), anti-CD80 antibodies such as IDEC-114, anti-CTLA-4 antibodies such as MDX-101, anti-CD20 antibodies such as Bexocar, Rituxan®, Zevalin®, and PRO70769, anti-CD22 antibodies such as Lymphocide™, anti-CD23 antibodies such as IDEC-152, anti-CD25 antibodies such as Zenapax® (daclizumab), and anti-MHC (HLA-DR) antibodies such as apolizumab.

[0218] In one embodiment, the Fc polypeptides of the present invention are directed against antigens expressed in solid tumors. Target antigens and clinical products and candidates that are relevant for such application may include but are not limited to: anti-EpCAM antibodies such as Crucell's anti-EpCAM and Edrecolomab, anti-CEA antibodies such as cantumab and Pentacea, anti-EGFR antibodies such as ABX-EGF, Cetuximab, IMC-C225, Merck Mab 425, anti-Muc1 antibodies such as BravaRex, TriAb, anti-Her2 antibodies

such as Herceptin®, MDX-210, anti-GD-2 ganglioside antibodies such as 3F8 and TriGem, anti-GD-3 ganglioside antibodies such as mitumomab, anti-PSMA antibodies such as MDX-070, anti-CA125 antibodies such as oregovomab, anti-TAG-72 antibdies such as MDX-220, and anti-MUC-1 antibodies such as cantuzumab.

[0219] In a preferred embodiment, the target of the Fc variants of the present invention is itself one or more Fc ligands. Fc polypeptides of the invention can be utilized to modulate the activity of the immune system, and in some cases to mimic the effects of IVIg therapy in a more controlled, specific, and efficient manner. IVIg is effectively a high dose of immunoglobulins delivered intravenously. In general, IVIg has been used to downregulate autoimmune conditions. It has been hypothesized that the therapeutic mechanism of action of IVIg involves ligation of Fc receptors at high frequency (J. Bayry et al., 2003, Transfusion Clinique et Biologique 10: 165-169; Binstadt et al., 2003, J Allergy Clin. Immunol, 697-704). Indeed animal models of Ithrombocytopenia purpura (ITP) show that the isolated Fc are the active portion of IVIg (Samuelsson et al, 2001, Pediatric Research 50(5), 551). For use in therapy, immunoglobulins are harvested from thousands of donors, with all of the concomitant problems associated with non-recombinant biotherapeutics collected from humans. An Fc variant of the present invention should serve all of the roles of IVIg while being manufactured as a recombinant protein rather than harvested from donors.

[0220] The immunomodulatory effects of IVIg may be dependent on productive interaction with one or more Fc ligands, including but not limited to FcγRs, complement proteins, and FcRn. In some embodiments, Fc variants of the invention with enhanced affinity for FcγRIIb can be used to promote anti-inflammatory activity (Samuelsson et al., 2001, *Science* 291: 484-486) and or to reduce autoimmunity (Hogarth, 2002, *Current Opinion in Immunology,* 14:798-802). In other embodiments, Fc polypeptides of the invention with enhanced affinity for one or more FcγRs can be utilized by themselves or in combination with additional modifications to reduce autoimmunity (Hogarth, 2002, *Current Opinion in Immunology,* 14:798-802). In alternative embodiments, Fc variants of the invention with enhanced affinity for FcγRIIIa but reduced capacity for intracellular signaling can be used to reduce immune system activation by competitively interfering with FcγRIIIa binding. The context of the Fc variant dramatically impacts the desired specificity. For example, Fc variants that provide enhanced binding to one or more activating FcγRs may provide optimal immunomodulatory effects in the context of an antibody, Fc fusion, isolated Fc, or Fc fragment by acting as an FcγR antagonist (van Mirre et al., 2004, J. Immunol. 173:332-339). However, fusion or conjugation of two or more Fc variants may provide different effects, and for such an Fc polypeptide it may be optimal to utilize Fc variants that provide enhanced affinity for an inhibitory receptor.

[0221] The Fc variants of the present invention may be used as immunomodulatory therapeutics. Binding to or blocking Fc receptors on immune system cells may be used to influence immune response in immunological conditions including but not limited to idiopathic thrombocytopenia purpura (ITP) and rheumatoid arthritis (RA) among others. By use of the affinity enhanced Fc variants of the present invention, the dosages required in typical IVIg applications may be reduced while obtaining a substantially similar therapeutic effect. The Fc variants may provide enhanced binding to an FcγR, including but not limited to FcγRIIa, FcγRIIb, FcγRIIIa, FcγRIIIb, and/or FcγRI. In particular, binding enhancements to FcγRIIb would increase expression or inhibitory activity, as needed, of that receptor and improve efficacy. Alternatively, blocking binding to activation receptors such as FcγRIIIb or FcγRI may improve efficacy. In addition, modulated affinity of the Fc variants for FcRn and/or also complement may also provide benefits.

[0222] In one embodiment, Fc variants that provide enhanced binding to the inhibitory receptor FcγRIIb provide an enhancement to the IVIg therapeutic approach. In particular, the Fc variants of the present invention that bind with greater affinity to the FcγRIIb receptor than parent Fc polypeptide may be used. Such Fc variants would thus function as FcγRIIb agonists, and would be expected to enhance the beneficial effects of IVIg as an autoimmune disease therapeutic and also as a modulator of B-cell proliferation. In addition, such FcγRIIb-enhanced Fc variants may also be further modified to have the same or limited binding to other receptors. In additional embodiments, the Fc variants with enhanced FcγRIIb affinity may be combined with mutations that reduce or ablate to other receptors, thereby potentially further minimizing side effects during therapeutic use.

[0223] Such immunomodulatory applications of the Fc variants of the present invention may also be utilized in the treatment of oncological indications, especially those for which antibody therapy involves antibody-dependant cytotoxic mechanisms. For example, an Fc variant that enhances affinity to FcγRIIb may be used to antagonize this inhibitory receptor, for example by binding to the Fc/FcγRIIb binding site but failing to trigger, or reducing cell signaling, potentially enhancing the effect of antibody-based anti-cancer therapy. Such Fc variants, functioning as FcγRIIb antagonists, may either block the inhibitory properties of FcγRIIb, or induce its inhibitory function as in the case of IVIg. An FcγRIIb antagonist may be used as co-therapy in combination with any other therapeutic, including but not limited to antibodies, acting on the basis of ADCC related cytotoxicity. FcγRIIb antagonistic Fc variants of this type are preferably isolated Fc or Fc fragments, although in alternate embodiments antibodies and Fc fusions may be used.

Optimized Properties

[0224] The present invention provides Fc variants that are optimized for a number of therapeutically relevant properties. An Fc variant comprises one or more amino acid modifications relative to a parent Fc polypeptide, wherein said amino acid modification(s) provide one or more optimized properties. An Fc variant of the present invention differs in amino acid sequence from its parent Fc polypeptide by virtue of at least one amino acid modification. Thus Fc variants of the present invention have at least one amino acid modification compared to the parent. Alternatively, the Fc variants of the present invention may have more than one amino acid modification as compared to the parent, for example from about one to fifty amino acid modifications, preferrably from about one to ten amino acid modifications, and most preferably from about one to about five amino acid modifications compared to the parent. Thus the sequences of the Fc variants and those of the parent Fc polypeptide are substantially homologous. For example, the variant Fc variant sequences herein will possess about 80% homology with the parent Fc variant sequence, preferably at least about 90% homology, and most preferably at least about 95% homology.

[0225] The Fc variants of the present invention may be optimized for a variety of properties. An Fc variant that is engineered or predicted to display one or more optimized properties is herein referred to as an "optimized Fc variant". Properties that may be optimized include but are not limited to enhanced or reduced affinity for an FcγR. In a preferred embodiment, the Fc variants of the present invention are optimized to possess enhanced affinity for a human activating FcγR, preferably FcγRI, FcγRIIa, FcγRIIc, FcγRIIIa, and FcγRIIIb, most preferably FcγRIIIa. In an alternately preferred embodiment, the Fc variants are optimized to possess reduced affinity for the human inhibitory receptor FcγRIIb. These preferred embodiments are anticipated to provide Fc polypeptides with enhanced therapeutic properties in humans, for example enhanced effector function and greater anti-cancer potency. In an alternate embodiment, the Fc variants of the present invention are optimized to have reduced or ablated affinity for a human FcγR, including but not limited to FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, and FcγRIIIb. These embodiments are anticipated to provide Fc polypeptides with enhanced therapeutic properties in humans, for example reduced effector function and reduced toxicity. In other embodiments, Fc variants of the present invention provide enhanced affinity for one or more FcγRs, yet reduced affinity for one or more other FcγRs. For example, an Fc variant of the present invention may have enhanced binding to FcγRIIIa, yet reduced binding to FcγRIIb. Alternately, an Fc variant of the present invention may have enhanced binding to FcγRIIa and FcγRI, yet reduced binding to FcγRIIb. In yet another embodiment, an Fc variant of the present invention may have enhanced affinity for FcγRIIb, yet reduced affinity to one or more activating FcγRs.

[0226] By "greater affinity" or "improved affinity" or "enhanced affinity" or "better affinity" than a parent Fc polypeptide, as used herein is meant that an Fc variant binds to an Fc receptor with a significantly higher equilibrium constant of association (K_A or Ka) or lower equilibrium constant of dissociation (K_D or Kd) than the parent Fc polypeptide when the amounts of variant and parent polypeptide in the binding assay are essentially the same. For example, the Fc variant with improved Fc receptor binding affinity may display from about 5 fold to about 1000 fold, e.g. from about 10 fold to about 500 fold improvement in Fc receptor binding affinity compared to the parent Fc polypeptide, where Fc receptor binding affinity is determined, for example, by the binding methods disclosed herein, including but not limited to Biacore, by one skilled in the art. Accordingly, by "reduced affinity" as compared to a parent Fc polypeptide as used herein is meant that an Fc variant binds an Fc receptor with significantly lower K_A or higher K_D than the parent Fc polypeptide. Greater or reduced affinity can also be defined relative to an absolute level of affinity. For example, according to the data herein, WT (native) IgG1 binds FcγRIIb with an affinity of about 1.5 μM, or about 1500 nM. Furthermore, some Fc variants described herein bind FcγRIIb with an affinity about 10-fold greater to WT IgG1. As disclosed herein, greater or enhanced affinity means having a K_D lower than about 100 nM, for example between about 10 nM-about 100 nM, between about 1 nM-about 100 nM, or less than 1 nM.

[0227] Preferred embodiments comprise optimization of Fc binding to a human FcγR, however in alternate embodiments the Fc variants of the present invention possess enhanced or reduced affinity for FcγRs from nonhuman organisms, including but not limited to rodents and nonhuman primates. Fc variants that are optimized for binding to a nonhuman FcγR may find use in experimentation. For example, mouse models are available for a variety of diseases that enable testing of properties such as efficacy, toxicity, and pharmacokinetics for a given drug candidate. As is known in the art, cancer cells can be grafted or injected into mice to mimic a human cancer, a process referred to as xenografting. Testing of Fc variants that comprise Fc variants that are optimized for one or more mouse FcγRs, may provide valuable information with regard to the efficacy of the protein, its mechanism of action, and the like. The Fc variants of the present invention may also be optimized for enhanced functionality and/or solution properties in aglycosylated form. In a preferred embodiment, the aglycosylated Fc variants of the present invention bind an Fc ligand with greater affinity than the aglycosylated form of the parent Fc variant. Said Fc ligands include but are not limited to FcγRs, C1q, FcRn, and proteins A and G, and may be from any source including but not limited to human, mouse, rat, rabbit, or monkey, preferably human. In an alternately preferred embodiment, the Fc variants are optimized to be more stable and/or more soluble than the aglycosylated form of the parent Fc variant.

[0228] Fc variants of the invention may comprise modifications that modulate interaction with Fc ligands other than FcγRs, including but not limited to complement proteins, FcRn, and Fc receptor homologs (FcRHs). FcRHs include but are not limited to FcRH1, FcRH2, FcRH3, FcRH4, FcRH5, and FcRH6 (Davis et al., 2002, Immunol. Reviews 190:123-136).

[0229] Preferably, the Fc ligand specificity of the Fc variant of the present invention will determine its therapeutic utility. The utility of a given Fc variant for therapeutic purposes will depend on the epitope or form of the Target antigen and the disease or indication being treated. For some targets and indications, enhanced FcγR-mediated effector functions may be preferable. This may be particularly favorable for anticancer Fc variants. Thus Fc variants may be used that comprise Fc variants that provide enhanced affinity for activating FcγRs and/or reduced affinity for inhibitory FcγRs. For some targets and indications, it may be further beneficial to utilize Fc variants that provide differential selectivity for different activating FcγRs; for example, in some cases enhanced binding to FcγRIIa and FcγRIIIa may be desired, but not FcγRI, whereas in other cases, enhanced binding only to FcγRIIa may be preferred. For certain targets and indications, it may be preferable to utilize Fc variants that enhance both FcγR-mediated and complement-mediated effector functions, whereas for other cases it may be advantageous to utilize Fc variants that enhance either FcγR-mediated or complement-mediated effector functions. For some Targets or cancer indications, it may be advantageous to reduce or ablate one or more effector functions, for example by knocking out binding to C1q, one or more FcγR's, FcRn, or one or more other Fc ligands. For other targets and indications, it may be preferable to utilize Fc variants that provide enhanced binding to the inhibitory FcγRIIb, yet WT level, reduced, or ablated binding to activating FcγRs. This may be particularly useful, for example, when the goal of an Fc variant is to inhibit inflammation or auto-immune disease, or modulate the immune system in some way.

[0230] In one embodiment, the Fc variants provide selectively enhanced affinity to FcγRIIb relative to one or more activating receptors. Selectively enhanced affinity means either that the Fc variant has improved affinity for FcγRIIb

relative to the activating receptor(s) as compared to the parent Fc polypeptide but has reduced affinity for the activating receptor(s) as compared to the parent Fc polypeptide, or it means that the Fc variant has improved affinity for both FcγRIIb and activating receptor(s) as compared to the parent Fc polypeptide, however the improvement in affinity is greater for FcγRIIb than it is for the activating receptor(s). In alternate embodiments, the Fc variants reduce or ablate binding to one or more activating FcγRs, reduce or ablate binding to one or more complement proteins, reduce or ablate one or more FcγR-mediated effector functions, and/or reduce or ablate one or more complement-mediated effector functions.

[0231] Clearly an important parameter that determines the most beneficial selectivity of a given Fc variant to treat a given disease is the context of the Fc variant, that is what type of Fc variant is being used. Thus the Fc ligand selectivity or specificity of a given Fc variant will provide different properties depending on whether it composes an antibody, Fc fusion, or an Fc variants with a coupled fusion or conjugate partner. For example, toxin, radionucleotide, or other conjugates may be less toxic to normal cells if the Fc variant that comprises them has reduced or ablated binding to one or more Fc ligands. As another example, in order to inhibit inflammation or autoimmune disease, it may be preferable to utilize an Fc variant with enhanced affinity for activating FcγRs, such as to bind these FcγRs and prevent their activation. Conversely, an Fc variant that comprises two or more Fc regions with enhanced FcγRIIb affinity may co-engage this receptor on the surface of immune cells, thereby inhibiting proliferation of these cells. Whereas in some cases an Fc variants may engage its target antigen on one cell type yet engage FcγRs on separate cells from the target antigen, in other cases it may be advantageous to engage FcγRs on the surface of the same cells as the target antigen. For example, if an antibody targets an antigen on a cell that also expresses one or more FcγRs, it may be beneficial to utilize an Fc variant that enhances or reduces binding to the FcγRs on the surface of that cell. This may be the case, for example when the Fc variant is being used as an anticancer agent, and co-engagement of target antigen and FcγR on the surface of the same cell promote signaling events within the cell that result in growth inhibition, apoptosis, or other anti-proliferative effect. Alternatively, antigen and FcγR co-engagement on the same cell may be advantageous when the Fc variant is being used to modulate the immune system in some way, wherein co-engagement of target antigen and FcγR provides some proliferative or anti-proliferative effect. Likewise, Fc variants that comprise two or more Fc regions may benefit from Fc variants that modulate FcγR selectivity or specificity to co-engage FcγRs on the surface of the same cell.

[0232] Disclosed herein are methods of inhibiting CD32b+ cells. Without being limited thereto, FIG. **44** is a schematic representation of a proposed mechanism by which immunoglobulins disclosed herein inhibit CD32b+ cells (See also Example 16.3; see also FIG. **57**). Accordingly, disclosed herein are methods of inhibiting CD32b+ cells comprising contacting a CD32b+ cell with an immunoglobulin comprising an Fc region with enhanced affinity to FcγRIIb. In one embodiment, the immunoglobulin binds at least two B cell proteins, .e.g., at least to proteins bound to the surface B cells. In one embodiment, the first of said B cell proteins is FcγRIIb. In a another embodiment, the second of said B cell proteins is part of the B cell receptor (BCR) complex, which may include an antigen bound to BCR. In another embodiment, the second of said B cell proteins is not involved directly in antigen recognition. In another embodiment, said the second of said B cell proteins is expressed on the surface of the B cell, but is not part of the B cell receptor. Nonlimiting examples of the second of said B cell proteins include BCR proteins (e.g., IgM (μ), CD79a, CD79b, CD19, CD21, CD22, CD72, CD81, Leu13, etc.), or other proteins bound to the surface of B cells (e.g., CD20, CD23, CD24, CD35, CD40, CD45RA, CD80, CD86, HLA-DR, etc.). In some embodiments, the immunoglobulins inhibit release of calcium from the B cells upon their stimulation through the B cell receptor. In another embodiment, an immunoglobulin disclosed herein binds at least two B cell proteins on the surface of the same B cell (see, .e.g., FIG. **44**).

[0233] Modifications for Optimizing Inhibitory Function

[0234] Disclosed herein is directed to immunoglobulins comprising modifications, wherein said modifications alter affinity to the FcγRIIb receptor, and/or alter the ability of the immunoglobulin to mediate one or more FcγRIIb-mediated effector functions. Modifications of the invention include amino acid modifications and glycoform modifications.

Amino Acid Modifications

[0235] As described herein (see, e.g., Example 9), simultaneous high affinity coengagement of cognate BCR and FcγRIIb may be used to inhibit FcγRIIb+ cells. Such coengagement may occur via the use of an immunoglobulin described herein, e.g., an immunoglobulin used to coengage both FcγRIIb via its Fc region, and a target antigen on the surface of the FcγRIIb+ cell (e.g., one or more cognate BCR proteins and/or an antigen bound to cognate BCR) via its Fv region. Amino acid modifications at heavy chain constant region positions: 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331 and 332 allow modification of immunoglobulin FcγRIIb binding properties, effector function, and potentially clinical properties of antibodies

[0236] In one embodiment, immunoglobulins that bind FcγRIIb+ cells and coengage a target antigen on the cell's surface and an FcγRIIb on cell's surface disclosed herein may be variant immunoglobulins relative to a parent immunoglobulin. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332, according to the EU index. In one embodiment, the variant immunoglobulin comprises a variant Fc region, wherein said variant Fc region comprises one or more (e.g., two or more) modification(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 235, 236, 239, 266, 267, 268, and 328, according to the EU index.

[0237] In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting

of 234F, 234G, 234I, 234K, 234N, 234P, 234Q, 234S, 234V, 234W, 234Y, 234D, 234E, 235A, 235E, 235H, 235I, 235N, 235P, 235Q, 235R, 235S, 235W, 235Y, 235D, 235F, 235T, 236D, 236F, 236H, 236I, 236K, 236L, 236M, 236P, 236Q, 236R, 236S, 236T, 236V, 236W, 236Y, 236A, 236E, 236N, 237A, 237E, 237H, 237K, 237L, 237P, 237Q, 237S, 237V, 237Y, 237D, 237N, 239D, 239E, 239N, 239Q, 265E, 266D, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298D, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327G, 327L, 327N, 327Q, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 329E, 330D, 330H, 330K, 330S, 331S, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234N, 234F, 234D, 234E, 234W, 235Q, 235R, 235W, 235Y, 235D, 235F, 235T, 236D, 236H, 236I, 236L, 236S, 236Y, 236E, 236N, 237H, 237L, 237D, 237N, 239D, 239N, 239E, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327L, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 330D, 330H, 330K, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234D, 234E, 234W, 235D, 235F, 235R, 235Y, 236D, 236N, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, and 332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 235Y, 236D, 239D, 266M, 267E, 268D, 268E, 328F, 328W, and 328Y, wherein numbering is according to an EU index.

[0238] In one embodiment, said modification(s) is at least two modifications (e.g., a combination of modifications) at positions selected from the group consisting of 234/239, 234/267, 234/328, 235/236, 235/239, 235/267, 235/268, 235/328, 236/239, 236/267, 236/268, 236/328, 237/267, 239/267, 239/268, 239/327, 239/328, 239/332, 266/267, 267/268, 267/325, 267/327, 267/328, 267/332, 268/327, 268/328, 268/332, 326/328, 327/328, and 328/332, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least two modifications (e.g., a combination of modifications) at positions selected from the group consisting of 235/267, 236/267, 239/268, 239/267, 267/268, and 267/328, wherein numbering is according to an EU index. In one embodiment, said modification(s) is at least two substitutions (e.g., a combination of substitutions) selected from the group consisting of 234D/267E, 234E/267E, 234F/267E, 234E/328F, 234W/239D, 234W/239E, 234W/267E, 234W/328Y, 235D/267E, 235D/328F, 235F/239D, 235F/267E, 235F/328Y, 235Y/236D, 235Y/239D, 235Y/267D, 235Y/267E, 235Y/268E, 235Y/328F, 236D/239D, 236D/267E, 236D/268E, 236D/328F, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 239D/268D, 239D/268E, 239D/327D, 239D/328F, 239D/328W, 239D/328Y, 239D/332E, 239E/267E, 266M/267E, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267E/327D, 267E/327E, 267E/328F, 267E/328I, 267E/328Y, 267E/332E, 268D/327D, 268D/328F, 268D/328W, 268D/328Y, 268D/332E, 268E/328F, 268E/328Y, 327D/328Y, 328F/332E, 328W/332E, and 328Y/332E, wherein numbering is according to an EU index.

[0239] In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E1328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E1267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E1268E, 236D/267E/268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y/268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 239D/267E/332E, 234W/328Y/I332 E, 235F/328Y/I332 E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332 E, 326D/328Y/332 E, 327D/328Y/332E, 234W/236D/239 E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 266D, 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 266M/267E, 234E/268D, 236D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E1328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E1328Y, 267A/268D/328Y, 267E/268E1328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 234W/328Y/332 E, 235F/328Y/332E, 239D/328F/332 E, 239D/328Y/332 E, 267A/328Y/332 E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332 E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E1267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 234N, 235Q, 235R, 235W, 235Y, 236D, 236H, 236I, 236L, 236S, 236Y, 237H, 237L, 239D, 239N, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 326A, 326E, 326W, 327D, 327L, 328E, 328F, 330D, 330H, 330K, 234F/236N, 234F/236D, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/

267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E1267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E1268E, 236D/267E1268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E1328F, 236D/267E1328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E1328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 239D/267E/332E, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E

[0240] In one embodiment, said modification(s) result in at least one of the following substitutions, or combinations of substitutions: 235Y/267E, 236D/267E, 239D/268D, 239D/267E, 267E/268D, 267E/268E, and 267E/328F, wherein numbering is according to an EU index.

[0241] In some embodiments, antibodies may comprise isotypic modifications, that is, modifications in a parent IgG to the amino acid type in an alternate IgG. For example as illustrated in FIG. **1**, an IgG1IgG3 hybrid variant may be constructed by substituting IgG1 positions in the CH2 and/or CH3 region with the amino acids from IgG3 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more substitutions selected from the group consisting of: 274Q, 276K, 300F, 339T, 356E, 358M, 384S, 392N, 397M, 422I, 435R, and 436F. In other embodiments of the invention, an IgG1/IgG2 hybrid variant may be constructed by substituting IgG2 positions in the CH2 and/or CH3 region with amino acids from IgG1 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more modifications selected from the group consisting of 233E, 234L, 235L, −236G (referring to an insertion of a glycine at position 236), and 327A.

[0242] Means for Optimizing Effector Function

[0243] Described herein are immunoglobulins comprising means for alter affinity to the FcγRIIb receptor, and/or alter the ability of the immunoglobulin to mediate one or more FcγRIIb-mediated effector functions. Means of the invention include amino acid modifications (e.g., positional means for optimizing effector function, substitutional means for optimizing effector function, etc.) and glycoform modifications (e.g., means for glycoform modifications).

[0244] Amino Acid Modifications

[0245] As described herein, positional means for optimizing effector function include but is not limited to, modification of an amino acid at one or more heavy chain constant region positions (e.g., at positions: 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332) which allow modification of immunoglobulin FcγRIIb binding properties, effector function, and potentially clinical properties of antibodies.

[0246] In particular, substitutional means for optimizing FcγRIIb effector functions, e.g., by altering affinity to FcγRIIb, include, but is not limited to, a substitution of an amino acid at one or more heavy chain constant region positions, e.g., one or more of the amino acid substitutions in the following heavy chain constant region positions: 234, 235, 236, 237, 239, 265, 266, 267, 268, 298, 325, 326, 327, 328, 329, 330, 331, and 332, wherein numbering is according to the EU index. In one embodiment, substitutional means include at least one (e.g., two or more) substitution(s) compared to a parent Fc region, wherein said modification(s) are at positions selected from the group consisting of 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332, according to the EU index. In one embodiment, substitutional means include one or more (e.g., two or more) substitutions (s) at positions selected from the group consisting of 235, 236, 239, 266, 267, 268, and 328, according to the EU index.

[0247] In one embodiment, said substitutional means is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234F, 234G, 234I, 234K, 234N, 234P, 234Q, 234S, 234V, 234W, 234Y, 234D, 234E, 235A, 235E, 235H, 235I, 235N, 235P, 235Q, 235R, 235S, 235W, 235Y, 235D, 235F, 235T, 236D, 236F, 236H, 236I, 236K, 236L, 236M, 236P, 236Q, 236R, 236S, 236T, 236V, 236W, 236Y, 236A, 236E, 236N, 237A, 237E, 237H, 237K, 237L, 237P, 237Q, 237S, 237V, 237Y, 237D, 237N, 239D, 239E, 239N, 239Q, 265E, 266D, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298D, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327G, 327L, 327N, 327Q, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 329E, 330D, 330H, 330K, 330S, 331S, and 332E, wherein numbering is according to an EU index. In one embodiment, said substitutional means is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234N, 234F, 234D, 234E, 234W, 235O, 235R, 235W, 235Y, 235D, 235F, 235T, 236D, 236H, 236I, 236L, 236S, 236Y, 236E, 236N, 237H, 237L, 237D, 237N, 239D, 239N, 239E, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 325L, 326A, 326E, 326W, 326D, 327D, 327L, 327E, 328E, 328F, 328Y, 328H, 328I, 328Q, 328W, 330D, 330H, 330K, and 332E, wherein numbering is according to an EU index. In one embodiment, said substitutional means is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 234D, 234E, 234W, 235D, 235F, 235R, 235Y, 236D, 236N, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, and 332E, wherein numbering is according to an EU index. In one embodiment, said substitutional means is at least one substitution (e.g., one or more substitution(s), two or more substitution(s), etc.) selected from the group consisting of 235Y, 236D, 239D, 266M, 267E, 268D, 268E, 328F, 328W, and 328Y, wherein numbering is according to an EU index.

[0248] In one embodiment, said substitutional means is at least two substitutions (e.g., a combination of modifications) at positions selected from the group consisting of 234/239, 234/267, 234/328, 235/236, 235/239, 235/267, 235/268, 235/328, 236/239, 236/267, 236/268, 236/328, 237/267, 239/267, 239/268, 239/327, 239/328, 239/332, 266/267, 267/268, 267/325, 267/327, 267/328, 267/332, 268/327, 268/328, 268/332, 326/328, 327/328, and 328/332, wherein numbering is according to an EU index. In one embodiment, said substitutional means is at least two substitutions (e.g., a combination of modifications) at positions selected from the group con-

sisting of 235/267, 236/267, 239/268, 239/267, 267/268, and 267/328, wherein numbering is according to an EU index. In one embodiment, said substitutional means is at least two substitutions (e.g., a combination of substitutions) selected from the group consisting of 234D/267E, 234E/267E, 234F/267E, 234E/328F, 234W/239D, 234W/239E, 234W/267E, 234W/328Y, 235D/267E, 235D/328F, 235F/239D, 235F/267E, 235F/328Y, 235Y/236D, 235Y/239D, 235Y/267D, 235Y/267E, 235Y/268E, 235Y/328F, 236D/239D, 236D/267E, 236D/268E, 236D/328F, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 239D/268D, 239D/268E, 239D/327D, 239D/328F, 239D/328W, 239D/328Y, 239D/332E, 239E/267E, 266M/267E, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267E/327D, 267E/327E, 267E/328F, 267E/328I, 267E/328Y, 267E/332E, 268D/327D, 268D/328F, 268D/328W, 268D/328Y, 268D/332E, 268E/328F, 268E/328Y, 327D/328Y, 328F/332E, 328W/332E, and 328Y/332E, wherein numbering is according to an EU index.

[0249] In one embodiment, said substitutional means result in at least one of the following substitutions, or combinations of substitutions: 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 239D/267E/332E, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said substitutional means result in at least one of the following substitutions, or combinations of substitutions: 266D, 234F/236N, 234F/236D, 236A/237A, 236S/237A, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235S/267E, 235T/267E, 235Y/267D, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 266M/267E, 234E/268D, 236D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 234W/239D/328Y, 235F/239D1328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A1328Y, 239D/267E/328F, 234W/268D/328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E, wherein numbering is according to an EU index. In one embodiment, said substitutional means result in at least one of the following substitutions, or combinations of substitutions: 234N, 235Q, 235R, 235W, 235Y, 236D, 236H, 236I, 236L, 236S, 236Y, 237H, 237L, 239D, 239N, 266I, 266M, 267A, 267D, 267E, 267G, 268D, 268E, 268N, 268Q, 298E, 298L, 298M, 298Q, 326A, 326E, 326W, 327D, 327L, 328E, 328F, 330D, 330H, 330K, 234F/236N, 234F/236D, 235D/239D, 234D/267E, 234E/267E, 234F/267E, 235D/267E, 235F/267E, 235T/267E, 235Y/267D, 235Y/267E, 236D/267E, 236E/267E, 236N/267E, 237D/267E, 237N/267E, 239D/267D, 239D/267E, 266M/267E, 234E/268D, 236D/268D, 239D/268D, 267D/268D, 267D/268E, 267E/268D, 267E/268E, 267E/325L, 267D/327D, 267D/327E, 267E/327D, 267E/327E, 268D/327D, 239D/328Y, 267E/328F, 267E/328H, 267E/328I, 267E/328Q, 267E/328Y, 268D/328Y, 239D/332E, 328Y/332E, 234D/236N/267E, 235Y/236D/267E, 234W/239E/267E, 235Y/239D/267E, 236D/239D/267E, 235Y/267E/268E, 236D/267E/268E, 239D/267E/268E, 234W/239D/328Y, 235F/239D/328Y, 234E/267E/328F, 235D/267E/328F, 235Y/267E/328F, 236D/267E/328F, 239D/267A/328Y, 239D/267E/328F, 234W/268D1328Y, 235F/268D/328Y, 239D/268D/328F, 239D/268D/328W, 239D/268D/328Y, 239D/268E/328Y, 267A/268D/328Y, 267E/268E/328F, 239D/326D/328Y, 268D/326D/328Y, 239D/327D/328Y, 268D/327D/328Y, 239D/267E/332E, 234W/328Y/332E, 235F/328Y/332E, 239D/328F/332 E, 239D/328Y/332E, 267A/328Y/332E, 268D/328F/332 E, 268D/328W/332E, 268D/328Y/332E, 268E/328Y/332E, 326D/328Y/332E, 327D/328Y/332E, 234W/236D/239E/267E, 239D/268D/328F/332E, 239D/268D/328W/332E, and 239D/268D/328Y/332E

[0250] In one embodiment, said substitutional means result in at least one of the following substitutions, or combinations of substitutions: 235Y/267E, 236D/267E, 239D/268D, 239D/267E, 267E/268D, 267E/268E, and 267E/328F, wherein numbering is according to an EU index.

[0251] In some embodiments of the invention, immunoglobulin may comprise means for isotypic modifications, that is, modifications in a parent IgG to the amino acid type in an alternate IgG. For example as illustrated in FIG. **2**A, an IgG1IgG3 hybrid variant may be constructed by a substitutional means for substituting IgG1 positions in the CH2 and/or CH3 region with the amino acids from IgG3 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more substitutional means, e.g., 274Q, 276K, 300F, 339T, 356E, 358M, 384S, 392N, 397M, 422I, 435R, and 436F. In other embodiments of the invention, an IgG1/IgG2 hybrid variant may be constructed by a substitutional means for substituting IgG2 positions in the CH2 and/or CH3 region with amino acids from IgG1 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more substitutional means, e.g., one or more

of the following amino acid substations: 233E, 234L, 235L, −236G (referring to an insertion of a glycine at position 236), and 327A.

[0252] The Fc ligand specificity of the Fc variants of the present invention can be modulated to create different effector function profiles that may be suited for particular target antigens, indications, or patient populations. Table 1 describes several preferred embodiments of receptor binding profiles that include improvements to, reductions to or no effect to the binding to various receptors, where such changes may be beneficial in certain contexts. The receptor binding profiles in the table could be varied by degree of increase or decrease to the specified receptors. Additionally, the binding changes specified could be in the context of additional binding changes to other receptors such as C1q or FcRn, for example by combining with ablation of binding to C1q to shut off complement activation, or by combining with enhanced binding to C1q to increase complement activation. Other embodiments with other receptor binding profiles are possible, the listed receptor binding profiles are exemplary.

TABLE 1

Affinity Enhancement	Affinity Reduction	Cell Activity	Therapeutic Activity
FcγRI only	—	Enhanced dendritic cell activity and uptake, and subsequent presentation of antigens Enhanced monocyte and macrophage response to antibody	Enhanced cell-based immune response against target
FcγRIIIa	—	Enhanced ADCC and phagocytosis of broad range of cell types	Increased target cell lysis
FcγRIIIa	FcγRIIb	Enhanced ADCC and phagocytosis of broad range of cell types	Increased target cell lysis
FcγRIIb FcγRIIc	—	Reduced activity of all FcγR bearing cell types except NK cells Possible activation of NK cells via FcγRIIc receptor signaling	Enhancement of target cell lysis selective for NK cell accessible target cells
FcγRIIb FcγRIIIa	—	Possible NK cell specific activation and enhancement of NK cell mediated ADCC	Enhanced target cell lysis selective for NK cell accessible target cells
FcγRIIIb	—	Neutrophil mediated phagocytosis enhancement	Enhanced target cell destruction for neutrophil accessible cells
FcαR	—	Neutrophil mediated phagocytosis enhancement	Enhanced target cell destruction for neutrophil accessible cells
FcγRI FcγRIIa FcγRIIIa	FcγRIIb	Enhanced dendritic cell activity and uptake, and subsequent presentation of antigens to T cells Enhanced monocyte and macrophage response to antibody	Enhanced cell-based immune response against target
FcγRIIb	FcγRI FcγRIIa FcγRIIIa	Reduced activity of monocytes, macrophages, neutrophils, NK, dendritic and other gamma receptor bearing cells	Eliminated or reduced cell-mediated cytotoxicity against target bearing cells

[0253] The presence of different polymorphic forms of FcγRs provides yet another parameter that impacts the therapeutic utility of the Fc variants of the present invention. Whereas the specificity and selectivity of a given Fc variant for the different classes of FcγRs significantly affects the capacity of an Fc variant to target a given antigen for treatment of a given disease, the specificity or selectivity of an Fc variant for different polymorphic forms of these receptors may in part determine which research or pre-clinical experiments may be appropriate for testing, and ultimately which patient populations may or may not respond to treatment. Thus the specificity or selectivity of Fc variants of the present invention to Fc ligand polymorphisms, including but not limited to FcγR, C1q, FcRn, and FcRH polymorphisms, may be used to guide the selection of valid research and pre-clinical experiments, clinical trial design, patient selection, dosing dependence, and/or other aspects concerning clinical trials.

Additional Modifications

[0254] In addition to comprising an Fc variant of the present invention, the Fc polypeptides of the present invention may comprise one or more additional modifications. Said modifications may be amino acid modifications, or may modifications that are not amino acid modifications such as modifications that are made enzymatically or chemically. Combinations of additional amino acid modifications and modifications that are not amino acid modifications are contemplated. Such additional modification(s) likely provide some improvement in the Fc polypeptide, for example an enhancement in its stability, solubility, function, or clinical use. The present invention contemplates a variety of improvements that made be made by coupling the Fc variants of the present invention with additional modifications.

[0255] The Fc variants of the present invention may be combined with other amino acid modifications in the Fc region that provide altered or optimized interaction with one or more Fc ligands, including but not limited to FcγRs, C1q or other complement proteins, FcRn, FcR homologues (FcRHs), and/or as yet undiscovered Fc ligands. It is noted that Fc polypeptides of the present invention may themselves have as yet unknown useful interaction properties with one or more Fc ligands, for example FcRHs. Additional modifications may provide altered or optimized affinity and/or specificity to the Fc ligands. Additional modifications may provide altered or optimized effector functions, including but not limited to ADCC, ADCP, CDC, and/or serum half-life. Such combination may provide additive, synergistic, or novel properties. In one embodiment, the Fc variants of the present invention may be combined with known Fc variants (Duncan et al., 1988, *Nature* 332:563-564; Lund et al., 1991, *J Immunol* 147:2657-2662; Lund et al., 1992, *Mol Immunol* 29:53-59; Alegre et al., 1994, *Transplantation* 57:1537-1543; Hutchins et al., 1995, *Proc Natl Acad Sci USA* 92:11980-11984; Jefferis et al., 1995, *Immunol Lett* 44:111-117; Lund et al., 1995, *Faseb J*9:115-119; Jefferis et al., 1996, *Immunol Lett* 54:101-104; Lund et al., 1996, *J Immunol* 157:4963-4969; Armour et al., 1999, *Eur J Immunol* 29:2613-2624; Idusogie et al., 2000, *J Immunol* 164:4178-4184; Reddy et al., 2000, *J Immunol* 164:1925-1933; Xu et al., 2000, *Cell Immunol* 200:16-26; Idusogie et al., 2001, *J Immunol* 166:2571-2575; Shields et al., 2001, *J Biol Chem* 276:6591-6604; Jefferis et al., 2002, *Immunol Lett* 82:57-65; Presta et al., 2002, *Biochem Soc Trans* 30:487-490; Hinton et al., 2004, *J Biol Chem* 279:6213-6216) (U.S. Pat. No. 5,624,821; U.S. Pat. No. 5,885,573; U.S. Pat. No. 6,194,551; PCT WO 00/42072; PCT WO 99/58572; US 2004/0002587 A1), U.S. Pat. No. 6,737,056, PCT US2004/000643, U.S. Ser. No. 10/370,749, and PCT/US2004/005112), all incorporated by reference. For example, as described in U.S. Pat. No. 6,737,056, PCT US2004/000643, U.S. Ser. No. 10/370,749, and PCT/US2004/005112, the substitutions S298A, S298D, K326E, K326D, E333A, K334A, and P396L provide optimized FcγR binding and/or enhanced ADCC. Furthermore, as disclosed in Idusogie et al., 2001, J. Immunology 166:2571-2572, incorporated by reference, substitutions K326W, K326Y, and E333S provide enhanced binding to the complement protein C1q and enhanced CDC. Finally, as described in Hinton et al., 2004, J. Biol. Chem. 279(8): 6213-6216, incorporated by reference, substitutions T250Q, T250E, M428L, and M428F provide enhanced binding to FcRn and improved pharmacokinetics.

[0256] Because the binding sites for FcγRs, C1q, and FcRn reside in the Fc region, the differences between the IgGs in the Fc region are likely to contribute to differences in FcγR- and C1q-mediated effector functions. It is also possible that the modifications can be made in other non-Fc regions of an Fc variant, including for example the Fab and hinge regions of an antibody, or the Fc fusion partner of an Fc fusion. For example, as disclosed in U.S. Ser. No. 11/090,981, hereby incorporated by reference, the Fab and hinge regions of an antibody may impact effector functions such as antibody dependent cell-mediated cytotoxicity (ADCC), antibody dependent cell-mediated phagocytosis (ADCP), and complement dependent cytotoxicity (CDC). Thus modifications outside the Fc region of an Fc variant of the present invention are contemplated. For example, antibodies of the present invention may comprise one or more amino acid modifications in the V_L, C_L, V_H, C_H1, and/or hinge regions of an antibody.

[0257] Other modifications may provide additional or novel binding determinants into an Fc variant, for example additional or novel Fc receptor binding sites, for example as described in U.S. Ser. No. 60/531,752, filed Dec. 22, 2003, entitled "Fc variants with novel Fc receptor binding sites". In one embodiment, an Fc variant of one antibody isotype may be engineered such that it binds to an Fc receptor of a different isotype. This may be particularly applicable when the Fc binding sites for the respective Fc receptors do not significantly overlap. For example, the structural determinants of IgA binding to FcγRI may be engineered into an IgG Fc variant.

[0258] The Fc variants of the present invention may comprise modifications that modulate the in vivo pharmacokinetic properties of an Fc variant. These include, but are not limited to, modifications that enhance affinity for the neonatal Fc receptor FcRn (U.S. Ser. No. 10/020,354; WO2001 US0048432; EP2001000997063; U.S. Pat. No. 6,277,375; U.S. Ser. No. 09/933,497; WO1997US0003321; U.S. Pat. No. 6,737,056; WO2000US0000973; Shields et al., 2001, J Biol Chem 276(9): 6591-6604; Zhou et al., 2003, J Mol Biol., 332: 901-913). These further include modifications that modify FcRn affinity in a pH-specific manner. In some embodiments, where enhanced in vivo half-life is desired, modifications that specifically enhance FcRn affinity at lower pH (5.5-6) relative to higher pH (7-8) are preferred (Hinton et al., 2004, J Biol Chem 279(8): 6213-6216; Dall'Acqua et al., 2002 J Immuno 169: 5171-5180; Ghetie et al., 1997, Nat Biotechnol 15(7): 637-640; WO2003US0033037; WO2004US0011213). For example, as described in Hinton et al., 2004, "Engineered Human IgG Antibodies with Longer Serum Half-lives in Primates" J Biol Chem 279(8): 6213-6216, substitutions T250Q, T250E, M428L, and M428F provide enhanced binding to FcRn and improved pharmacokinetics. Additionally preferred modifications are those that maintain the wild-type Fc's improved binding at lower pH relative to the higher pH. In alternative embodiments, where rapid in vivo clearance is desired, modifications that reduce affinity for FcRn are preferred. (U.S. Pat. No. 6,165,745; WO1993US0003895; EP1993000910800; WO1997US0021437; Medesan et al., 1997, J Immunol 158 (5): 2211-2217; Ghetie & Ward, 2000, Annu Rev Immunol 18: 739-766; Martin et al. 2001, Molecular Cell 7: 867-877; Kim et al. 1999, Eur J Immunol 29: 2819-2825). Preferred variants that enhance FcRn are described in U.S. Ser. No. 60/627,763, filed Nov. 12, 2004; 60/642,886, filed Jan. 11, 2005; 60/649,508, filed Feb. 2, 2005; 60/662,468, filed Mar. 15, 2005, and 60/669,311 filed Apr. 6, 2005, entitled "Fc Variants with Altered Binding to FcRn", all hereby incorporated by reference.

[0259] Additional modifications may comprise amino acid modifications wherein residues in an Fc polypeptide are modified to the corresponding residue in a homologous Fc polypeptide. Effector functions such as ADCC, ADCP, CDC, and serum half-life differ significantly between the different classes of antibodies, including for example human IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgD, IgE, IgG, and IgM (references—Michaelsen et al., 1992, Molecular Immunology 29(3): 319-326). Human IgG1 is the most commonly used antibody for therapeutic purposes, and engineering studies wherein variants have been constructed that show enhanced effector function have been carried out predomi-

nantly in this context. As described above, it is possible to determine corresponding or equivalent residues in Fc polypeptides that have significant sequence or structural homology with each other. By the same token, it is possible to use such methods to engineer additional amino acid modifications in an Fc polypeptide to provide additional optimized properties, for example as described in U.S. Ser. No. 60/621,387, filed Oct. 21, 2004. In one embodiment, amino acid modifications can be made that replace one or more residues in an Fc polypeptide of the present invention with one or more residues in another homologous Fc polypeptide. In an alternate embodiment, hybrid Fc polypeptides are constructed, such that one or more regions of an Fc polypeptide of the present invention are replace with the corresponding regions of a homolous Fc polypeptide. For example, some studies have explored IgG1, IgG2, IgG3, and IgG4 variants in order to investigate the determinants of the effector function differences between them. See for example Canfield & Morrison, 1991, J Exp Med 173: 1483-1491; Chappel et al., 1991, Proc Natl Acad Sci USA 88(20): 9036-9040; Chappel et al., 1993, J Biol Chem 268: 25124-25131; Tao, Canfield, and Morrison, 1991, J Exp Med 173: 1025-1028; Tao et al., 1993, J Exp Med 178: 661-667; Redpath et al., 1998, Human Immunology, 59, 720-727.

[0260] In one embodiment, the Fc variants of the present invention comprise one or more engineered glycoforms. By "engineered glvcoform" as used herein is meant a carbohydrate composition that is covalently attached to an Fc variant, wherein said carbohydrate composition differs chemically from that of a parent Fc variant. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. Engineered glycoforms may be generated by a variety of methods known in the art (Umaña et al., 1999, *Nat Biotechnol* 17:176-180; Davies et al., 2001, *Biotechnol Bioeng* 74:288-294; Shields et al., 2002, *J Biol Chem* 277:26733-26740; Shinkawa et al., 2003, *J Biol Chem* 278:3466-3473); (U.S. Pat. No. 6,602,684; U.S. Ser. No. 10/277,370; U.S. Ser. No. 10/113,929; PCT WO 00/61739A1; PCT WO 01/29246A1; PCT WO 02/31140A1; PCT WO 02/30954A1); (Potelligent™ technology [Biowa, Inc., Princeton, N.J.]; GlycoMAb™ glycosylation engineering technology [GLYCART biotechnology AG, Zürich, Switzerland]). Many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region, for example by expressing an Fc variant in various organisms or cell lines, engineered or otherwise (for example Lec-13 CHO cells or rat hybridoma YB2/0 cells), by regulating enzymes involved in the glycosylation pathway (for example FUT8 [α1,6-fucosyltranserase] and/or β1-4-N-acetylglucosaminyltransferase III [GnTIII]), or by modifying carbohydrate(s) after the Fc variant has been expressed. Engineered glycoform typically refers to the different carbohydrate or oligosaccharide; thus an Fc variant, for example an antibody or Fc fusion, may comprise an engineered glycoform. Alternatively, engineered glycoform may refer to the Fc variant that comprises the different carbohydrate or oligosaccharide.

[0261] Fc variants of the present invention may comprise one or more modifications that provide optimized properties that are not specifically related to effector function per se. Said modifications may be amino acid modifications, or may be modifications that are made enzymatically or chemically. Such modification(s) likely provide some improvement in the Fc variant, for example an enhancement in its stability, solubility, function, or clinical use. The present invention contemplates a variety of improvements that made be made by coupling the Fc variants of the present invention with additional modifications.

[0262] In a preferred embodiment, the Fc variants of the present invention may comprise modifications to reduce immunogenicity in humans. In a most preferred embodiment, the immunogenicity of an Fc variant of the present invention is reduced using a method described in U.S. Ser. No. 11/004,590, filed Dec. 3, 2004, entitled "Methods of Generating Variant Proteins with Increased Host String Content and Compositions Thereof". In alternate embodiments, the antibodies of the present invention are humanized (Clark, 2000, *Immunol Today* 21:397-402). By "humanized" antibody as used herein is meant an antibody comprising a human framework region (FR) and one or more complementarity determining regions (CDR's) from a non-human (usually mouse or rat) antibody. The non-human antibody providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Humanization relies principally on the grafting of donor CDRs onto acceptor (human) V_L and V_H frameworks (Winter U.S. Pat. No. 5,225,539). This strategy is referred to as "CDR grafting". "Backmutation" of selected acceptor framework residues to the corresponding donor residues is often required to regain affinity that is lost in the initial grafted construct (U.S. Pat. No. 5,530,101; U.S. Pat. No. 5,585,089; U.S. Pat. No. 5,693,761; U.S. Pat. No. 5,693,762; U.S. Pat. No. 6,180,370; U.S. Pat. No. 5,859,205; U.S. Pat. No. 5,821,337; U.S. Pat. No. 6,054,297; U.S. Pat. No. 6,407,213). The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region. A variety of techniques and methods for humanizing and reshaping non-human antibodies are well known in the art (See Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), and references cited therein). Humanization methods include but are not limited to methods described in Jones et al., 1986, *Nature* 321:522-525; Riechmann et al., 1988; *Nature* 332:323-329; Verhoeyen et al., 1988, *Science*, 239:1534-1536; Queen et al., 1989, *Proc Natl Acad Sci, USA* 86:10029-33; He et al., 1998, J Immunol 160: 1029-1035; Carter et al., 1992, *Proc Natl Acad Sci USA* 89:4285-9, Presta et al., 1997, Cancer Res 57(20):4593-9; Gorman et al., 1991, Proc Natl Acad Sci USA 88:4181-4185; O'Connor et al., 1998, *Protein Eng* 11:321-8. Humanization or other methods of reducing the immunogenicity of nonhuman antibody variable regions may include resurfacing methods, as described for example in Roguska et al., 1994, Proc Natl Acad Sci USA 91:969-973. In one embodiment, selection based methods may be employed to humanize and/or affinity mature antibody variable regions, including but not limited to methods described in Wu et al., 1999, J. Mol. Biol. 294:151-162; Baca et al., 1997, J. Biol. Chem. 272(16): 10678-10684; Rosok et al., 1996, J. Biol. Chem. 271(37): 22611-22618; Rader et al., 1998, Proc. Natl. Acad. Sci. USA 95: 8910-8915; Krauss et al., 2003, Protein Engineering 16(10):753-759. Other humanization methods may involve the grafting of only parts of the CDRs, including but not limited to methods described in U.S. Ser. No. 09/810,502; Tan et al., 2002, J. Immunol. 169:1119-1125; De Pascalis et al., 2002, J. Immunol. 169:3076-3084. Structure-based methods

may be employed for humanization and affinity maturation, for example as described in U.S. Ser. No. 10/153,159 and related applications.

[0263] Modifications to reduce immunogenicity may include modifications that reduce binding of processed peptides derived from the parent sequence to MHC proteins. For example, amino acid modifications would be engineered such that there are no or a minimal number of immune epitopes that are predicted to bind, with high affinity, to any prevalent MHC alleles. Several methods of identifying MHC-binding epitopes in protein sequences are known in the art and may be used to score epitopes in an Fc variant of the present invention. See for example WO 98/52976; WO 02/079232; WO 00/3317; U.S. Ser. No. 09/903,378; U.S. Ser. No. 10/039,170; U.S. Ser. No. 60/222,697; U.S. Ser. No. 10/339,788; PCT WO 01/21823; and PCT WO 02/00165; Mallios, 1999, *Bioinformatics* 15: 432-439; Mallios, 2001, *Bioinformatics* 17: 942-948; Sturniolo et al., 1999, *Nature Biotech.* 17: 555-561; WO 98/59244; WO 02/069232; WO 02/77187; Marshall et al., 1995, *J. Immunol.* 154: 5927-5933; and Hammer et al., 1994, *J. Exp. Med.* 180: 2353-2358. Sequence-based information can be used to determine a binding score for a given peptide—MHC interaction (see for example Mallios, 1999, *Bioinformatics* 15: 432-439; Mallios, 2001, *Bioinformatics* 17: p 942-948; Sturniolo et. al., 1999, *Nature Biotech.* 17: 555-561). It is possible to use structure-based methods in which a given peptide is computationally placed in the peptide-binding groove of a given MHC molecule and the interaction energy is determined (for example, see WO 98/59244 and WO 02/069232). Such methods may be referred to as "threading" methods. Alternatively, purely experimental methods can be used; for example a set of overlapping peptides derived from the protein of interest can be experimentally tested for the ability to induce T-cell activation and/or other aspects of an immune response. (see for example WO 02/77187). In a preferred embodiment, MHC-binding propensity scores are calculated for each 9-residue frame along the protein sequence using a matrix method (see Sturniolo et. al., supra; Marshall et. al., 1995, *J. Immunol.* 154: 5927-5933, and Hammer et. al., 1994, *J. Exp. Med.* 180: 2353-2358). It is also possible to consider scores for only a subset of these residues, or to consider also the identities of the peptide residues before and after the 9-residue frame of interest. The matrix comprises binding scores for specific amino acids interacting with the peptide binding pockets in different human class II MHC molecule. In the most preferred embodiment, the scores in the matrix are obtained from experimental peptide binding studies. In an alternate preferred embodiment, scores for a given amino acid binding to a given pocket are extrapolated from experimentally characterized alleles to additional alleles with identical or similar residues lining that pocket. Matrices that are produced by extrapolation are referred to as "virtual matrices". In an alternate embodiment, additional amino acid modifications may be engineered to reduce the propensity of the intact molecule to interact with B cell receptors and circulating antibodies.

[0264] Antibodies and Fc fusions of the present invention may comprise amino acid modifications in one or more regions outside the Fc region, for example the antibody Fab region or the Fc fusion partner, that provide optimal properties. In one embodiment, the variable region of an antibody of the present invention may be affinity matured, that is to say that amino acid modifications have been made in the V_H and/or V_L domains of the antibody to enhance binding of the antibody to its target antigen. Likewise, modifications may be made in the Fc fusion partner to enhance affinity of the Fc fusion for its target antigen. Such types of modifications may improve the association and/or the dissociation kinetics for binding to the target antigen. Other modifications include those that improve selectivity for target antigen vs. alternative targets. These include modifications that improve selectivity for antigen expressed on target vs. non-target cells. Other improvements to the target recognition properties may be provided by additional modifications. Such properties may include, but are not limited to, specific kinetic properties (i.e. association and dissociation kinetics), selectivity for the particular target versus alternative targets, and selectivity for a specific form of target versus alternative forms. Examples include full-length versus splice variants, aberrant forms of antigens that are expressed only on certain cell types such as tumor cells, cell-surface vs. soluble forms, selectivity for various polymorphic variants, or selectivity for specific conformational forms of the target.

[0265] Fc variants of the invention may comprise one or more modifications that provide reduced or enhanced internalization of an Fc variant. In one embodiment, Fc variants of the present invention can be utilized or combined with additional modifications in order to reduce the cellular internalization of an Fc variant that occurs via interaction with one or more Fc ligands. This property might be expected to enhance effector function, and potentially reduce immunogenicity of the Fc variants of the invention. Alternatively, Fc variants of the present Fc variants of the present invention can be utilized directly or combined with additional modifications in order to enhance the cellular internalization of an Fc variant that occurs via interaction with one or more Fc ligands. For example, in a preferred embodiment, an Fc variant is used that provides enhanced binding to FcγRI, which is expressed on dendritic cells and active early in immune response. This strategy could be further enhanced by combination with additional modifications, either within the Fc variant or in an attached fusion or conjugate partner, that promote recognition and presentation of Fc peptide fragments by MHC molecules. These strategies are expected to enhance target antigen processing and thereby improve antigenicity of the target antigen (Bonnerot and Amigorena, 1999, *Immunol Rev.* 172: 279-84), promoting an adaptive immune response and greater target cell killing by the human immune system. These strategies may be particularly advantageous when the targeted antigen is shed from the cellular surface. An additional application of these concepts arises with idiotype vaccine immunotherapies, in which clone-specific antibodies produced by a patient's lymphoma cells are used to vaccinate the patient.

[0266] In a preferred embodiment, modifications are made to improve biophysical properties of the Fc variants of the present invention, including but not limited to stability, solubility, and oligomeric state. Modifications can include, for example, substitutions that provide more favorable intramolecular interactions in the Fc variant such as to provide greater stability, or substitution of exposed nonpolar amino acids with polar amino acids for higher solubility. A number of optimization goals and methods are described in U.S. Ser. No. 10/379,392 that may find use for engineering additional modifications to further optimize the Fc variants of the present invention. The Fc variants of the present invention can also be combined with additional modifications that reduce oligomeric state or size, such that tumor penetration is enhanced, or in vivo clearance rates are increased as desired.

[0267] Other modifications to the Fc variants of the present invention include those that enable the specific formation or homodimeric or homomultimeric molecules. Such modifications include but are not limited to engineered disulfides, as well as chemical modifications or aggregation methods which may provide a mechanism for generating covalent homodimeric or homomultimers. For example, methods of engineering and compositions of such molecules are described in Kan et al., 2001, *J. Immunol.*, 2001, 166: 1320-1326; Stevenson et al., 2002, *Recent Results Cancer Res.* 159: 104-12; U.S. Pat. No. 5,681,566; Caron et al., 1992, J Exp Med 176:1191-1195, and Shopes, 1992, J Immunol 148(9): 2918-22. Additional modifications to the variants of the present invention include those that enable the specific formation or heterodimeric, heteromultimeric, bifunctional, and/or multifunctional molecules. Such modifications include, but are not limited to, one or more amino acid substitutions in the C_H3 domain, in which the substitutions reduce homodimer formation and increase heterodimer formation. For example, methods of engineering and compositions of such molecules are described in Atwell et al., 1997, J Mol Biol 270(1):26-35, and Carter et al., 2001, J Immunol Methods 248:7-15. Additional modifications include modifications in the hinge and CH3 domains, in which the modifications reduce the propensity to form dimers.

[0268] In further embodiments, the Fc variants of the present invention comprise modifications that remove proteolytic degradation sites. These may include, for example, protease sites that reduce production yields, as well as protease sites that degrade the administered protein in vivo. In a preferred embodiment, additional modifications are made to remove covalent degradation sites such as deamidation (i.e. deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues), oxidation, and proteolytic degradation sites. Deamidation sites that are particular useful to remove are those that have enhance propensity for deamidation, including, but not limited to asparaginyl and gituamyl residues followed by glycines (NG and QG motifs, respectively). In such cases, substitution of either residue can significantly reduce the tendancy for deamidation. Common oxidation sites include methionine and cysteine residues. Other covalent modifications, that can either be introduced or removed, include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the "-amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group. Additional modifications also may include but are not limited to posttranslational modifications such as N-linked or O-linked glycosylation and phosphorylation.

[0269] Modifications may include those that improve expression and/or purification yields from hosts or host cells commonly used for production of biologics. These include, but are not limited to various mammalian cell lines (e.g. CHO), yeast cell lines, bacterial cell lines, and plants. Additional modifications include modifications that remove or reduce the ability of heavy chains to form inter-chain disulfide linkages. Additional modifications include modifications that remove or reduce the ability of heavy chains to form intra-chain disulfide linkages.

[0270] The Fc variants of the present invention may comprise modifications that include the use of unnatural amino acids incorporated using, for example, the technologies developed by Schultz and colleagues, including but not limited to methods described by Cropp & Shultz, 2004, Trends Genet. 20(12):625-30, Anderson et al., 2004, Proc Natl Acad Sci USA 101(2):7566-71, Zhang et al., 2003, 303(5656):371-3, and Chin et al., 2003, Science 301(5635):964-7. In some embodiments, these modifications enable manipulation of various functional, biophysical, immunological, or manufacturing properties discussed above. In additional embodiments, these modifications enable additional chemical modification for other purposes. Other modifications are contemplated herein. For example, the Fc variant may be linked to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol. Additional amino acid modifications may be made to enable specific or non-specific chemical or posttranslational modification of the Fc variants. Such modifications, include, but are not limited to PEGylation and glycosylation. Specific substitutions that can be utilized to enable PEGylation include, but are not limited to, introduction of novel cysteine residues or unnatural amino acids such that efficient and specific coupling chemistries can be used to attach a PEG or otherwise polymeric moiety. Introduction of specific glycosylation sites can be achieved by introducing novel N-X-T/S sequences into the Fc variants of the present invention.

[0271] The Fc variants of the present invention may be fused or conjugated to one or more other molecules or polypeptides. Conjugate and fusion partners may be any molecule, including small molecule chemical compounds and polypeptides. For example, a variety of antibody conjugates and methods are described in Trail et al., 1999, Curr. Opin. Immunol. 11:584-588. Possible conjugate partners include but are not limited to cytokines, cytotoxic agents, toxins, radioisotopes, chemotherapeutic agent, anti-angiogenic agents, a tyrosine kinase inhibitors, and other therapeutically active agents. In some embodiments, conjugate partners may be thought of more as payloads, that is to say that the goal of a conjugate is targeted delivery of the conjugate partner to a targeted cell, for example a cancer cell or immune cell, by the Fc variant. Thus, for example, the conjugation of a toxin to an antibody or Fc fusion targets the delivery of said toxin to cells expressing the target antigen.

[0272] In one embodiment, the Fc variants of the present invention are fused or conjugated to a cytokine. By "cytokine" as used herein is meant a generic term for proteins released by one cell population that act on another cell as intercellular mediators. For example, as described in Penichet et al., 2001, J Immunol Methods 248:91-101, cytokines may be fused to antibody to provide an array of desirable properties. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-alpha and -beta; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-beta; platelet-growth factor; transforming growth fac-

tors (TGFs) such as TGF-alpha and TGF-beta; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-alpha, beta, and -gamma; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1 alpha, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; IL-15, a tumor necrosis factor such as TNF-alpha or TNF-beta; C5a; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture, and biologically active equivalents of the native sequence cytokines.

[0273] In an alternate embodiment, the Fc polypeptides of the present invention are fused, conjugated, or operably linked to a toxin, including but not limited to small molecule toxins and enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof. For example, a variety of immunotoxins and immunotoxin methods are described in Thrush et al., 1996, Ann. Rev. Immunol. 14:49-71. Small molecule toxins include but are not limited to calicheamicin, maytansine (U.S. Pat. No. 5,208,020), trichothene, and CC1065. In one embodiment of the invention, the Fc polypeptide is conjugated to one or more maytansine molecules (e.g. about 1 to about 10 maytansine molecules per antibody molecule). Maytansine may, for example, be converted to May-SS-Me which may be reduced to May-SH3 and reacted with modified Fc polypeptide (Chari et al., 1992, *Cancer Research* 52: 127-131) to generate a maytansinoid-antibody or maytansinoid-Fc fusion conjugate. Another conjugate of interest comprises an Fc polypeptide, for example an antibody or Fc fusion, conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. Structural analogues of calicheamicin that may be used include but are not limited to γ_1^1, α_2^1, α_3, N-acetyl-γ_1^1, PSAG, and Θ^1_1, (Hinman et al., 1993, Cancer Research 53:3336-3342; Lode et al., 1998, Cancer Research 58:2925-2928) (U.S. Pat. No. 5,714,586; U.S. Pat. No. 5,712,374; U.S. Pat. No. 5,264,586; U.S. Pat. No. 5,773,001). Dolastatin 10 analogs such as auristatin E (AE) and monomethylauristatin E (MMAE) may find use as conjugates for the Fc variants of the present invention (Doronina et al., 2003, Nat Biotechnol 21(7):778-84; Francisco et al., 2003 Blood 102(4):1458-65). Useful enyzmatically active toxins include but are not limited to diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), *momordica charantia* inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, PCT WO 93/21232, hereby incorporated by reference. The present invention further contemplates a conjugate between an Fc variant of the present invention and a compound with nucleolytic activity, for example a ribonuclease or DNA endonuclease such as a deoxyribonuclease (Dnase).

[0274] In an alternate embodiment, an Fc variant of the present invention may be fused, conjugated, or operably linked to a radioisotope to form a radioconjugate. A variety of radioactive isotopes are available for the production of radioconjugate antibodies and Fc fusions. Examples include, but are not limited to, At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, and radioactive isotopes of Lu. See for example, reference.

[0275] In yet another embodiment, an Fc variant of the present invention may be conjugated to a "receptor" (e.g., streptavidin) for utilization in tumor pretargeting wherein the Fc variant-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g. avidin) which is conjugated to a cytotoxic agent (e.g. a radionucleotide). In an alternate embodiment, the Fc variant is conjugated or operably linked to an enzyme in order to employ Antibody Dependent Enzyme Mediated Prodrug Therapy (ADEPT). ADEPT may be used by conjugating or operably linking the Fc variant to a prodrug-activating enzyme that converts a prodrug (e.g. a peptidyl chemotherapeutic agent, see PCT WO 81/01145) to an active anti-cancer drug. See, for example, PCT WO 88/07378 and U.S. Pat. No. 4,975,278. The enzyme component of the immunoconjugate useful for ADEPT includes any enzyme capable of acting on a prodrug in such a way so as to covert it into its more active, cytotoxic form. Enzymes that are useful in the method of this invention include but are not limited to alkaline phosphatase useful for converting phosphate-containing prodrugs into free drugs; arylsulfatase useful for converting sulfate-containing prodrugs into free drugs; cytosine deaminase useful for converting non-toxic 5-fluorocytosine into the anti-cancer drug, 5-fluorouracil; proteases, such as *serratia* protease, thermolysin, subtilisin, carboxypeptidases and cathepsins (such as cathepsins B and L), that are useful for converting peptide-containing prodrugs into free drugs; D-alanylcarboxypeptidases, useful for converting prodrugs that contain D-amino acid substituents; carbohydrate-cleaving enzymes such as .beta.-galactosidase and neuramimidase useful for converting glycosylated prodrugs into free drugs; beta-lactamase useful for converting drugs derivatized with .alpha.-lactams into free drugs; and penicillin amidases, such as penicillin V amidase or penicillin G amidase, useful for converting drugs derivatized at their amine nitrogens with phenoxyacetyl or phenylacetyl groups, respectively, into free drugs. Alternatively, antibodies with enzymatic activity, also known in the art as "abzymes", can be used to convert the prodrugs of the invention into free active drugs (see, for example, Massey, 1987, Nature 328: 457-458). Fc variant-abzyme conjugates can be prepared for delivery of the abzyme to a tumor cell population. A variety of additional conjugates are contemplated for the Fc variants of the present invention. A variety of chemotherapeutic agents, anti-angiogenic agents, tyrosine kinase inhibitors, and other therapeutic agents are described below, which may find use as Fc variant conjugates.

[0276] Also contemplated as fusion and conjugate partners are Fc polypeptides. Thus an Fc variant may be a multimeric Fc polypeptide, comprising two or more Fc regions. The advantage of such a molecule is that it provides multiple binding sites for Fc receptors with a single protein molecule. In one embodiment, Fc regions may be linked using a chemical engineering approach. For example, Fab's and Fc's may be linked by thioether bonds originating at cysteine residues in the hinges, generating molecules such as $FabFc_2$ (Kan et al., 2001, *J. Immunol.*, 2001, 166: 1320-1326; Stevenson et al., 2002, *Recent Results Cancer Res.* 159: 104-12; U.S. Pat. No. 5,681,566). Fc regions may be linked using disulfide engineering and/or chemical cross-linking, for example as

described in Caron et al., 1992, J. Exp. Med. 176:1191-1195, and Shopes, 1992, J. Immunol. 148(9):2918-22. In a preferred embodiment, Fc regions may be linked genetically. For example multiple Cγ2 domains have been fused between the Fab and Fc regions of an antibody (White et al., 2001, *Protein Expression and Purification* 21: 446-455). In a preferred embodiment, Fc regions in an Fc variant are linked genetically to generated tandemly linked Fc regions as described in U.S. Ser. No. 60/531,752, filed Dec. 22, 2003, entitled "Fc polypeptides with novel Fc receptor binding sites". Tandemly linked Fc polypeptides may comprise two or more Fc regions, preferably one to three, most preferably two Fc regions. It may be advantageous to explore a number of engineering constructs in order to obtain homo- or hetero-tandemly linked Fc variants with the most favorable structural and functional properties. Tandemly linked Fc variants may be homo-tandemly linked Fc variants, that is an Fc variant of one isotype is fused genetically to another Fc variant of the same isotype. It is anticipated that because there are multiple FcγR, C1q, and/or FcRn binding sites on tandemly linked Fc polypeptides, effector functions and/or pharmacokinetics may be enhanced. In an alternate embodiment, Fc variants from different isotypes may be tandemly linked, referred to as hetero-tandemly linked Fc variants. For example, because of the capacity to target FcγR and FcαRI receptors, an Fc variant that binds both FcγRs and FcαRI may provide a significant clinical improvement.

[0277] As will be appreciated by one skilled in the art, in reality the concepts and definitions of fusion and conjugate are overlapping. The designation of an Fc variant as a fusion or conjugate is not meant to constrain it to any particular embodiment of the present invention. Rather, these terms are used loosely to convey the broad concept that any Fc variant of the present invention may be linked genetically, chemically, or otherwise, to one or more polypeptides or molecules to provide some desirable property.

[0278] Fusion and conjugate partners may be linked to any region of an Fc variant of the present invention, including at the N- or C-termini, or at some residue in-between the termini. In a preferred embodiment, a fusion or conjugate partner is linked at the N- or C-terminus of the Fc variant, most preferably the N-terminus. A variety of linkers may find use in the present invention to covalently link Fc variants to a fusion or conjugate partner or generate an Fc fusion. By "linker", "linker sequence", "spacer", "tethering sequence" or grammatical equivalents thereof, herein is meant a molecule or group of molecules (such as a monomer or polymer) that connects two molecules and often serves to place the two molecules in a preferred configuration. A number of strategies may be used to covalently link molecules together. These include, but are not limited to polypeptide linkages between N- and C-termini of proteins or protein domains, linkage via disulfide bonds, and linkage via chemical cross-linking reagents. In one aspect of this embodiment, the linker is a peptide bond, generated by recombinant techniques or peptide synthesis. Choosing a suitable linker for a specific case where two polypeptide chains are to be connected depends on various parameters, including but not limited to the nature of the two polypeptide chains (e.g., whether they naturally oligomerize), the distance between the N- and the C-termini to be connected if known, and/or the stability of the linker towards proteolysis and oxidation. Furthermore, the linker may contain amino acid residues that provide flexibility. Thus, the linker peptide may predominantly include the following amino acid residues: Gly, Ser, Ala, or Thr. The linker peptide should have a length that is adequate to link two molecules in such a way that they assume the correct conformation relative to one another so that they retain the desired activity. Suitable lengths for this purpose include at least one and not more than 50 amino acid residues. Preferably, the linker is from about 1 to 30 amino acids in length, with linkers of 1 to 20 amino acids in length being most preferred. In addition, the amino acid residues selected for inclusion in the linker peptide should exhibit properties that do not interfere significantly with the activity of the polypeptide. Thus, the linker peptide on the whole should not exhibit a charge that would be inconsistent with the activity of the polypeptide, or interfere with internal folding, or form bonds or other interactions with amino acid residues in one or more of the monomers that would seriously impede the binding of receptor monomer domains. Useful linkers include glycine-serine polymers (including, for example, (GS)n, (GSGGS)n, (GGGGS)n, and (GGGS)n, where n is an integer of at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers such as the tether for the shaker potassium channel, and a large variety of other flexible linkers, as will be appreciated by those in the art. Glycine-serine polymers are preferred since both of these amino acids are relatively unstructured, and therefore may be able to serve as a neutral tether between components. Secondly, serine is hydrophilic and therefore able to solubilize what could be a globular glycine chain. Third, similar chains have been shown to be effective in joining subunits of recombinant proteins such as single chain antibodies. Suitable linkers may also be identified by screening databases of known three-dimensional structures for naturally occurring motifs that can bridge the gap between two polypeptide chains. In a preferred embodiment, the linker is not immunogenic when administered in a human patient. Thus linkers may be chosen such that they have low immunogenicity or are thought to have low immunogenicity. For example, a linker may be chosen that exists naturally in a human. In a most preferred embodiment, the linker has the sequence of the hinge region of an antibody, that is the sequence that links the antibody Fab and Fc regions; alternatively the linker has a sequence that comprises part of the hinge region, or a sequence that is substantially similar to the hinge region of an antibody. Another way of obtaining a suitable linker is by optimizing a simple linker, e.g., (Gly4Ser)n, through random mutagenesis. Alternatively, once a suitable polypeptide linker is defined, additional linker polypeptides can be created to select amino acids that more optimally interact with the domains being linked. Other types of linkers that may be used in the present invention include artificial polypeptide linkers and inteins. In another embodiment, disulfide bonds are designed to link the two molecules. In another embodiment, linkers are chemical cross-linking agents. For example, a variety of bifunctional protein coupling agents may be used, including but not limited to N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), succinimidyl-4-(N-maleimidomethyl)cyclohexane-1-carboxylate, iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For

example, a ricin immunotoxin can be prepared as described in Vitetta et al., 1971, Science 238:1098. Chemical linkers may enable chelation of an isotope. For example, Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody (see PCT WO 94/11026). The linker may be cleavable, facilitating release of the cytotoxic drug in the cell. For example, an acid-labile linker, peptidase-sensitive linker, dimethyl linker or disulfide-containing linker (Chari et al., 1992, Cancer Research 52: 127-131) may be used. Alternatively, a variety of nonproteinaceous polymers, including but not limited to polyethylene glycol (PEG), polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, may find use as linkers, that is may find use to link the Fc variants of the present invention to a fusion or conjugate partner to generate an Fc fusion, or to link the Fc variants of the present invention to a conjugate.

Engineering Methods

[0279] Design strategies, computational screening methods, and library generation methods are described in U.S. Ser. No. 10/672,280 and U.S. Ser. No. 10/822,231, entitled "Optimized Fc Variants and Methods for their Generation", herein expressly incorporated by reference. These strategies, approaches, techniques, and methods may be applied individually or in various combinations to generate optimized Fc variants.

Experimental Production of Fc Variants

[0280] The present invention provides methods for producing and experimentally testing Fc variants. The described methods are not meant to constrain the present invention to any particular application or theory of operation. Rather, the provided methods are meant to illustrate generally that one or more Fc variants may be produced and experimentally tested to obtain variant Fc variants. General methods for antibody molecular biology, expression, purification, and screening are described in Antibody Engineering, edited by Duebel & Kontermann, Springer-Verlag, Heidelberg, 2001; and Hayhurst & Georgiou, 2001, *Curr Opin Chem Biol* 5:683-689; Maynard & Georgiou, 2000, *Annu Rev Biomed Eng* 2:339-76; Antibodies: A Laboratory Manual by Harlow & Lane, New York: Cold Spring Harbor Laboratory Press, 1988.

[0281] In one embodiment of the present invention, nucleic acids are created that encode the Fc variants, and that may then be cloned into host cells, expressed and assayed, if desired. Thus, nucleic acids, and particularly DNA, may be made that encode each protein sequence. These practices are carried out using well-known procedures. For example, a variety of methods that may find use in the present invention are described in Molecular Cloning—A Laboratory Manual, 3rd Ed. (Maniatis, Cold Spring Harbor Laboratory Press, New York, 2001), and Current Protocols in Molecular Biology (John Wiley & Sons). As will be appreciated by those skilled in the art, the generation of exact sequences for a library comprising a large number of sequences is potentially expensive and time consuming. Accordingly, there are a variety of techniques that may be used to efficiently generate libraries of the present invention. Such methods that may find use in the present invention are described or referenced in U.S. Pat. No. 6,403,312; U.S. Ser. No. 09/782,004; U.S. Ser. No. 09/927,790; U.S. Ser. No. 10/218,102; PCT WO 01/40091; and PCT WO 02/25588. Such methods include but are not limited to gene assembly methods, PCR-based method and methods which use variations of PCR, ligase chain reaction-based methods, pooled oligo methods such as those used in synthetic shuffling, error-prone amplification methods and methods which use oligos with random mutations, classical site-directed mutagenesis methods, cassette mutagenesis, and other amplification and gene synthesis methods. As is known in the art, there are a variety of commercially available kits and methods for gene assembly, mutagenesis, vector subcloning, and the like, and such commercial products find use in the present invention for generating nucleic acids that encode Fc variants.

[0282] The Fc variants of the present invention may be produced by culturing a host cell transformed with nucleic acid, preferably an expression vector, containing nucleic acid encoding the Fc variants, under the appropriate conditions to induce or cause expression of the protein. The conditions appropriate for expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. A wide variety of appropriate host cells may be used, including but not limited to mammalian cells, bacteria, insect cells, and yeast. For example, a variety of cell lines that may find use in the present invention are described in the ATCC® cell line catalog, available from the American Type Culture Collection.

[0283] In a preferred embodiment, the Fc variants are expressed in mammalian expression systems, including systems in which the expression constructs are introduced into the mammalian cells using virus such as retrovirus or adenovirus. Any mammalian cells may be used, with human, mouse, rat, hamster, and primate cells being particularly preferred. Suitable cells also include known research cells, including but not limited to Jurkat T cells, NIH3T3, CHO, BHK, COS, HEK293, PER C.6, HeLa, Sp2/0, NSO cells and variants thereof. In an alternately preferred embodiment, library proteins are expressed in bacterial cells. Bacterial expression systems are well known in the art, and include *Escherichia coli* (*E. coli*), *Bacillus subtilis, Streptococcus cremoris*, and *Streptococcus lividans*. In alternate embodiments, Fc variants are produced in insect cells (e.g. Sf21/Sf9, *Trichoplusia ni* Bti-Tn5b1-4) or yeast cells (e.g. *S. cerevisiae, Pichia*, etc). In an alternate embodiment, Fc variants are expressed in vitro using cell free translation systems. In vitro translation systems derived from both prokaryotic (e.g. *E. coli*) and eukaryotic (e.g. wheat germ, rabbit reticulocytes) cells are available and may be chosen based on the expression levels and functional properties of the protein of interest. For example, as appreciated by those skilled in the art, in vitro translation is required for some display technologies, for example ribosome display. In addition, the Fc variants may be produced by chemical synthesis methods. Also transgenic expression systems both animal (e.g. cow, sheep or goat milk, embryonated hen's eggs, whole insect larvae, etc.) and plant (e.g. corn, tobacco, duckweed, etc.)

[0284] The nucleic acids that encode the Fc variants of the present invention may be incorporated into an expression vector in order to express the protein. A variety of expression vectors may be utilized for protein expression. Expression vectors may comprise self-replicating extra-chromosomal vectors or vectors which integrate into a host genome. Expression vectors are constructed to be compatible with the host cell type. Thus expression vectors which find use in the

present invention include but are not limited to those which enable protein expression in mammalian cells, bacteria, insect cells, yeast, and in in vitro systems. As is known in the art, a variety of expression vectors are available, commercially or otherwise, that may find use in the present invention for expressing Fc variants.

[0285] Expression vectors typically comprise a protein operably linked with control or regulatory sequences, selectable markers, any fusion partners, and/or additional elements. By "operably linked" herein is meant that the nucleic acid is placed into a functional relationship with another nucleic acid sequence. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the Fc variant, and are typically appropriate to the host cell used to express the protein. In general, the transcriptional and translational regulatory sequences may include promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. As is also known in the art, expression vectors typically contain a selection gene or marker to allow the selection of transformed host cells containing the expression vector. Selection genes are well known in the art and will vary with the host cell used.

[0286] Fc variants may be operably linked to a fusion partner to enable targeting of the expressed protein, purification, screening, display, and the like. Fusion partners may be linked to the Fc variant sequence via a linker sequences. The linker sequence will generally comprise a small number of amino acids, typically less than ten, although longer linkers may also be used. Typically, linker sequences are selected to be flexible and resistant to degradation. As will be appreciated by those skilled in the art, any of a wide variety of sequences may be used as linkers. For example, a common linker sequence comprises the amino acid sequence GGGGS. A fusion partner may be a targeting or signal sequence that directs Fc variant and any associated fusion partners to a desired cellular location or to the extracellular media. As is known in the art, certain signaling sequences may target a protein to be either secreted into the growth media, or into the periplasmic space, located between the inner and outer membrane of the cell. A fusion partner may also be a sequence that encodes a peptide or protein that enables purification and/or screening. Such fusion partners include but are not limited to polyhistidine tags (His-tags) (for example H_6 and H_{10} or other tags for use with Immobilized Metal Affinity Chromatography (IMAC) systems (e.g. Ni^{+2} affinity columns)), GST fusions, MBP fusions, Strep-tag, the BSP biotinylation target sequence of the bacterial enzyme BirA, and epitope tags which are targeted by antibodies (for example c-myc tags, flag-tags, and the like). As will be appreciated by those skilled in the art, such tags may be useful for purification, for screening, or both. For example, an Fc variant may be purified using a His-tag by immobilizing it to a Ni^{+2} affinity column, and then after purification the same His-tag may be used to immobilize the antibody to a Ni^{+2} coated plate to perform an ELISA or other binding assay (as described below). A fusion partner may enable the use of a selection method to screen Fc variants (see below). Fusion partners that enable a variety of selection methods are well-known in the art, and all of these find use in the present invention. For example, by fusing the members of an Fc variant library to the gene III protein, phage display can be employed (Kay et al., Phage display of peptides and proteins: a laboratory manual, Academic Press, San Diego, Calif., 1996; Lowman et al., 1991, *Biochemistry* 30:10832-10838; Smith, 1985, *Science* 228:1315-1317). Fusion partners may enable Fc variants to be labeled. Alternatively, a fusion partner may bind to a specific sequence on the expression vector, enabling the fusion partner and associated Fc variant to be linked covalently or noncovalently with the nucleic acid that encodes them. For example, U.S. Ser. No. 09/642,574; U.S. Ser. No. 10/080,376; U.S. Ser. No. 09/792,630; U.S. Ser. No. 10/023,208; U.S. Ser. No. 09/792,626; U.S. Ser. No. 10/082,671; U.S. Ser. No. 09/953,351; U.S. Ser. No. 10/097,100; U.S. Ser. No. 60/366,658; PCT WO 00/22906; PCT WO 01/49058; PCT WO 02/04852; PCT WO 02/04853; PCT WO 02/08023; PCT WO 01/28702; and PCT WO 02/07466 describe such a fusion partner and technique that may find use in the present invention.

[0287] The methods of introducing exogenous nucleic acid into host cells are well known in the art, and will vary with the host cell used. Techniques include but are not limited to dextran-mediated transfection, calcium phosphate precipitation, calcium chloride treatment, polybrene mediated transfection, protoplast fusion, electroporation, viral or phage infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei. In the case of mammalian cells, transfection may be either transient or stable.

[0288] In a preferred embodiment, Fc variants are purified or isolated after expression. Proteins may be isolated or purified in a variety of ways known to those skilled in the art. Standard purification methods include chromatographic techniques, including ion exchange, hydrophobic interaction, affinity, sizing or gel filtration, and reversed-phase, carried out at atmospheric pressure or at high pressure using systems such as FPLC and HPLC. Purification methods also include electrophoretic, immunological, precipitation, dialysis, and chromatofocusing techniques. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration are also useful. As is well known in the art, a variety of natural proteins bind Fc and antibodies, and these proteins can find use in the present invention for purification of Fc variants. For example, the bacterial proteins A and G bind to the Fc region. Likewise, the bacterial protein L binds to the Fab region of some antibodies, as of course does the antibody's target antigen. Purification can often be enabled by a particular fusion partner. For example, Fc variants may be purified using glutathione resin if a GST fusion is employed, Ni^{+2} affinity chromatography if a His-tag is employed, or immobilized anti-flag antibody if a flag-tag is used. For general guidance in suitable purification techniques, see Protein Purification Principles and Practice, 3rd Ed., Scopes, Springer-Verlag, NY, 1994. The degree of purification necessary will vary depending on the screen or use of the Fc variants. In some instances no purification is necessary. For example in one embodiment, if the Fc variants are secreted, screening may take place directly from the media. As is well known in the art, some methods of selection do not involve purification of proteins. Thus, for example, if a library of Fc variants is made into a phage display library, protein purification may not be performed.

Experimental Assays

[0289] Fc variants may be screened using a variety of methods, including but not limited to those that use in vitro assays, in vivo and cell-based assays, and selection technologies. Automation and high-throughput screening technologies may be utilized in the screening procedures. Screening may

employ the use of a fusion partner or label. The use of fusion partners has been discussed above. By "labeled" herein is meant that the Fc variants of the invention have one or more elements, isotopes, or chemical compounds attached to enable the detection in a screen. In general, labels fall into three classes: a) immune labels, which may be an epitope incorporated as a fusion partner that is recognized by an antibody, b) isotopic labels, which may be radioactive or heavy isotopes, and c) small molecule labels, which may include fluorescent and colorimetric dyes, or molecules such as biotin that enable other labeling methods. Labels may be incorporated into the compound at any position and may be incorporated in vitro or in vivo during protein expression.

[0290] In a preferred embodiment, the functional and/or biophysical properties of Fc variants are screened in an in vitro assay. In vitro assays may allow a broad dynamic range for screening properties of interest. Properties of Fc variants that may be screened include but are not limited to stability, solubility, and affinity for Fc ligands, for example FcγRs. Multiple properties may be screened simultaneously or individually. Proteins may be purified or unpurified, depending on the requirements of the assay. In one embodiment, the screen is a qualitative or quantitative binding assay for binding of Fc variants to a protein or nonprotein molecule that is known or thought to bind the Fc variant. In a preferred embodiment, the screen is a binding assay for measuring binding to the Target antigen. In an alternately preferred embodiment, the screen is an assay for binding of Fc variants to an Fc ligand, including but are not limited to the family of FcγRs, the neonatal receptor FcRn, the complement protein C1q, and the bacterial proteins A and G. Said Fc ligands may be from any organism, with humans, mice, rats, rabbits, and monkeys preferred. Binding assays can be carried out using a variety of methods known in the art, including but not limited to FRET (Fluorescence Resonance Energy Transfer) and BRET (Bioluminescence Resonance Energy Transfer)-based assays, AlphaScreen™ (Amplified Luminescent Proximity Homogeneous Assay), Scintillation Proximity Assay, ELISA (Enzyme-Linked Immunosorbent Assay), SPR (Surface Plasmon Resonance, also known as BIACORE®), isothermal titration calorimetry, differential scanning calorimetry, gel electrophoresis, and chromatography including gel filtration. These and other methods may take advantage of some fusion partner or label of the Fc variant. Assays may employ a variety of detection methods including but not limited to chromogenic, fluorescent, luminescent, or isotopic labels.

[0291] The biophysical properties of Fc variants, for example stability and solubility, may be screened using a variety of methods known in the art. Protein stability may be determined by measuring the thermodynamic equilibrium between folded and unfolded states. For example, Fc variants of the present invention may be unfolded using chemical denaturant, heat, or pH, and this transition may be monitored using methods including but not limited to circular dichroism spectroscopy, fluorescence spectroscopy, absorbance spectroscopy, NMR spectroscopy, calorimetry, and proteolysis. As will be appreciated by those skilled in the art, the kinetic parameters of the folding and unfolding transitions may also be monitored using these and other techniques. The solubility and overall structural integrity of an Fc variant may be quantitatively or qualitatively determined using a wide range of methods that are known in the art. Methods which may find use in the present invention for characterizing the biophysical properties of Fc variants include gel electrophoresis, isoelectric focusing, capillary electrophoresis, chromatography such as size exclusion chromatography, ion-exchange chromatography, and reversed-phase high performance liquid chromatography, peptide mapping, oligosaccharide mapping, mass spectrometry, ultraviolet absorbance spectroscopy, fluorescence spectroscopy, circular dichroism spectroscopy, isothermal titration calorimetry, differential scanning calorimetry, analytical ultra-centrifugation, dynamic light scattering, proteolysis, and cross-linking, turbidity measurement, filter retardation assays, immunological assays, fluorescent dye binding assays, protein-staining assays, microscopy, and detection of aggregates via ELISA or other binding assay. Structural analysis employing X-ray crystallographic techniques and NMR spectroscopy may also find use. In one embodiment, stability and/or solubility may be measured by determining the amount of protein solution after some defined period of time. In this assay, the protein may or may not be exposed to some extreme condition, for example elevated temperature, low pH, or the presence of denaturant. Because function typically requires a stable, soluble, and/or well-folded/structured protein, the aforementioned functional and binding assays also provide ways to perform such a measurement. For example, a solution comprising an Fc variant could be assayed for its ability to bind target antigen, then exposed to elevated temperature for one or more defined periods of time, then assayed for antigen binding again. Because unfolded and aggregated protein is not expected to be capable of binding antigen, the amount of activity remaining provides a measure of the Fc variant's stability and solubility.

[0292] In a preferred embodiment, the library is screened using one or more cell-based or in vitro assays. For such assays, Fc variants, purified or unpurified, are typically added exogenously such that cells are exposed to individual variants or groups of variants belonging to a library. These assays are typically, but not always, based on the biology of the ability of the antibody or Fc fusion to bind to the target antigen and mediate some biochemical event, for example effector functions like cellular lysis, phagocytosis, ligand/receptor binding inhibition, inhibition of growth and/or proliferation, apoptosis and the like. Such assays often involve monitoring the response of cells to Fc variant, for example cell survival, cell death, cellular phagocytosis, cell lysis, change in cellular morphology, or transcriptional activation such as cellular expression of a natural gene or reporter gene. For example, such assays may measure the ability of Fc variants to elicit ADCC, ADCP, or CDC. For some assays additional cells or components, that is in addition to the target cells, may need to be added, for example serum complement, or effector cells such as peripheral blood monocytes (PBMCs), NK cells, macrophages, and the like. Such additional cells may be from any organism, preferably humans, mice, rat, rabbit, and monkey. Crosslinked or monomeric antibodies and Fc fusions may cause apoptosis of certain cell lines expressing the antibody's target antigen, or they may mediate attack on target cells by immune cells which have been added to the assay. Methods for monitoring cell death or viability are known in the art, and include the use of dyes, fluorophores, immunochemical, cytochemical, and radioactive reagents. For example, caspase assays or annexin-flourconjugates may enable apoptosis to be measured, and uptake or release of radioactive substrates (e.g. Chromium-51 release assays) or the metabolic reduction of fluorescent dyes such as alamar blue may enable cell growth, proliferation or activation to be

monitored. In a preferred embodiment, the DELFIA® EuTDA-based cytotoxicity assay (Perkin Elmer, MA) is used. Alternatively, dead or damaged target cells may be monitored by measuring the release of one or more natural intracellular proteins, for example lactate dehydrogenase. Transcriptional activation may also serve as a method for assaying function in cell-based assays. In this case, response may be monitored by assaying for natural genes or proteins which may be upregulated or down-regulated, for example the release of certain interleukins may be measured, or alternatively readout may be via a luciferase or GFP-reporter construct. Cell-based assays may also involve the measure of morphological changes of cells as a response to the presence of an Fc variant. Cell types for such assays may be prokaryotic or eukaryotic, and a variety of cell lines that are known in the art may be employed. Alternatively, cell-based screens are performed using cells that have been transformed or transfected with nucleic acids encoding the Fc variants.

[0293] In vitro assays include but are not limited to binding assays, ADCC, CDC, cytotoxicity, proliferation, peroxide/ozone release, chemotaxis of effector cells, inhibition of such assays by reduced effector function antibodies; ranges of activities such as >100× improvement or >100× reduction, blends of receptor activation and the assay outcomes that are expected from such receptor profiles.

Pre-Clinical Experiments and Animal Models

[0294] The biological properties of the Fc variants of the present invention may be characterized in cell, tissue, and whole organism experiments. As is know in the art, drugs are often tested in animals, including but not limited to mice, rats, rabbits, dogs, cats, pigs, and monkeys, in order to measure a drug's efficacy for treatment against a disease or disease model, or to measure a drug's pharmacokinetics, toxicity, and other properties. Said animals may be referred to as disease models. With respect to the Fc variants of the present invention, a particular challenge arises when using animal models to evaluate the potential for in-human efficacy of candidate polypeptides—this is due, at least in part, to the fact that Fc variants that have a specific effect on the affinity for a human Fc receptor may not have a similar affinity effect with the orthologous animal receptor. These problems can be further exacerbated by the inevitable ambiguities associated with correct assignment of true orthologues (Mechetina et al., *Immunogenetics,* 2002 54:463-468), and the fact that some orthologues simply do not exist in the animal (for example, humans possess an FcγRIIa whereas mice do not). Therapeutics are often tested in mice, including but not limited to nude mice, SCID mice, xenograft mice, and transgenic mice (including knockins and knockouts). For example, an antibody or Fc fusion of the present invention that is intended as an anti-cancer therapeutic may be tested in a mouse cancer model, for example a xenograft mouse. In this method, a tumor or tumor cell line is grafted onto or injected into a mouse, and subsequently the mouse is treated with the therapeutic to determine the ability of the antibody or Fc fusion to reduce or inhibit cancer growth and metastasis. An alternative approach is the use of a SCID murine model in which immune-deficient mice are injected with human PBLs, conferring a semi-functional and human immune system—with an appropriate array of human FcγRs—to the mice that have subsequently been injected with antibodies or Fc polypeptides that target injected human tumor cells. In such a model, the Fc polypeptides that target the desired antigen (such as her2/neu on SkOV3 ovarian cancer cells) interact with human PBLs within the mice to engage tumoricidal effector functions. Such experimentation may provide meaningful data for determination of the potential of said Fc variant to be used as a therapeutic. Any organism, preferably mammals, may be used for testing. For example because of their genetic similarity to humans, monkeys can be suitable therapeutic models, and thus may be used to test the efficacy, toxicity, pharmacokinetics, or other property of the Fc polypeptides of the present invention. Tests of the Fc variants of the present invention in humans are ultimately required for approval as drugs, and thus of course these experiments are contemplated. Thus the Fc variants of the present invention may be tested in humans to determine their therapeutic efficacy, toxicity, pharmacokinetics, and/or other clinical properties.

[0295] The Fc variants of the present invention may confer superior performance on Fc polypeptides therapeutics in animal models or in humans. The receptor binding profiles of such Fc variants, as described in this specification, may, for example, be selected to increase the potency of cytotoxic drugs or to target specific effector functions or effector cells to improve the selectivity of the drug's action. Further, receptor binding profiles can be selected that may reduce some or all effector functions thereby reducing the side-effects or toxicity of such Fc polypeptide drugs. For example, an Fc variant with reduced binding to FcγRIIa, FcγRI and FcγRIIa can be selected to eliminate most cell-mediated effector function, or an Fc variant with reduced binding to C1q may be selected to limit complement-mediated effector functions. In some contexts, such effector functions are known to have potential toxic effects, therefore eliminating them may increase the safety of the Fc polypeptide drug, and such improved safety may be characterized in animal models. In some contexts, such effector functions are known to mediate the desirable therapeutic activity, therefore enhancing them may increase the activity or potency of the Fc polypeptide drug and such improved activity or potency may be characterized in animal models.

[0296] Optimized Fc variants can be tested in a variety of orthotopic tumor models. These clinically relevant animal models are important in the study of pathophysiology and therapy of aggressive cancers like pancreatic, prostate and breast cancer. Immune deprived mice including, but not limited to athymic nude or SCID mice are frequently used in scoring of local and systemic tumor spread from the site of intraorgan (e.g. pancreas, prostate or mammary gland) injection of human tumor cells or fragments of donor patients.

[0297] In preferred embodiments, Fc variants of the present invention may be assessed for efficacy in clinically relevant animal models of various human diseases. In many cases, relevant models include various transgenic animals for specific tumor antigens. Relevant transgenic models such as those that express human Fc receptors (e.g., FcγRIIIa including the gamma chain, FcγRI, FcγRIIa, FcγRIIb, and others) could be used to evaluate and test the efficacy of Fc polypeptides of the present invention. Evaluation of Fc variants by the introduction of human genes which directly or indirectly mediate effector function in mice or other rodents, may enable physiological studies of efficacy in tumor toxicity or other diseases such as autoimmune disorders and RA. Human Fc receptors such as FcγRIIIa may possess polymorphisms, such as that at position 158 (V or F as described) which would further enable the introduction of specific and combinations of human polymorphisms into rodents. The various studies

involving polymorphism-specific FcγRs is not limited to this section, however, and encompasses all discussions and applications of FcγRs in general as specified in throughout this application. Fc variants of the present invention may confer superior activity on Fc polypeptides in such transgenic models. In particular, variants with binding profiles optimized for human FcγRIIIa mediated activity may show superior activity in transgenic CD16 (FcγRIII) mice. Similar improvements in efficacy in mice transgenic for the other human Fc receptors, e.g. FcγRIIa, FcγRI, etc., may be observed for Fc variants with binding profiles optimized for the respective receptors. Mice transgenic for multiple human receptors would show improved activity for Fc variants with binding profiles optimized for the corresponding multiple receptors, for example as outlined in Table 1.

[0298] The introduction of target tumor antigens such as human CD20 into rodent B-cells in the form of a transgenic animal model can be used to provide a more relevant evaluation of efficacy. As such, the target antigen need not be limited to a fully human construct but could be a fusion protein containing the relevant human epitope of the target antigen. In a preferred embodiment, the testing of Fc polypeptides may include transgenic model systems, which include the combination of but not limited to both human target antigen and human Fc receptors (e.g. CD16 and other related receptors mediating effector functions) to evaluate efficacy and tumoricidal activity.

[0299] In a preferred embodiment, Fc polypeptides of the present invention that target the Her2 antigen (e.g. Fc variants of mu4D5 or its humanized analogues) may be assessed for efficacy in a clinically relevant mouse model of breast cancer. Examples of relevant models include, but are not limited to: 1) the HER2/neu (neu-N)-transgenic mice, which are derived from the parental FVB/N mouse strain and are transgenic for the rat form of the proto-oncogene HER2/neu (neu); and 2) transgenic mice that overexpress human HER2 under the murine mammary tumor virus promoter (Finkle et al., 2004, Clin Cancer Res. 10 (7):2499-511). Fc polypeptides of the present invention that show superior efficacy in these models represent likely candidates for further development.

[0300] Because of the difficulties and ambiguities associated with using animal models to characterize the potential efficacy of candidate therapeutic antibodies in a human patient, some variant polypeptides of the present invention may find utility as proxies for assessing potential in-human efficacy. Such proxy molecules would preferably mimic, in the animal system, the FcγR and/or complement biology of a corresponding candidate human Fc variant. This mimicry is most likely to be manifested by relative association affinities between specific Fc variants and animal vs. human receptors. For example, if one were using a mouse model to assess the potential in-human efficacy of an Fc variant that has enhanced affinity for human FcγRIIIa, an appropriate proxy variant would have enhanced affinity for mouse FcγRIII-2 (mouse CD16-2). Alternatively if one were using a mouse model to assess the potential in-human efficacy of an Fc variant that has reduced affinity for the human inhibitory receptor FcγRIIb, an appropriate proxy variant would have reduced affinity for mouse FcγRII. It should also be noted that the proxy Fc variants could be created in the context of a human Fc variant, an animal Fc variant, or both.

[0301] In a preferred embodiment, the testing of Fc variants may include study of efficacy in primates (e.g. cynomolgus monkey model) to facilitate the evaluation of depletion of specific target cells harboring target antigen. Additional primate models include but not limited to that of the rhesus monkey and Fc polypeptides in therapeutic studies of autoimmune, transplantation and cancer.

[0302] Toxicity studies are performed to determine the Fc polypeptide related effects that cannot be evaluated in standard pharmacology profile or occur only after repeated administration of the agent. Most toxicity tests are performed in two species—a rodent and a non-rodent—to ensure that any unexpected adverse effects are not overlooked before new therapeutic entities are introduced into humans. In general, these models may measure a variety of toxicities including genotoxicity, chronic toxicity, immunogenicity, reproductive/developmental toxicity and carcinogenicity. Included within the aforementioned parameters are standard measurement of food consumption, bodyweight, antibody formation, clinical chemistry, and macro- and microscopic examination of standard organs/tissues (e.g. cardiotoxicity). Additional parameters of measurement are injection site trauma and the measurement of neutralizing antibodies, if any. Traditionally, monoclonal antibody therepeutics, naked or conjugated are evaluated for cross-reactivity with normal tissues, immunogenicity/antibody production, conjugate or linker toxicity and "bystander" toxicity of radiolabeled species. Nonetheless, such studies may have to be individualized to address specific concerns and following the guidance set by ICH S6 (Safety studies for biotechnological products also noted above). As such, the general principles are that the products are sufficiently well characterized and for which impurities/contaminants have been removed, that the test material is comparable throughout development, and GLP compliance.

[0303] The pharmacokinetics (PK) of the Fc variants of the invention can be studied in a variety of animal systems, with the most relevant being non-human primates such as the cynomolgus, rhesus monkeys. Single or repeated i.v./s.c. administrations over a dose range of 6000-fold (0.05-300 mg/kg) can be evaluated for the half-life (days to weeks) using plasma concentration and clearance as well as volume of distribution at a steady state and level of systemic absorbance can be measured. Examples of such parameters of measurement generally include maximum observed plasma concentration (Cmax), the time to reach Cmax (Tmax), the area under the plasma concentration-time curve from time 0 to infinity [AUC(0-inf] and apparent elimination half-life (T1/2). Additional measured parameters could include compartmental analysis of concentration-time data obtained following i.v. administration and bioavailability. Examples of pharmacological/toxicological studies using cynomolgus have been established for Rituxan and Zevalin in which monoclonal antibodies to CD20 are cross-reactive. Biodistribution, dosimetry (for radiolabled antibodies or Fc fusions), and PK studies can also be done in rodent models. Such studies would evaluate tolerance at all doses administered, toxicity to local tissues, preferential localization to rodent xenograft animal models, depletion of target cells (e.g. CD20 positive cells).

[0304] The Fc variants of the present invention may confer superior pharmacokinetics on Fc polypeptide therapeutics in animal systems or in humans. For example, increased binding to FcRn may increase the half-life and exposure of the Fc polypeptide. Alternatively, decreased binding to FcRn may decrease the half-life and exposure of the Fc polypeptide in cases where reduced exposure is favorable, such as when such drug has side-effects.

[0305] It is known in the art that the array of Fc receptors is differentially expressed on various immune cell types, as well as in different tissues. Differential tissue distribution of Fc receptors may ultimately have an impact on the pharmacodynamic (PD) and pharmacokinetic (PK) properties of Fc variants of the present invention. Because Fc variants of the presentation have varying affinities for the array of Fc receptors, further screening of the polypeptides for PD and/or PK properties may be extremely useful for defining the optimal balance of PD, PK, and therapeutic efficacy conferred by each candidate polypeptide.

[0306] Pharmacodynamic studies may include, but are not limited to, targeting specific tumor cells or blocking signaling mechanisms, measuring depletion of target antigen expressing cells or signals, etc. The Fc variants of the present invention may target particular effector cell populations and thereby direct Fc polypeptides to recruit certain activities to improve potency or to increase penetration into a particularly favorable physiological compartment. For example, neutrophil activity and localization can be targeted by an Fc variant that preferentially targets FcγRIIb. Such pharmacodynamic effects may be demonstrated in animal models or in humans.

Therapeutic Use of Fc Variants

[0307] The Fc variants of the present invention may be used for various therapeutic purposes. As will be appreciated by those in the art, the Fc variants of the present invention may be used for any therapeutic purpose for which antibodies, Fc fusions, and the like may be used. In a preferred embodiment, the Fc variants are administered to a patient to treat disorders including but not limited to autoimmune and inflammatory diseases, infectious diseases, and cancer.

[0308] A "patient" for the purposes of the present invention includes both humans and other animals, preferably mammals and most preferably humans. Thus the Fc variants of the present invention have both human therapy and veterinary applications. The term "treatment" in the present invention is meant to include therapeutic treatment, as well as prophylactic, or suppressive measures for a disease or disorder. Thus, for example, successful administration of an Fc variant prior to onset of the disease results in treatment of the disease. As another example, successful administration of an optimized Fc variant after clinical manifestation of the disease to combat the symptoms of the disease comprises treatment of the disease. "Treatment" also encompasses administration of an optimized Fc variant after the appearance of the disease in order to eradicate the disease. Successful administration of an agent after onset and after clinical symptoms have developed, with possible abatement of clinical symptoms and perhaps amelioration of the disease, comprises treatment of the disease. Those "in need of treatment" include mammals already having the disease or disorder, as well as those prone to having the disease or disorder, including those in which the disease or disorder is to be prevented.

[0309] In one embodiment, an Fc variant of the present invention is administered to a patient having a disease involving inappropriate expression of a protein or other molecule. Within the scope of the present invention this is meant to include diseases and disorders characterized by aberrant proteins, due for example to alterations in the amount of a protein present, protein localization, posttranslational modification, conformational state, the presence of a mutant or pathogen protein, etc. Similarly, the disease or disorder may be characterized by alterations molecules including but not limited to polysaccharides and gangliosides. An overabundance may be due to any cause, including but not limited to overexpression at the molecular level, prolonged or accumulated appearance at the site of action, or increased activity of a protein relative to normal. Included within this definition are diseases and disorders characterized by a reduction of a protein. This reduction may be due to any cause, including but not limited to reduced expression at the molecular level, shortened or reduced appearance at the site of action, mutant forms of a protein, or decreased activity of a protein relative to normal. Such an overabundance or reduction of a protein can be measured relative to normal expression, appearance, or activity of a protein, and said measurement may play an important role in the development and/or clinical testing of the Fc variants of the present invention.

[0310] "Cancer" and "cancerous" herein refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to carcinoma, lymphoma, blastoma, sarcoma (including liposarcoma), neuroendocrine tumors, mesothelioma, schwanoma, meningioma, adenocarcinoma, melanoma, and leukemia or lymphoid malignancies.

[0311] More particular examples of such cancers include hematologic malignancies, such as Hodgkin's lymphoma; non-Hodgkin's lymphomas (Burkitt's lymphoma, small lymphocytic lymphoma/chronic lymphocytic leukemia, mycosis fungoides, mantle cell lymphoma, follicular lymphoma, diffuse large B-cell lymphoma, marginal zone lymphoma, hairy cell leukemia and lymphoplasmacytic leukemia), tumors of lymphocyte precursor cells, including B-cell acute lymphoblastic leukemia/lymphoma, and T-cell acute lymphoblastic leukemia/lymphoma, thymoma, tumors of the mature T and NK cells, including peripheral T-cell leukemias, adult T-cell leukemia/T-cell lymphomas and large granular lymphocytic leukemia, Langerhans cell histocytosis, myeloid neoplasias such as acute myelogenous leukemias, including AML with maturation, AML without differentiation, acute promyelocytic leukemia, acute myelomonocytic leukemia, and acute monocytic leukemias, myelodysplastic syndromes, and chronic myeloproliferative disorders, including chronic myelogenous leukemia; tumors of the central nervous system such as glioma, glioblastoma, neuroblastoma, astrocytoma, medulloblastoma, ependymoma, and retinoblastoma; solid tumors of the head and neck (eg. nasopharyngeal cancer, salivary gland carcinoma, and esophagael cancer), lung (eg. small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung), digestive system (eg. gastric or stomach cancer including gastrointestinal cancer, cancer of the bile duct or biliary tract, colon cancer, rectal cancer, colorectal cancer, and anal carcinoma), reproductive system (eg. testicular, penile, or prostate cancer, uterine, vaginal, vulval, cervical, ovarian, and endometrial cancer), skin (eg. melanoma, basal cell carcinoma, squamous cell cancer, actinic keratosis), liver (eg. liver cancer, hepatic carcinoma, hepatocellular cancer, and hepatoma), bone (eg. osteoclastoma, and osteolytic bone cancers) additional tissues and organs (eg. pancreatic cancer, bladder cancer, kidney or renal cancer, thyroid cancer, breast cancer, cancer of the peritoneum, and Kaposi's sarcoma), and tumors of the vascular system (eg. angiosarcoma and hemagiopericytoma).

[0312] "Autoimmune diseases" herein include allogenic islet graft rejection, alopecia areata, ankylosing spondylitis, antiphospholipid syndrome, autoimmune Addison's disease,

antineutrophil cytoplasmic autoantibodies (ANCA), autoimmune diseases of the adrenal gland, autoimmune hemolytic anemia, autoimmune hepatitis, autoimmune myocarditis, autoimmune neutropenia, autoimmune oophoritis and orchitis, autoimmune thrombocytopenia, autoimmune urticaria, Behcet's disease, bullous pemphigoid, cardiomyopathy, Castleman's syndrome, celiac spruce-dermatitis, chronic fatigue immune disfunction syndrome, chronic inflammatory demyelinating polyneuropathy, Churg-Strauss syndrome, cicatrical pemphigoid, CREST syndrome, cold agglutinin disease, Crohn's disease, dermatomyositis, discoid lupus, essential mixed cryoglobulinemia, factor Vil deficiency, fibromyalgia-fibromyositis, glomerulonephritis, Grave's disease, Guillain-Barre, Goodpasture's syndrome, graft-versus-host disease (GVHD), Hashimoto's thyroiditis, hemophilia A, idiopathic pulmonary fibrosis, idiopathic thrombocytopenia purpura (ITP), IgA neuropathy, IgM polyneuropathies, immune mediated thrombocytopenia, juvenile arthritis, Kawasaki's disease, lichen plantus, lupus erthematosis, Meniere's disease, mixed connective tissue disease, multiple sclerosis, type 1 diabetes mellitus, myasthenia gravis, pemphigus vulgaris, pernicious anemia, polyarteritis nodosa, polychrondritis, polyglandular syndromes, polymyalgia rheumatica, polymyositis and dermatomyositis, primary agammaglobinulinemia, primary biliary cirrhosis, psoriasis, psoriatic arthritis, Reynauld's phenomenon, Reiter's syndrome, rheumatoid arthritis, sarcoidosis, scleroderma, Sjorgen's syndrome, solid organ transplant rejection, stiff-man syndrome, systemic lupus erythematosus, takayasu arteritis, temporal arteristis/giant cell arteritis, thrombotic thrombocytopenia purpura, ulcerative colitis, uveitis, vasculitides such as dermatitis herpetiformis vasculitis, vitiligo, and Wegner's granulomatosis.

[0313] "Inflammatory disorders" herein include acute respiratory distress syndrome (ARDS), acute septic arthritis, allergic encephalomyelitis, allergic rhinitis, allergic vasculitis, allergy, asthma, atherosclerosis, chronic inflammation due to chronic bacterial or viral infectionis, chronic obstructive pulmonary disease (COPD), coronary artery disease, encephalitis, inflammatory bowel disease, inflammatory osteolysis, inflammation associated with acute and delayed hypersensitivity reactions, inflammation associated with tumors, peripheral nerve injury or demyelinating diseases, inflammation associated with tissue trauma such as burns and ischemia, inflammation due to meningitis, multiple organ injury syndrome, pulmonary fibrosis, sepsis and septic shock, Stevens-Johnson syndrome, undifferentiated arthropy, and undifferentiated spondyloarthropathy.

[0314] "Infectious diseases" herein include diseases caused by pathogens such as viruses, bacteria, fungi, protozoa, and parasites. Infectious diseases may be caused by viruses including adenovirus, cytomegalovirus, dengue, Epstein-Barr, hanta, hepatitis A, hepatitis B, hepatitis C, herpes simplex type 1, herpes simplex type II, human immunodeficiency virus, (HIV), human papilloma virus (HPV), influenza, measles, mumps, papova virus, polio, respiratory syncytial virus, rinderpest, rhinovirus, rotavirus, rubella, SARS virus, smallpox, viral meningitis, and the like. Infections diseases may also be caused by bacteria including *Bacillus antracis, Borrelia burgdorferi, Campylobacter jejuni, Chlamydia trachomatis, Clostridium botulinum, Clostridium tetani, Diptheria, E. coli, Legionella, Helicobacter pylori, Mycobacterium rickettsia, Mycoplasma nesisseria, Pertussis, Pseudomonas aeruginosa, S. pneumonia, Streptococcus, Staphylococcus, Vibria cholerae, Yersinia pestis*, and the like. Infectious diseases may also be caused by fungi such as *Aspergillus fumigatus, Blastomyces dermatitidis, Candida albicans, Coccidioides immitis, Cryptococcus neoformans, Histoplasma capsulatum, Penicillium marneffei*, and the like. Infectious diseases may also be caused by protozoa and parasites such as *chlamydia, kokzidioa, leishmania, malaria, rickettsia, trypanosoma*, and the like.

[0315] Furthermore, Fc variants of the present invention may be used to prevent or treat additional conditions including but not limited to heart conditions such as congestive heart failure (CHF), myocarditis and other conditions of the myocardium; skin conditions such as rosecea, acne, and eczema; bone and tooth conditions such as bone loss, osteoporosis, Paget's disease, Langerhans' cell histiocytosis, periodontal disease, disuse osteopenia, osteomalacia, monostotic fibrous dysplasia, polyostotic fibrous dysplasia, bone metastasis, bone pain management, humoral malignant hypercalcemia, periodontal reconstruction, spinal cord injury, and bone fractures; metabolic conditions such as Gaucher's disease; endocrine conditions such as Cushing's syndrome; and neurological conditions.

Formulation, Administration, and Dosing

[0316] Pharmaceutical compositions are contemplated wherein an Fc variant of the present invention and one or more therapeutically active agents are formulated. Formulations of the Fc variants of the present invention are prepared for storage by mixing said Fc variant having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed., 1980), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, acetate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl orbenzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; sweeteners and other flavoring agents; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; additives; coloring agents; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURO NICS™ or polyethylene glycol (PEG). In a preferred embodiment, the pharmaceutical composition that comprises the Fc variant of the present invention may be in a water-soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric

acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine. The formulations to be used for in vivo administration are preferrably sterile. This is readily accomplished by filtration through sterile filtration membranes or other methods.

[0317] The Fc variants disclosed herein may also be formulated as immunoliposomes. A liposome is a small vesicle comprising various types of lipids, phospholipids and/or surfactant that is useful for delivery of a therapeutic agent to a mammal. Liposomes containing the Fc variant are prepared by methods known in the art, such as described in Epstein et al., 1985, *Proc Natl Acad Sci USA,* 82:3688; Hwang et al., 1980, *Proc Natl Acad Sci USA,* 77:4030; U.S. Pat. No. 4,485,045; U.S. Pat. No. 4,544,545; and PCT WO 97/38731. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. A chemotherapeutic agent or other therapeutically active agent is optionally contained within the liposome (Gabizon et al., 1989, *J National Cancer Inst* 81:1484).

[0318] The Fc variant and other therapeutically active agents may also be entrapped in microcapsules prepared by methods including but not limited to coacervation techniques, interfacial polymerization (for example using hydroxymethylcellulose or gelatin-microcapsules, or poly-(methylmethacylate) microcapsules), colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules), and macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed., 1980. Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymer, which matrices are in the form of shaped articles, e.g. films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and gamma ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (which are injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), poly-D-(−)-3-hydroxybutyric acid, and Pro-Lease® (commercially available from Alkermes), which is a microsphere-based delivery system composed of the desired bioactive molecule incorporated into a matrix of poly-DL-lactide-co-glycolide (PLG).

[0319] Administration of the pharmaceutical composition comprising an Fc variant of the present invention, preferably in the form of a sterile aqueous solution, may be done in a variety of ways, including, but not limited to orally, subcutaneously, intravenously, intranasally, intraotically, transdermally, topically (e.g., gels, salves, lotions, creams, etc.), intraperitoneally, intramuscularly, intrapulmonary, vaginally, parenterally, rectally, or intraocularly. In some instances, for example for the treatment of wounds, inflammation, etc., the Fc variant may be directly applied as a solution or spray. As is known in the art, the pharmaceutical composition may be formulated accordingly depending upon the manner of introduction.

[0320] Subcutaneous administration may be preferable in some circumstances because the patient may self-administer the pharmaceutical composition. Many protein therapeutics are not sufficiently potent to allow for formulation of a therapeutically effective dose in the maximum acceptable volume for subcutaneous administration. This problem may be addressed in part by the use of protein formulations comprising arginine-HCl, histidine, and polysorbate (see WO 04091658). Fc polypeptides of the present invention may be more amenable to subcutaneous administration due to, for example, increased potency, improved serum half-life, or enhanced solubility.

[0321] As is known in the art, protein therapeutics are often delivered by IV infusion or bolus. The Fc variants of the present invention may also be delivered using such methods. For example, administration may venious be by intravenous infusion with 0.9% sodium chloride as an infusion vehicle.

[0322] Pulmonary delivery may be accomplished using an inhaler or nebulizer and a formulation comprising an aerosolizing agent. For example, AERx® inhalable technology commercially available from Aradigm, or Inhance™ pulmonary delivery system commercially available from Nektar Therapeutics may be used. Fc variants of the present invention may be more amenable to intrapulmonary delivery. FcRn is present in the lung, and may promote transport from the lung to the bloodstream (e.g. Syntonix WO 04004798, Bitonti et. al. (2004) Proc. Nat. Acad. Sci. 101:9763-8). Accordingly, antibodies or Fc fusions that bind FcRn more effectively in the lung or that are released more efficiently in the bloodstream may have improved bioavailability following intrapulmonary administration. Fc variants of the present invention may also be more amenable to intrapulmonary administration due to, for example, improved solubility or altered isoelectric point.

[0323] Furthermore, Fc polypeptides of the present invention may be more amenable to oral delivery due to, for example, improved stability at gastric pH and increased resistance to proteolysis. Furthermore, FcRn appears to be expressed in the intestinal epithelia of adults (Dickinson et al., 1999, J Clin Invest 104:903-11), so Fc polypeptides of the present invention, for example antibodies or Fc fusions, with improved FcRn interaction profiles may show enhanced bioavailability following oral administration. FcRn mediated transport of Fc variants may also occur at other mucus membranes such as those in the gastrointestinal, respiratory, and genital tracts (Yoshida et al., 2004, Immunity 20:769-83).

[0324] In addition, any of a number of delivery systems are known in the art and may be used to administer the Fc variants of the present invention. Examples include, but are not limited to, encapsulation in liposomes, microparticles, microspheres (eg. PLA/PGA microspheres), and the like. Alternatively, an implant of a porous, non-porous, or gelatinous material, including membranes or fibers, may be used. Sustained release systems may comprise a polymeric material or matrix such as polyesters, hydrogels, poly(vinylalcohol), polylactides, copolymers of L-glutamic acid and ethyl-L-gutamate, ethylene-vinyl acetate, lactic acid-glycolic acid copolymers such as the LUPRON DEPOT®, and poly-D-(−)-3-hydroxyburyric acid. It is also possible to administer a nucleic acid encoding the Fc variant of the current invention, for example by retroviral infection, direct injection, or coating with lipids, cell surface receptors, or other transfection agents. In all cases, controlled release systems may be used to release the Fc variant at or close to the desired location of action.

[0325] The dosing amounts and frequencies of administration are, in a preferred embodiment, selected to be therapeutically or prophylactically effective. As is known in the art, adjustments for protein degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

[0326] The concentration of the therapeutically active Fc variant in the formulation may vary from about 0.1 to 100 weight %. In a preferred embodiment, the concentration of the Fc variant is in the range of 0.003 to 1.0 molar. In order to treat a patient, a therapeutically effective dose of the Fc variant of the present invention may be administered. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. Dosages may range from 0.0001 to 100 mg/kg of body weight or greater, for example 0.1, 1, 10, or 50 mg/kg of body weight, with 1 to 10 mg/kg being preferred.

[0327] In some embodiments, only a single dose of the Fc variant is used. In other embodiments, multiple doses of the Fc variant are administered. The elapsed time between administrations may be less than 1 hour, about 1 hour, about 1-2 hours, about 2-3 hours, about 3-4 hours, about 6 hours, about 12 hours, about 24 hours, about 48 hours, about 2-4 days, about 4-6 days, about 1 week, about 2 weeks, or more than 2 weeks.

[0328] In other embodiments the Fc variants of the present invention are administered in metronomic dosing regimes, either by continuous infusion or frequent administration without extended rest periods. Such metronomic administration may involve dosing at constant intervals without rest periods. Typically such regimens encompass chronic low-dose or continuous infusion for an extended period of time, for example 1-2 days, 1-2 weeks, 1-2 months, or up to 6 months or more. The use of lower doses may minimize side effects and the need for rest periods.

[0329] In certain embodiments the Fc variant of the present invention and one or more other prophylactic or therapeutic agents are cyclically administered to the patient. Cycling therapy involves administration of a first agent at one time, a second agent at a second time, optionally additional agents at additional times, optionally a rest period, and then repeating this sequence of administration one or more times. The number of cycles is typically from 2-10. Cycling therapy may reduce the development of resistance to one or more agents, may minimize side effects, or may improve treatment efficacy.

Combination- and Co-Therapies

[0330] The Fc variants of the present invention may be administered concomitantly with one or more other therapeutic regimens or agents. The additional therapeutic regimes or agents may be used to improve the efficacy or safety of the Fc variant. Also, the additional therapeutic regimes or agents may be used to treat the same disease or a comorbidity rather than to alter the action of the Fc variant. For example, an Fc variant of the present invention may be administered to the patient along with chemotherapy, radiation therapy, or both chemotherapy and radiation therapy. The Fc variant of the present invention may be administered in combination with one or more other prophylactic or therapeutic agents, including but not limited to cytotoxic agents, chemotherapeutic agents, cytokines, growth inhibitory agents, anti-hormonal agents, kinase inhibitors, anti-angiogenic agents, cardioprotectants, immunostimulatory agents, immunosuppressive agents, agents that promote proliferation of hematological cells, angiogenesis inhibitors, protein tyrosine kinase (PTK) inhibitors, additional Fc variants, FcγRIIb or other Fc receptor inhibitors, or other therapeutic agents.

[0331] The terms "in combination with" and "co-administration" are not limited to the administration of said prophylactic or therapeutic agents at exactly the same time. Instead, it is meant that the Fc variant of the present invention and the other agent or agents are administered in a sequence and within a time interval such that they may act together to provide a benefit that is increased versus treatment with only either the Fc variant of the present invention or the other agent or agents. It is preferred that the Fc variant and the other agent or agents act additively, and especially preferred that they act synergistically. Such molecules are suitably present in combination in amounts that are effective for the purpose intended. The skilled medical practitioner can determine empirically, or by considering the pharmacokinetics and modes of action of the agents, the appropriate dose or doses of each therapeutic agent, as well as the appropriate timings and methods of administration.

[0332] In one embodiment, the Fc variants of the present invention are administered with one or more additional molecules comprising antibodies or Fc. The Fc variants of the present invention may be co-administered with one or more other antibodies that have efficacy in treating the same disease or an additional comorbidity; for example two antibodies may be administered that recognize two antigens that are overexpressed in a given type of cancer, or two antigens that mediate pathogenesis of an autoimmune or infectious disease.

[0333] Examples of anti-cancer antibodies that may be co-administered include, but are not limited to, anti 17-IA cell surface antigen antibodies such as Panorex™ (edrecolomab); anti-4-1 BB antibodies; anti-4Dc antibodies; anti-A33 antibodies such as A33 and CDP-833; anti-α4β1 integrin antibodies such as natalizumab; anti-α4β7 integrin antibodies such as LDP-02; anti-αVβ1 integrin antibodies such as F-200, M-200, and SJ-749; anti-αVβ3 integrin antibodies such as abciximab, CNTO-95, Mab-17E6, and Vitaxin™; anti-complement factor 5 (C5) antibodies such as 5G1.1; anti-CA1 25 antibodies such as OvaRex® (oregovomab);

anti-CD3 antibodies such as Nuvion® (visilizumab) and Rexomab; anti-CD4 antibodies such as IDEC-151, MDX-CD4, OKT4A; anti-CD6 antibodies such as Oncolysin B and Oncolysin CD6; anti-CD7 antibodies such as HB2; anti-CD19 antibodies such as B43, MT-103, and Oncolysin B; anti-CD20 antibodies such as 2H7, 2H7.v16, 2H7.v114, 2H7.v115, Bexxar® (tositumomab), Rituxan® (rituximab), Zevalin® (Ibritumomab tiuxetan), and PRO70769; anti-CD22 antibodies such as Lymphocide™ (epratuzumab); anti-CD23 antibodies such as IDEC-152; anti-CD25 antibodies such as basiliximab and Zenapax® (daclizumab); anti-CD30 antibodies such as AC10, MDX-060, and SGN-30; anti-CD33 antibodies such as Mylotarg® (gemtuzumab ozogamicin), Oncolysin M, and Smart M195; anti-CD38 antibodies; anti-CD40 antibodies such as SGN-40 and toralizumab; anti-CD40L antibodies such as 5c8, Antova™, and IDEC-131; anti-CD44 antibodies such as bivatuzumab; anti-CD46 antibodies; anti-CD52 antibodies such as Campath® (alemtuzumab); anti-CD55 antibodies such as SC-1; anti-CD56 antibodies such as huN901-DM1; anti-CD64 antibodies such as MDX-33; anti-CD66e antibodies such as XR-303; anti-CD74 antibodies such as IMMU-110; anti-CD80 antibodies such as galiximab and IDEC-114; anti-CD89 antibodies such as MDX-214; anti-CD123 antibodies; anti-CD138 antibodies such as B-B4-DM1; anti-CD146 antibodies such as AA-98; anti-CD148 antibodies; anti-CEA antibodies such as cT84.66, labetuzumab, and Pentacea™; anti-CTLA-4 antibodies such as MDX-101; anti-CXCR4 antibodies; antibodies such as ABX-EGF, Erbitux® (cetuximab), IMC-C225, and Merck Mab 425; anti-EpCAM antibodies such as Crucell's anti-EpCAM, ING-1, and IS-IL-2; anti-ephrin B2/EphB4 antibodies; anti-Her2 antibodies such as Herceptin®, MDX-210; anti-FAP (fibroblast activation protein) antibodies such as sibrotuzumab; anti-ferritin antibodies such as NXT-211; anti-FGF-1 antibodies; anti-FGF-3 antibodies; anti-FGF-8 antibodies; anti-FGFR antibodies, anti-fibrin antibodies; anti-G250 antibodies such as WX-G250 and Rencarex®; anti-GD2 ganglioside antibodies such as EMD-273063 and TriGem; anti-GD3 ganglioside antibodies such as BEC2, KW-2871, and mitumomab; anti-gpIIb/IIIa antibodies such as ReoPro; anti-heparinase antibodies; anti-Her2/ErbB2 antibodies such as Herceptin® (trastuzumab), MDX-210, and pertuzumab; anti-HLA antibodies such as Oncolym®, Smart 1D10; anti-HM1.24 antibodies; anti-ICAM antibodies such as ICM3; anti-IgA receptor antibodies; anti-IGF-1 antibodies such as CP-751871 and EM-164; anti-IGF-1R antibodies such as IMC-A12; anti-IL-6 antibodies such as CNTO-328 and elsilimomab; anti-IL-15 antibodies such as HuMax™-IL15; anti-KDR antibodies; anti-laminin 5 antibodies; anti-Lewis Y antigen antibodies such as Hu3S193 and IGN-311; anti-MCAM antibodies; anti-Muc1 antibodies such as BravaRex and TriAb; anti-NCAM antibodies such as ERIC-1 and ICRT; anti-PEM antigen antibodies such as Theragyn and Therex; anti-PSA antibodies; anti-PSCA antibodies such as IG8; anti-Ptk antbodies; anti-PTN antibodies; anti-RANKL antibodies such as AMG-162; anti-RLIP76 antibodies; anti-SK-1 antigen antibodies such as Monopharm C; anti-STEAP antibodies; anti-TAG72 antibodies such as CC49-SCA and MDX-220; anti-TGF-β antibodies such as CAT-152; anti-TNF-α antibodies such as CDP571, CDP870, D2E7, Humira® (adalimumab), and Remicade® (infliximab); anti-TRAIL-R1 and TRAIL-R2 antibodies; anti-VE-cadherin-2 antibodies; and anti-VLA-4 antibodies such as Antegren™. Furthermore, anti-idiotype antibodies including but not limited to the GD3 epitope antibody BEC2 and the gp72 epitope antibody 105AD7, may be used. In addition, bispecific antibodies including but not limited to the anti-CD3/CD20 antibody Bi20 may be used.

[0334] Examples of antibodies that may be co-administered to treat autoimmune or inflammatory disease, transplant rejection, GVHD, and the like include, but are not limited to, anti-α4β7 integrin antibodies such as LDP-02, anti-beta2 integrin antibodies such as LDP-01, anti-complement (C5) antibodies such as 5G1.1, anti-CD2 antibodies such as BTI-322, MEDI-507, anti-CD3 antibodies such as OKT3, SMART anti-CD3, anti-CD4 antibodies such as IDEC-151, MDX-CD4, OKT4A, anti-CD11a antibodies, anti-CD14 antibodies such as IC14, anti-CD18 antibodies, anti-CD23 antibodies such as IDEC 152, anti-CD25 antibodies such as Zenapax, anti-CD40L antibodies such as 5c8, Antova, IDEC-131, anti-CD64 antibodies such as MDX-33, anti-CD80 antibodies such as IDEC-114, anti-CD147 antibodies such as ABX-CBL, anti-E-selectin antibodies such as CDP850, anti-gpIIb/IIIa antibodies such as ReoPro/Abcixima, anti-ICAM-3 antibodies such as ICM3, anti-ICE antibodies such as VX-740, anti-FcR1 antibodies such as MDX-33, anti-IgE antibodies such as rhuMab-E25, anti-IL-4 antibodies such as SB-240683, anti-IL-5 antibodies such as SB-240563, SCH55700, anti-IL-8 antibodies such as ABX-IL8, anti-interferon gamma antibodies, and anti-TNFα antibodies such as CDP571, CDP870, D2E7, Infliximab, MAK-195F, anti-VLA-4 antibodies such as Antegren. Examples of other Fc-containing molecules that may be co-administered to treat autoimmune or inflammatory disease, transplant rejection, GVHD, and the like include, but are not limited to, the p75 TNF receptor/Fc fusion Enbrel® (etanercept) and Regeneron's IL-1 trap.

[0335] Examples of antibodies that may be co-administered to treat infectious diseases include, but are not limited to, anti-anthrax antibodies such as ABthrax, anti-CMV antibodies such as CytoGam and sevirumab, anti-ryptosporidium antibodies such as CryptoGAM, Sporidin-G, anti-helicobacter antibodies such as Pyloran, anti-hepatitis B antibodies such as HepeX-B, Nabi-HB, anti-HIV antibodies such as HRG-214, anti-RSV antibodies such as felvizumab, HNK-20, palivizumab, RespiGam, and anti-*staphylococcus* antibodies such as Aurexis, Aurograb, BSYX-A110, and SE-Mab.

[0336] Alternatively, the Fc variants of the present invention may be co-administered or with one or more other molecules that compete for binding to one or more Fc receptors. For example, co-administering inhibitors of the inhibitory receptor FcγRIIb may result in increased effector function. Similarly, co-administering inhibitors of activating receptors, for example FcγRIIIa, may minimize unwanted effector function. Fc receptor inhibitors include but are not limited to Fc variants that are engineered to act as competitive FcγR inhibitors, as well as other immunoglobulins and specifically intravenous immunoglobulin (IVIg). In one embodiment, the inhibitor is administered and allowed to act before the Fc variant is administered. An alternative way of achieving the effect of sequential dosing would be to provide an immediate release dosage form of the Fc receptor inhibitor and then a sustained release formulation of the Fc variant of the invention. The immediate release and controlled release formulations could be administered separately or be combined into one unit dosage form. Administration of an FcγRIIb inhibitor may also be used to limit unwanted immune responses, for

example anti-Factor VIII antibody response following Factor VIII administration to hemophiliacs.

[0337] In one embodiment, the Fc variants of the present invention are administered with a chemotherapeutic agent. By "chemotherapeutic agent" as used herein is meant a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include but are not limited to alkylating agents such as thiotepa and cyclosphosphamide (CYTOXAN™); alkyl sulfonates such as busulfan, improsulfan and piposulfan; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; antibiotics such as aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, calicheamicin, carabicin, caminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalamycin, olivomycins, peplomycin, poffiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, trioxifene, keoxifene, LY 117018, onapristone, and toremifene (Fareston); anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethylenethiophosphaoramide and trimethylolomelamine; folic acid replenisher such as frolinic acid; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; proteins such as arginine deiminase and asparaginase; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; taxanes, e.g. paclitaxel (TAXOL®, Bristol-Myers Squibb Oncology, Princeton, N.J.) and docetaxel (TAXOTERE®, Rhne-Poulenc Rorer, Antony, France); topoisomerase inhibitor RFS 2000; thymidylate synthase inhibitor (such as Tomudex); additional chemotherapeutics including aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; difluoromethylornithine (DMFO); elformithine; elliptinium acetate; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; sizofuran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; retinoic acid; esperamicins; capecitabine. Pharmaceutically acceptable salts, acids or derivatives of any of the above may also be used.

[0338] A chemotherapeutic or other cytotoxic agent may be administered as a prodrug. By "prodrug" as used herein is meant a precursor or derivative form of a pharmaceutically active substance that is less cytotoxic to tumor cells compared to the parent drug and is capable of being enzymatically activated or converted into the more active parent form. See, for example Wilman, 1986, Biochemical Society Transactions, 615th Meeting Belfast, 14:375-382; and Stella et al., "Prodrugs: A Chemical Approach to Targeted Drug Delivery," Directed Drug Delivery, Borchardt et al., (ed.): 247-267, Humana Press, 1985. The prodrugs that may find use with the present invention include but are not limited to phosphate-containing prodrugs, thiophosphate-containing prodrugs, sulfate-containing prodrugs, peptide-containing prodrugs, D-amino acid-modified prodrugs, glycosylated prodrugs, beta-lactam-containing prodrugs, optionally substituted phenoxyacetamide-containing prodrugs or optionally substituted phenylacetamide-containing prodrugs, 5-fluorocytosine and other 5-fluorouridine prodrugs which can be converted into the more active cytotoxic free drug. Examples of cytotoxic drugs that can be derivatized into a prodrug form for use with the Fc variants of the present invention include but are not limited to any of the aforementioned chemotherapeutic agents.

[0339] A variety of other therapeutic agents may find use for administration with the Fc variants of the present invention. In one embodiment, the Fc variant is administered with an anti-angiogenic agent. By "anti-angiogenic agent" as used herein is meant a compound that blocks, or interferes to some degree, the development of blood vessels. The anti-angiogenic factor may, for instance, be a small molecule or a protein, for example an antibody, Fc fusion, or cytokine, that binds to a growth factor or growth factor receptor involved in promoting angiogenesis. The preferred anti-angiogenic factor herein is an antibody that binds to Vascular Endothelial Growth Factor (VEGF). Other agents that inhibit signaling through VEGF may also be used, for example RNA-based therapeutics that reduce levels of VEGF or VEGF-R expression, VEGF-toxin fusions, Regeneron's VEGF-trap, and antibodies that bind VEGF-R. In an alternate embodiment, the Fc variant is administered with a therapeutic agent that induces or enhances adaptive immune response, for example an antibody that targets CTLA-4. Additional anti-angiogenesis agents include, but are not limited to, angiostatin (plasminogen fragment), antithrombin III, angiozyme, ABT-627, Bay 12-9566, benefin, bevacizumab, bisphosphonates, BMS-275291, cartilage-derived inhibitor (CDI), CAI, CD59 complement fragment, CEP-7055, Col 3, combretastatin A-4, endostatin (collagen XVIII fragment), farnesyl transferase inhibitors, fibronectin fragment, gro-beta, halofuginone, heparinases, heparin hexasaccharide fragment, HMV833, human chorionic gonadotropin (hCG), IM-862, interferon alpha, interferon beta, interferon gamma, interferon inducible protein 10 (IP-10), interleukin-12, kringle 5 (plasminogen fragment), marimastat, metalloproteinase inhibitors (eg. TIMPs), 2-methodyestradiol, MMI 270 (CGS 27023A), plasminogen activiator inhibitor (PAI), platelet factor-4 (PF4), prinomastat, prolactin 16 kDa fragment, proliferin-related protein (PRP), PTK 787/ZK 222594, retinoids, solimastat, squalamine, SS3304, SU5416, SU6668, SU11248, tetrahy-

drocortisol-S, tetrathiomolybdate, thalidomide, thrombospondin-1 (TSP-1), TNP-470, transforming growth factor beta (TGF-β), vasculostatin, vasostatin (calreticulin fragment), ZS6126, and ZD6474.

[0340] In a preferred embodiment, the Fc variant is administered with a tyrosine kinase inhibitor. By "tyrosine kinase inhibitor" as used herein is meant a molecule that inhibits to some extent tyrosine kinase activity of a tyrosine kinase. Examples of such inhibitors include but are not limited to quinazolines, such as PD 153035, 4-(3-chloroanilino) quinazoline; pyridopyrimidines; pyrimidopyrimidines; pyrrolopyrimidines, such as CGP 59326, CGP 60261 and CGP 62706; pyrazolopyrimidines, 4-(phenylamino)-7H-pyrrolo [2,3-d]pyrimidines; curcumin (diferuloyl methane, 4,5-bis(4-fluoroanilino)-phthalimide); tyrphostines containing nitrothiophene moieties; PD-0183805 (Warner-Lambert); antisense molecules (e.g. those that bind to ErbB-encoding nucleic acid); quinoxalines (U.S. Pat. No. 5,804,396); tryphostins (U.S. Pat. No. 5,804,396); ZD6474 (Astra Zeneca); PTK-787 (Novartis/Schering A G); pan-ErbB inhibitors such as C1-1033 (Pfizer); Affinitac (ISIS 3521; Isis/Lilly); Imatinib mesylate (STI571, Gleevec®; Novartis); PKI 166 (Novartis); GW2016 (Glaxo SmithKline); C1-1033 (Pfizer); EKB-569 (Wyeth); Semaxinib (Sugen); ZD6474 (AstraZeneca); PTK-787 (Novartis/Schering AG); INC-1C11 (Imclone); or as described in any of the following patent publications: U.S. Pat. No. 5,804,396; PCT WO 99/09016 (American Cyanimid); PCT WO 98/43960 (American Cyanamid); PCT WO 97/38983 (Warner-Lambert); PCT WO 99/06378 (Warner-Lambert); PCT WO 99/06396 (Warner-Lambert); PCT WO 96/30347 (Pfizer, Inc); PCT WO 96/33978 (AstraZeneca); PCT WO96/3397 (AstraZeneca); PCT WO 96/33980 (AstraZeneca), gefitinib (IRESSA™, ZD1839, AstraZeneca), and OSI-774 (Tarceva™, OSI Pharmaceuticals/Genentech).

[0341] In another embodiment, the Fc variant is administered with one or more immunomodulatory agents. Such agents may increase or decrease production of one or more cytokines, up- or down-regulate self-antigen presentation, mask MHC antigens, or promote the proliferation, differentiation, migration, or activation state of one or more types of immune cells. Immunomodulatory agents include but not limited to: non-steroidal anti-inflammatory drugs (NSAIDs) such as asprin, ibuprofed, celecoxib, diclofenac, etodolac, fenoprofen, indomethacin, ketoralac, oxaprozin, nabumentone, sulindac, tolmentin, rofecoxib, naproxen, ketoprofen, and nabumetone; steroids (eg. glucocorticoids, dexamethasone, cortisone, hydroxycortisone, methylprednisolone, prednisone, prednisolone, trimcinolone, azulfidine-icosanoids such as prostaglandins, thromboxanes, and leukotrienes; as well as topical steroids such as anthralin, calcipotriene, clobetasol, and tazarotene); cytokines such as TGFb, IFNa, IFNb, IFNg, IL-2, IL-4, IL-10; cytokine, chemokine, or receptor antagonists including antibodies, soluble receptors, and receptor-Fc fusions against BAFF, B7, CCR2, CCR5, CD2, CD3, CD4, CD6, CD7, CD8, CD11, CD14, CD15, CD17, CD18, CD20, CD23, CD28, CD40, CD40L, CD44, CD45, CD52, CD64, CD80, CD86, CD147, CD152, complement factors (C5, D) CTLA4, eotaxin, Fas, ICAM, ICOS, IFNα, IFNβ, IFNγ, IFNAR, IgE, IL-1, IL-2, IL-2R, IL-4, IL-5R, IL-6, IL-8, IL-9 IL-12, IL-13, IL-13R1, IL-15, IL-18R, IL-23, integrins, LFA-1, LFA-3, MHC, selectins, TGFβ, TNFα, TNFβ, TNF-R1, T-cell receptor, including Enbrel® (etanercept), Humira® (adalimumab), and Remicade® (infliximab); heterologous anti-lymphocyte globulin; other immunomodulatory molecules such as 2-amino-6-aryl-5 substituted pyrimidines, anti-idiotypic antibodies for MHC binding peptides and MHC fragments, azathioprine, brequinar, bromocryptine, cyclophosphamide, cyclosporine A, D-penicillamine, deoxyspergualin, FK506, glutaraldehyde, gold, hydroxychloroquine, leflunomide, malononitriloamides (eg. leflunomide), methotrexate, minocycline, mizoribine, mycophenolate mofetil, rapamycin, and sulfasasazine.

[0342] In an alternate embodiment, Fc variants of the present invention are administered with a cytokine. By "cytokine" as used herein is meant a generic term for proteins released by one cell population that act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, and traditional polypeptide hormones. Included among the cytokines are growth hormone such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; fibroblast growth factor; prolactin; placental lactogen; tumor necrosis factor-alpha and -beta; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-beta; platelet-growth factor; transforming growth factors (TGFs) such as TGF-alpha and TGF-beta; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-alpha, beta, and -gamma; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1alpha, IL-2, IL-3, IL4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; IL-15, a tumor necrosis factor such as TNF-alpha or TNF-beta; and other polypeptide factors including LIF and kit ligand (KL). As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture, and biologically active equivalents of the native sequence cytokines.

[0343] In a preferred embodiment, cytokines or other agents that stimulate cells of the immune system are co-administered with an Fc variant of the present invention. Such a mode of treatment may enhance desired effector function. For example, agents that stimulate NK cells, including but not limited to IL-2 may be co-administered. In another embodiment, agents that stimulate macrophages, including but not limited to C5a, formyl peptides such as N-formyl-methionyl-leucyl-phenylalanine (Beigier-Bompadre et. al. (2003) Scand. J. Immunol. 57: 221-8), may be co-administered. Also, agents that stimulate neutrophils, including but not limited to G-CSF, GM-CSF, and the like may be administered. Furthermore, agents that promote migration of such immunostimulatory cytokines may be used. Also additional agents including but not limited to interferon gamma, IL-3 and IL-7 may promote one or more effector functions. In an alternate embodiment, cytokines or other agents that inhibit effector cell function are co-administered with an Fc variant of the present invention. Such a mode of treatment may limit unwanted effector function.

[0344] In an additional embodiment, the Fc variant is administered with one or more antibiotics, including but not limited to: aminoglycoside antibiotics (eg. apramycin,

arbekacin, bambermycins, butirosin, dibekacin, gentamicin, kanamycin, neomycin, netilmicin, paromomycin, ribostamycin, sisomycin, spectrinomycin), aminocyclitols (eg. sprctinomycin), amphenicol antibiotics (eg. azidamfenicol, chloramphenicol, florfrnicol, and thiamphemicol), ansamycin antibiotics (eg. rifamide and rifampin), carbapenems (eg. imipenem, meropenem, panipenem); cephalosporins (eg. cefaclor, cefadroxil, cefamandole, cefatrizine, cefazedone, cefozopran, cefpimizole, cefpiramide, cefpirome, cefprozil, cefuroxine, cefixime, cephalexin, cephradine), cephamycins (cefbuperazone, cefoxitin, cefminox, cefmetazole, and cefotetan); lincosamides (eg. clindamycin, lincomycin); macrolide (eg. azithromycin, brefeldin A, clarithromycin, erythromycin, roxithromycin, tobramycin), monobactams (eg. aztreonam, carumonam, and tigernonam); mupirocin; oxacephems (eg. flomoxef, latamoxef, and moxalactam); penicillins (eg. amdinocillin, amdinocillin pivoxil, amoxicillin, bacampicillin, bexzylpenicillinic acid, benzylpenicillin sodium, epicillin, fenbenicillin, floxacillin, penamecillin, penethamate hydriodide, penicillin o-benethamine, penicillin 0, penicillin V, penicillin V benzoate, penicillin V hydrabamine, penimepicycline, and phencihicillin potassium); polypeptides (eg. bacitracin, colistin, polymixin B, teicoplanin, vancomycin); quinolones (amifloxacin, cinoxacin, ciprofloxacin, enoxacin, enrofloxacin, feroxacin, flumequine, gatifloxacin, gemifloxacin, grepafloxacin, lomefloxacin, moxifloxacin, nalidixic acid, norfloxacin, ofloxacin, oxolinic acid, pefloxacin, pipemidic acid, rosoxacin, rufloxacin, sparfloxacin, temafloxacin, tosufloxacin, trovafloxacin); rifampin; streptogramins (eg. quinupristin, dalfopristin); sulfonamides (sulfanilamide, sulfamethoxazole); tetracyclenes (chlortetracycline, demeclocycline hydrochloride, demethylchlortetracycline, doxycycline, duramycin, minocycline, neomycin, oxytetracycline, streptomycin, tetracycline, vancomycin).

[0345] Anti-fungal agents such as amphotericin B, ciclopirox, clotrimazole, econazole, fluconazole, flucytosine, itraconazole, ketoconazole, niconazole, nystatin, terbinafine, terconazole, and tioconazole may also be used.

[0346] Antiviral agents including protease inhibitors, reverse transcriptase inhibitors, and others, including type I interferons, viral fusion inhibitors, and neuramidase inhibitors, may also be used. Examples of antiviral agents include, but are not limited to, acyclovir, adefovir, amantadine, amprenavir, clevadine, enfuvirtide, entecavir, foscarnet, gangcyclovir, idoxuridine, indinavir, lopinavir, pleconaril, ribavirin, rimantadine, ritonavir, saquinavir, trifluridine, vidarabine, and zidovudine, may be used.

[0347] The Fc variants of the present invention may be combined with other therapeutic regimens. For example, in one embodiment, the patient to be treated with an antibody or Fc fusion of the present invention may also receive radiation therapy. Radiation therapy can be administered according to protocols commonly employed in the art and known to the skilled artisan. Such therapy includes but is not limited to cesium, iridium, iodine, or cobalt radiation. The radiation therapy may be whole body irradiation, or may be directed locally to a specific site or tissue in or on the body, such as the lung, bladder, or prostate. Typically, radiation therapy is administered in pulses over a period of time from about 1 to 2 weeks. The radiation therapy may, however, be administered over longer periods of time. For instance, radiation therapy may be administered to patients having head and neck cancer for about 6 to about 7 weeks. Optionally, the radiation therapy may be administered as a single dose or as multiple, sequential doses. The skilled medical practitioner can determine empirically the appropriate dose or doses of radiation therapy useful herein. In accordance with another embodiment of the invention, the Fc variant of the present invention and one or more other anti-cancer therapies are employed to treat cancer cells ex vivo. It is contemplated that such ex vivo treatment may be useful in bone marrow transplantation and particularly, autologous bone marrow transplantation. For instance, treatment of cells or tissue(s) containing cancer cells with Fc variant and one or more other anti-cancer therapies, such as described above, can be employed to deplete or substantially deplete the cancer cells prior to transplantation in a recipient patient.

[0348] Radiation therapy may also comprise treatment with an isotopically labeled molecule, such as an antibody. Examples of radioimmunotherapeutics include but Zevalin™ (Y-90 labeled anti-CD20), LymphoCide™ (Y-90 labeled anti-CD22) and Bexxar™ (I-131 labeled anti-CD20)

[0349] It is of course contemplated that the Fc variants of the invention may employ in combination with still other therapeutic techniques such as surgery or phototherapy.

Clinical Trial Design and Post-Approval Treatment Strategies

[0350] Pharmacogenomic approaches to clinical trials abd therapy are embodiments of the present invention. A number of the receptors that may interact with the Fc variants of the present invention are polymorphic in the human population. For a given patient or population of patients, the efficacy of the Fc variants of the present invention may be affected by the presence or absence of specific polymorphisms in proteins. For example, FcγRIIIs is polymorphic at position 158, which is commonly either V (high affinity) or F (low affinity). Patients with the V/V homozygous genotype are observed to have a better clinical response to treatment with the anti-CD20 antibody Rituxan® (rituximab) (Carton et al., 2002, Blood 99:754-758; Weng et al., 2003, J Clin Oncol 21:3940-3947; Dall'Ozzo et al., 2004, Cancer Res 64:4664-9). Additional polymorphisms include but are not limited to FcγRIIa R131 or H131, and such polymorphisms are known to either increase or decrease Fc binding and subsequent biological activity, depending on the polymorphism. Fc variants of the present invention may bind preferentially to a particular polymorphic form of a receptor, for example F158 FcγRIIIa, or to bind with equivalent affinity to all of the polymorphisms at a particular position in the receptor, for example both the V158 and F158 polymorphisms of FcγRIIIa. In a preferred embodiment, Fc variants of the present invention that provide equivalent binding to polymorphisms may be used in an antibody to eliminate the differential efficacy seen in patients with different polymorphisms. Such a property may give greater consistency in therapeutic response and reduce non-responding patient populations. Such variant Fc with identical binding to receptor polymorphisms may have increased biological activity, such as ADCC, CDC or circulating half-life, or alternatively decreased activity, via modulation of the binding to the relevant Fc receptors. In a preferred embodiment, Fc variants of the present invention may bind with higher or lower affinity to one of the polymorphisms of a receptor, either accentuating the existing difference in binding or reversing the difference. Such a property may allow creation of therapeutics particularly tailored for efficacy with a patient population possessing such polymorphism. For example, a patient population pos-

sessing an FcγRIIb polymorphism that binds with higher affinity to Fc, could receive a drug containing an Fc variant with reduced binding to such polymorphic form of the receptor, creating a more efficacious drug.

[0351] In a preferred embodiment, patients are screened for one or more polymorphisms in order to predict the efficacy of the Fc variants of the present invention. This information may be used, for example, to select patients to include or exclude from clinical trials or, post-approval, to provide guidance to physicians and patients regarding appropriate dosages and treatment options. For example, the anti-CD20 antibody rituximab is minimally effective in patients that are homozygous or heterozygous for F158 FcγRIIa (Carton et al., 2002, Blood 99:754-758; Weng et al., 2003, J Clin Oncol 21:3940-3947; Dall'Ozzo et al., 2004, Cancer Res 64:4664-9). Such patients may show an improved clinical response to antibodies comprising an Fc variant of the present invention. In one embodiment, patients are selected for inclusion in clinical trials if their genotype indicates that they are likely to respond significantly better to an antibody of the present invention as compared to one or more currently used antibody therapeutics. In another embodiment, appropriate dosages and treatment regimens are determined using such genotype information. In another embodiment, patients are selected for inclusion in a clinical trial or for receipt of therapy post-approval based on their polymorphism genotype, where such therapy contains an Fc variant engineered to be specifically efficacious for such population, or alternatively where such therapy contains an Fc variant that does not show differential activity to the different forms of the polymorphism.

[0352] Included in the present invention are diagnostic tests to identify patients who are likely to show a favorable clinical response to an Fc variant of the present invention, or who are likely to exhibit a significantly better response when treated with an Fc variant of the present invention versus one or more currently used antibody therapeutics. Any of a number of methods for determining FcγR polymorphisms in humans known in the art may be used.

[0353] In a preferred embodiment, patients are screened to predict the efficacy of the Fc polypeptides of the present invention. This information may be used, for example, to select patients to include or exclude from clinical trials or, post-approval, to provide guidance to physicians and patients regarding appropriate dosages and treatment options. Screening may involve the determination of the expression level or distribution of the target antigen. For example, the level of Her2/neu expression is currently used to select which patients will most favorably respond to trastuzumab therapy. Screening may also involve determination of genetic polymorphisms, for example polymorphisms related to FcγRs or FcαRs. For example, patients who are homozygous or heterozygous for the F158 polymorphic form of FcγRIIIa may respond clinically more favorably to the Fc polypeptides of the present invention. Information obtained from patient screening may be used to select patients for inclusion in clinical trials, to determine appropriate dosages and treatment regimens, or for other clinical applications. Included in the present invention are diagnostic tests to identify patients who are likely to show a favorable clinical response to an Fc polypeptide of the present invention, or who are likely to exhibit a significantly better response when treated with an Fc polypeptide of the present invention versus one or more currently used biotherapeutics. Any of a number of methods for determining antigen expression levels, antigen distribution, and/or genetic polymorphisms in humans known in the art may be used.

[0354] Furthermore, the present invention comprises prognostic tests performed on clinical samples such as blood and tissue samples. Such tests may assay for effector function activity, including but not limited to opsonization, ADCC, CDC, ADCP, or for killing, regardless of mechanism, of cancerous or otherwise pathogenic cells. In a preferred embodiment, ADCC assays, such as those described herein, are used to predict, for a specific patient, the efficacy of a given Fc polypeptide of the present invention. Such information may be used to identify patients for inclusion or exclusion in clinical trials, or to inform decisions regarding appropriate dosages and treatment regemins. Such information may also be used to select a drug that contains a particular Fc variant that shows superior activity in such an assay.

EXAMPLES

[0355] Examples are provided below to illustrate the present invention. These examples are not meant to constrain the present invention to any particular application or theory of operation.

[0356] For all positions discussed in the present invention, numbering is according to the EU index or EU numbering scheme (Kabat et al., 1991, *Sequences of Proteins of Immunological Interest,* 5th Ed., United States Public Health Service, National Institutes of Health, Bethesda), which refers to the numbering of the EU antibody (Edelman et al., 1969, Proc Natl Acad Sci USA 63:78-85). Those skilled in the art of antibodies will appreciate that these conventions consist of nonsequential numbering in specific regions of an immunoglobulin sequence, enabling a normalized reference to conserved positions in immunoglobulin families. Accordingly, the positions of any given immunoglobulin as defined by EU index will not necessarily correspond to its sequential sequence. FIG. **3** shows the sequential and EU index numbering schemes for the antibody alemtuzumab in order to illustrate this principal more clearly. It should also be noted that polymorphisms have been observed at a number of Fc positions, including but not limited to Kabat 270, 272, 312, 315, 356, and 358, and thus slight differences between the presented sequence and sequences in the scientific literature may exist.

[0357] Fc variants and Fc variant libraries were designed using computational- and sequence-based methods as described in U.S. Ser. No. 10/672,280 and U.S. Ser. No. 10/822,231. Experimental libraries were designed in successive rounds of computational and experimental screening. Design of subsequent Fc libraries benefited from feedback from prior libraries, and thus typically comprised combinations of Fc variants that showed favorable properties in the previous screen. FIG. **4** shows residues at which amino acid modifications were made in the Fc variants of the present invention, mapped onto the human Fc/FcγRIIIb structure. The entire set of Fc variants that were constructed and experimentally tested is shown in FIG. **41**.

Example 1

Molecular Biology and Protein Expression/Purification

[0358] The majority of experimentation on the Fc variants was carried out in the context of the anti-cancer antibody

alemtuzumab (Campath®, a registered trademark of Ilex Pharmaceuticals LP). Alemtuzumab binds a short linear epitope within its target antigen CD52 (Hale et al., 1990, Tissue Antigens 35:118-127; Hale, 1995, *Immunotechnology* 1:175-187). Alemtuzumab has been chosen as the primary engineering template because its efficacy is due in part to its ability to recruit effector cells (Dyer et al., 1989, *Blood* 73:1431-1439; Friend et al., 1991, *Transplant Proc* 23:2253-2254; Hale et al., 1998, *Blood* 92:4581-4590; Glennie et al., 2000, *Immunol Today* 21:403-410), and because production and use of its antigen in binding assays are relatively straightforward. In order to evaluate the optimized Fc variants of the present invention in the context of other antibodies, select Fc variants were evaluated in the anti-Her2 antibody trastuzumab (Herceptin®, a registered trademark of Genentech), the anti-CD20 antibody rituximab (Rituxan®, a registered trademark of IDEC Pharmaceuticals Corporation), the anti-EGFR antibody cetuximab (Erbitux®, a registered trademark of Imclone), and the anti-CD20 antibody PRO70769 (PCT/US2003/040426, entitled "Immunoglobulin Variants and Uses Thereof"). The use of alemtuzumab, trastuzumab, rituximab, cetuximab, and PRO70769 for screening purposes is not meant to constrain the present invention to any particular antibody.

[0359] The IgG1 full length light (V_L-C_L) and heavy (V_H-Cγ1-Cγ2-Cγ3) chain antibody genes for alemtuzumab (campath-1H, James et al., 1999, *J Mol Biol* 289: 293-301), trastuzumab (hu4D5-8; Carter et al., 1992, *Proc Nat Acad Sci USA* 89:4285-4289; Gerstner et al., 2002, *J. Mol. Biol.*, 321: 851-862), rituximab (C2B8, U.S. Pat. No. 6,399,061), and cetuximab (C225, PCT US96/09847) were constructed using recursive PCR with convenient end restriction sites to facilitate subcloning. The genes were ligated into the mammalian expression vector pcDNA3.1Zeo (Invitrogen), comprising the full length light kappa (CK) and heavy chain IgG1 constant regions. The V_H-Cγ1-Cγ2-Cγ3 clone in pcDNA3.1zeo was used as a template for mutagenesis of the Fc region. Mutations were introduced into this clone using PCR-based mutagenesis or quick-change mutagenesis (Stratagene) techniques. Fc variants were sequenced to confirm the fidelity of the sequence. Plasmids containing heavy chain gene (V_H-Cγ1-Cγ2-Cγ3) (wild-type or variants) were co-transfected with plasmid containing light chain gene (V_L-C_L) into 293T cells. Media were harvested 5 days after transfection. Expression of immunoglobulin was monitored by screening the culture supernatant of transfectomas by western using peroxidase-conjugated goat-anti human IgG (Jackson ImmunoResearch, catalog #109-035-088). FIG. **5** shows expression of wild-type alemtuzumab and variants 1 through 10 in 293T cells. Antibodies were purified from the supernatant using protein A affinity chromatography (Pierce, Catalog #20334. FIG. **6** shows results of the protein purification for WT alemtuzumab. Antibody Fc variants showed similar expression and purification results to WT. Some Fc variants were deglycosylated in order to determine their solution and functional properties in the absence of carbohydrate. To obtain deglycosylated antibodies, purified alemtuzumab antibodies were incubated with peptide-N-glycosidase (PNGase F) at 37° C. for 24 h. FIG. **7** presents an SDS PAGE gel confirming deglycosylation for several Fc variants and WT alemtuzumab.

[0360] In order to confirm the functional fidelity of alemtuzumab produced under these conditions, the antigenic CD52 peptide, fused to GST, was expressed in *E. coli* BL21 (DE3) under IPTG induction. Both un-induced and induced samples were run on a SDS PAGE gel, and transferred to PVDF membrane. For western analysis, either alemtuzumab from Sotec (final concentration 2.5 ng/ul) or media of transfected 293T cells (final alemtuzumab concentration about 0.1-0.2 ng/ul) were used as primary antibody, and peroxidase-conjugated goat-anti human IgG was used as secondary antibody. FIG. **8** presents these results. The ability to bind target antigen confirms the structural and functional fidelity of the expressed alemtuzumab. Fc variants that have the same variable region as WT alemtuzumab are anticipated to maintain a comparable binding affinity for antigen.

[0361] The gene encoding the extracellular region of human V158 FcγRIIIa was obtained by PCR from a clone obtained from the Mammalian Gene Collection (MGC: 22630). F158 FcγRIIIa was constructed by mutagenesis of the V158 FcγRIIIa gene. The genes encoding the extracellular regions of human FcγRI, human FcγRIIa, human FcγRIIb, human FcγRIIc, mouse FcγRIII, and human FcRn α chain and β-microglobulin chain were constructed using recursive PCR. FcγRs and FcRn α chain were fused at the C-terminus with a 6×His-tag and a GST-tag. All genes were subcloned into the pcDNA3.1zeo vector. For expression, vectors containing human FcγRs were transfected into 293T cells, FcRn a chain and β-microglobulin chain were co-transfected into 293T cells, and mouse FcγRIII was transfected into NIH3T3 cells. Media containing secreted receptors were harvested 3 days later and purified using Nickel affinity chromatography. For western analysis, membrane was probed with an anti-GST antibody. FIG. **9** presents an SDS PAGE gel that shows the results of expression and purification of human V158 FcγRIIIa. Purified human C1q protein complex was purchased commercially (Quidel Corp., San Diego).

Example 2

Fc Ligand Binding Assays

[0362] Binding to the human Fc ligands FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, C1q, and FcRn was measured for the designed Fc variants. Binding affinities were measured using an AlphaScreen™ assay (Amplified Luminescent Proximity Homogeneous Assay (ALPHA), PerkinElmer, Wellesley, Mass.), a bead-based luminescent proximity assay. Laser excitation of a donor bead excites oxygen, which if sufficiently close to the acceptor bead generates a cascade of chemiluminescent events, ultimately leading to fluorescence emission at 520-620 nm. WT alemtuzumab antibody was biotinylated by standard methods for attachment to streptavidin donor beads, and GST-tagged FcγRs and FcRn were bound to glutathione chelate acceptor beads. For the C1q binding assay, untagged C1q protein was conjugated with Digoxygenin (DIG, Roche) using N-hydrosuccinimide (NHS) chemistry and bound to DIG acceptor beads. For the protein A binding assay, protein A acceptor beads were purchased directly from PerkinElmer. The AlphaScreen assay was applied as a competition assay for screening Fc variants. In the absence of competing Fc variants, WT antibody and FcγR interact and produce a signal at 520-620 nm. Addition of untagged Fc variant competes with the WT Fc/FcγR interaction, reducing fluorescence quantitatively to enable determination of relative binding affinities. Fc variants were screened in the context of either alemtuzumab or trastuzumab, and select Fc variants were also screened in the context of rituximab and cetuximab.

[0363] FIG. **10** shows AlphaScreen data for binding to human V158 FcγRIIIa by select Fc variants. The binding data were normalized to the maximum and minimum luminescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The data were fit to a one site competition model using nonlinear regression, and these fits are represented by the curves in the figure. These fits provide the inhibitory concentration 50% (IC50) (i.e. the concentration required for 50% inhibition) for each antibody, illustrated by the dotted lines in FIG. **10**, thus enabling the relative binding affinities of Fc variants to be quantitatively determined. By dividing the IC50 for each variant by that of WT alemtuzumab, the fold-enhancement or reduction relative to WT Herceptin (Fold WT) are obtained. Here, WT alemtuzumab has an IC50 of $(4.63\times10^{-9})_x(2)$=9.2 nM, whereas S239D has an IC50 of $(3.98\times10^{-10})\times(2)$=0.8 nM. Thus S239D alemtuzumab binds 9.2 nM/0.8 nM=11.64-fold more tightly than WT alemtuzumab to human V158 FcγRIIIa. FIGS. **11***a* and **11***b* provide AlphaScreen data showing additional Fc variants, with substitutions at positions 239, 264, 272, 274, and 332, that bind more tightly to FcγRIIIa, and thus are candidates for improving the effector function of Fc polypeptides.

[0364] Fc variants were also screened in parallel for other Fc ligands. As discussed, the inhibitory receptor FcγRIIb plays an important role in effector function. Exemplary data for binding of select Fc variants of the invention to human FcγRIIb, as measured by the AlphaScreen, are provided in FIG. **12**. FcγRIIa is an activating receptor that is highly homologous to FcγRIIb. Exemplary data for binding of select Fc variants to the R131 polymorphic form of human FcγRIIa are provided in FIG. **13**. Another important Fc ligand is the neonatal Fc receptor FcRn. As discussed, this receptor binds to the Fc region between the Cγ2 and Cγ3 domains; because binding mediates endosomal recycling, affinity of Fc for FcRn is a key determinant of antibody and Fc fusion pharmacokinetics. Exemplary data showing binding of select Fc variants to FcRn, as measured by the AlphaScreen, are provided in FIG. **14**. The binding site for FcRn on Fc, between the Cγ2 and Cγ3 domains, is overlapping with the binding site for bacterial proteins A and G. Because protein A is frequently employed for antibody purification, select variants were tested for binding to this Fc ligand. FIG. **15** provides these AlphaScreen data. Although protein A was not included in the parallel screen for all variants, the ability of the Fc variants to be purified using protein A chromatography (see Example 1) implies that for the majority of Fc variants the capacity to bind protein A, and moreover the integrity of the Cγ2-Cγ3 hinge region, are unaffected by the Fc substitutions.

[0365] The data for binding of Fc variants to FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, C1q, and FcRn were analyzed as described above for FIG. **11**. The fold-enhancement or reduction relative to WT for binding of each variant to each Fc ligand, as measured by the AlphaScreen, are provided in FIG. **41**. The table presents for each variant the variant number (Variant), the substitution(s) of the variant, the antibody context (Context), the fold affinity relative to WT (Fold) and the confidence (Conf) in the fold affinity for binding to each Fc ligand, and the IIIa:IIb specificity ratio (IIIa:IIb) (see below). Multiple data sets were acquired for many of the variants, and all data for a given variant are grouped together. The context of the antibody indicates which antibodies have been constructed with the particular Fc variant; a=alemtuzumab, t=trastuzumab, r=rituximab, c=cetuximab, and p=PRO70769. The data provided were acquired in the context of the first antibody listed, typically alemtuzumab, although in some cases trastuzumab. An asterix (*) indicates that the data for the given Fc ligand was acquired in the context of trastuzumab. A fold (Fold) above 1 indicates an enhancement in binding affinity, and a fold below 1 indicates a reduction in binding affinity relative to the parent antibody for the given Fc ligand. Confidence values (Conf) correspond to the log confidence levels, provided from the fits of the data to a sigmoidal dose response curve. As is known in the art, a lower Conf value indicates lower error and greater confidence in the Fold value. The lack of data for a given variant and Fc ligand indicates either that the fits to the data did not provide a meaningful value, or that the variant was not tested for that Fc ligand.

[0366] FIG. **41** shows that a number of Fc variants have been obtained with enhanced affinities and altered specificities for the various Fc ligands. Some Fc variants of the present invention provide selective enhancement in binding affinity to different Fc ligands, whereas other provide selective reduction in binding affinity to different Fc ligands. By "selective enhancement" as used herein is meant an improvement in or a greater improvement in binding affinity of an Fc variant to one or more Fc ligands relative to one or more other Fc ligands. For example, for a given variant, the Fold WT for binding to, say FcγRIIa, may be greater than the Fold WT for binding to, say FcγRIIb. By "selective reduction" as used herein is meant a reduction in or a greater reduction in binding affinity of an Fc variant to one or more Fc ligands relative to one or more other Fc ligands. For example, for a given variant, the Fold WT for binding to, say FcγRI, may be lower than the Fold WT for binding to, say FcγRIIb. As an example of such selectivity, G236S provides a selective enhancement to FcγRII's (IIa, IIb, and IIc) relative to FcγRI and FcγRIIIa, with a somewhat greater enhancement to FcγRIIa relative to FcγRIIb and FcγRIIc. G236A, however, is highly selectively enhanced for FcγRIIa, not only with respect to FcγRI and FcγRIIIa, but also over FcγRIIb and FcγRIIc. Selective enhancements and reductions are observed for a number of Fc variants, including but not limited to variants comprising substitutions at residues L234, L235, G236, S267, H268, R292, E293, Q295, Y300, S324, A327, L328, A330, and T335. Overall, the data provided in FIG. **41** show that it is indeed possible to tune the Fc region for Fc ligand specificity, often by using very subtle mutational differences, despite the fact that a number of highly homologous receptors bind to the same FcγR binding site. The present invention provides a number of Fc variants that may be used to selectively enhance, as well as selectively reduce, affinity of an Fc polypeptide for certain Fc ligands relative to others. Collections of Fc variants such as these will not only enable the generation of antibodies and Fc fusions that have effector function tailored for the desired outcome, but they also provide a unique set of reagents with which to experimentally investigate and characterize effector function biology.

[0367] As discussed, optimal effector function may result from Fc variants wherein affinity for activating FcγRs is greater than affinity for the inhibitory FcγRIIb. Indeed a number of Fc variants have been obtained that show differentially enhanced binding to FcγRIIIa over FcγRIIb. AlphaScreen data directly comparing binding to FcγRIIIa and FcγRIIb for two Fc variants with this specificity profile, A330L and A330Y, are shown in FIGS. **16***a* and **16***b*. This concept can be defined quantitatively as the fold-enhancement or -reduction

of the activating FcγRIIIa (FIG. **41**, column 12) divided by the fold-enhancement or -reduction of the inhibitory FcγRIIb (FIG. **41**, column 8), herein referred to as the "FcγRIIIa-fold: FcγRIIb-fold ratio" or "IIIa:IIb ratio". This value is provided in column 18 of FIG. **41** (as IIIa:IIb). Combination of A330L and A330Y with other variants, for example A330L/I332E, A330Y/I332, and S239D/A330L/I332E, provide very favorable IIIa:IIb ratios. FIG. **41** shows that a number of Fc variants provide a positive, favorable FcγRIIIa to FcγRIIb specificity profile, with a IIIa:IIb ratio as high as 86:1.

[0368] Some of the most promising Fc variants of the present invention for enhancing effector function have both substantial increases in affinity for FcγRIIIa and favorable FcγRIIIa-fold:FcγRIIb-fold ratios. These include, for example, S239D/I332E (FcγRIIIa-fold=56-192, FcγRIIIa-fold:FcγRIIb-fold=3), S239D/A330Y/I332E (FcγRIIIa-fold=130), S239D/A330Y/I332E (FcγRIIa-fold=139, FcγRIIIa-fold:FcγRIIb-fold=18), and S239D/S298A/I332E (FcγRIIIa-fold=295, FcγRIIIa-fold:FcγRIIb-fold=48). FIGS. **17***a*-**17***c* show AlphaScreen data monitoring binding of these and other Fc variants in the context of trastuzumab to human V158 FcγRIIIa and human FcγRIIb.

[0369] In addition to alemtuzumab and trastuzumab, select Fc variants were screened in the context of other antibodies in order to investigate the breadth of their applicability. AlphaScreen data measuring binding of select Fc variants to human V158 FcγRIIIa in the context of rituximab and cetuximab are shown in FIG. **18** and FIG. **19** respectively. Together with the data shown previously for alemtuzumab and trastuzumab, the results indicate consistent binding enhancements regardless of the antibody context, and thus that the Fc variants of the present invention are broadly applicable to antibodies and Fc fusions.

[0370] As discussed above, an important parameter of Fc-mediated effector function is the affinity of Fc for both V158 and F158 polymorphic forms of FcγRIIIa. AlphaScreen data comparing binding of select variants to the two receptor allotypes are shown in FIG. **20***a* (V158 FcγRIIIa) and FIG. **20***b* (F158 FcγRIIIa). As can be seen, all variants improve binding to both FcγRIIIa allotypes. These data indicate that those Fc variants of the present invention with enhanced effector function will be broadly applicable to the entire patient population, and that enhancement to clinical efficacy will potentially be greatest for the low responsive patient population who need it most.

[0371] The FcγR binding affinities of these Fc variants were further investigated using Surface Plasmon Resonance (SPR) (Biacore, Uppsala, Sweden). SPR is a sensitive and extremely quantitative method that allows for the measurement of binding affinities of protein-protein interactions, and has been used to effectively measure Fc/FcγR binding (Radaev et al., 2001, *J Biol Chem* 276:16478-16483). SPR thus provides an excellent complementary binding assay to the AlphaScreen assay. His-tagged V158 FcγRIIIa was immobilized to an SPR chip, and WT and Fc variant alemtuzumab antibodies were flowed over the chip at a range of concentrations. Binding constants were obtained from fitting the data using standard curve-fitting methods. Table 3 presents dissociation constants (Kd) for binding of select Fc variants to V158 FcγRIIIa and F158 FcγRIIIa obtained using SPR, and compares these with IC50s obtained from the AlphaScreen assay. By dividing the Kd and IC50 for each variant by that of WT alemtuzumab, the fold-improvements over WT (Fold WT) are obtained.

TABLE 3

	SPR V158 FcγRIIIa		SPR F158 FcγRIIIa		AlphaScreen V158 FcγRIIIa		AlphaScreen F158 FcγRIIIa	
	Kd (nM)	Fold WT	Kd (nM)	Fold WT	IC50 (nM)	Fold WT	IC50 (nM)	Fold WT
WT	68		730		6.4		17.2	
V264I	64	1.1	550	1.3	4.5	1.4	11.5	1.5
I332E	31	2.2	72	10.1	1.0	6.4	2.5	6.9
V264I/I332E	17	4.0	52	14.0	0.5	12.8	1.1	15.6
S298A	52	1.3	285	2.6	2.9	2.2	12.0	1.4
S298A/ E333A/ K334A	39	1.7	156	4.7	2.5	2.6	7.5	2.3

[0372] The SPR data corroborate the improvements to FcγRIIIa affinity observed by AlphaScreen assay. Table 3 further indicates the superiority of V264I/I332E and I332E over S298A and S298A/E333A/K334A; whereas S298A/E333A/K334A improves Fc binding to V158 and F158 FcγRIIIa by 1.7-fold and 4.7-fold respectively, I332E shows binding enhancements of 2.2-fold and 10.1-fold respectively, and V264I/I332E shows binding enhancements of 4.0-fold and 14-fold respectively. Also worth noting is that the affinity of V264I/I332E for F158 FcγRIIIa (52 nM) is better than that of WT for the V158 allotype (68 nM), suggesting that this Fc variant, as well as those with even greater improvements in binding, may enable the clinical efficacy of antibodies for the low responsive patient population to achieve that currently possible for high responders. The correlation between the SPR and AlphaScreen binding measurements are shown in FIGS. **21***a*-**21***d*. FIGS. **21***a* and **21***b* show the Kd-IC50 correlations for binding to V158 FcγRIIIa and F158 FcγRIIIa respectively, and FIGS. **21***c* and **21***d* show the fold-improvement correlations for binding to V158 FcγRIIa and F158 FcγRIIIa respectively. The good fits of these data to straight lines (r^2=0.9, r^2=0.84, r^2=0.98, and r^2=0.90) support the accuracy the AlphaScreen measurements, and validate its use for determining the relative FcγR binding affinities of Fc variants.

[0373] SPR data were also acquired for binding of select trastuzumab Fc variants to human V158 FcγRIIIa, F158 FcγRIIIa, and FcγRIIb. These data are shown in Table 4. The Fc variants tested show substantial binding enhancements to the activating receptor FcγRIIIa, with over 100-fold tighter binding observed for interaction of S239D/I332E/S298A with F158 FcγRIIIa. Furthermore, for the best FcγRIIIa binders, F158 FcγRIIIa/FcγRIIb ratios of 3-4 are observed.

TABLE 4

	SPR V158 FcγRIIIa		SPR F158 FcγRIIIa		SPR FcγRIIb	
	Kd (nM)	Fold WT	Kd (nM)	Fold WT	IC50 (nM)	Fold WT
WT	363.5		503		769	
V264I/I332E	76.9	4.7	252	2.0	756	1.0
V264I/I332E/ A330L	113.0	3.2	88	5.7	353	2.2
S239D/I332E/ A330L	8.2	44.3	8.9	56.5	46	16.7
S239D/I332E/ S298A	8.7	41.8	4.9	102.7	32	24.0

TABLE 4-continued

	SPR V158 FcγRIIIa		SPR F158 FcγRIIIa		SPR FcγRIIb	
	Kd (nM)	Fold WT	Kd (nM)	Fold WT	IC50 (nM)	Fold WT
S239D/I332E/ V264I/A330L	12.7	28.6	6.3	79.8	35	22.0

[0374] As discussed, although there is a need for greater effector function, for some antibody therapeutics, reduced or eliminated effector function may be desired. Several Fc variants in FIG. **41** substantially reduce or ablate FcγR binding, and thus may find use in antibodies and Fc fusions wherein effector function is undesirable. AlphaScreen data measuring binding of some exemplary Fc variants to human V158 FcγRIIIa are shown in FIGS. **22***a* and **22***b*. These Fc variants, as well as their use in combination, may find use for eliminating effector function when desired, for example in antibodies and Fc fusions whose mechanism of action involves blocking or antagonism but not killing of the cells bearing target antigen. Based on the data provided in FIG. **41**, preferred positions for reducing Fc ligand binding and/or effector function, that is positions that may be modified to reduce binding to one or more Fc ligands and/or reduce effector function, include but are not limited to positions 232, 234, 235, 236, 237, 239, 264, 265, 267, 269, 270, 299, 325, 328, 329, and 330.

Example 3

ADCC of Fc Variants

[0375] In order to determine the effect on effector function, cell-based ADCC assays were performed on select Fc variants. ADCC was measured using the DELFIA® EuTDA-based cytotoxicity assay (Perkin Elmer, MA) with purified human peripheral blood monocytes (PBMCs) as effector cells. Target cells were loaded with BATDA at 1×10^6 cells/ml, washed 4 times and seeded into 96-well plate at 10,000 cells/well. The target cells were then opsonized using Fc variant or WT antibodies at the indicated final concentration. Human PBMCs, isolated from buffy-coat were added at the indicated fold-excess of target cells and the plate was incubated at 37° C. for 4 hrs. The co-cultured cells were centrifuged at 500×g, supernatants were transferred to a separate plate and incubated with Eu solution, and relative fluorescence units were measured using a Packard Fusion™ α-FP HT reader (Packard Biosciences, IL). Samples were run in triplicate to provide error estimates (n=3, +/−S.D.). PBMCs were allotyped for the V158 or F158 FcγRIIIa allotype using PCR.

[0376] ADCC assays were run on Fc variant and WT alemtuzumab using DoHH-2 lymphoma target cells. FIG. **23***a* is a bar graph showing the ADCC of these proteins at 10 ng/ml antibody. Results show that alemtuzumab Fc variants I332E, V264I, and I332E/V264I have substantially enhanced ADCC compared to WT alemtuzumab, with the relative ADCC enhancements proportional to their binding improvements to FcγRIIIa as indicated by AlphaScreen assay and SPR. The dose dependence of ADCC on antibody concentration is shown in FIG. **23***b*. The binding data were normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The data were fit to a sigmoidal dose-response model using nonlinear regression, represented by the curve in the figure. The fits enable determination of the effective concentration 50% (EC50) (i.e. the concentration required for 50% effectiveness), which provides the relative enhancements to ADCC for each Fc variant. The EC50s for these binding data are analogous to the IC50s obtained from the AlphaScreen competition data, and derivation of these values is thus analogous to that described in Example 2 and FIG. **11**. In FIG. **23***b*, the log(EC50)s, obtained from the fits to the data, for WT, V264I/I332E, and S239D/I332E alemtuzumab are 0.99, 0.60, and 0.49 respectively, and therefore their respective EC50s are 9.9, 4.0, and 3.0. Thus V264I/I332E and S239E/I332E provide a 2.5-fold and 3.3-fold enhancement respectively in ADCC over WT alemtuzumab using PBMCs expressing heterozygous V158/F158 FcγRIIIa. These data are summarized in Table 5 below.

TABLE 5

	log(EC50)	EC50 (ng/ml)	Fold WT
WT	0.99	9.9	
V264I/I332E	0.60	4.0	2.5
S239D/I332E	0.49	3.0	3.3

[0377] In order to determine whether these ADCC enhancements are broadly applicable to antibodies, select Fc variants were evaluated in the context of trastuzumab and rituximab. ADCC assays were run on Fc variant and WT trastuzumab using two breast carcinoma target cell lines BT474 and Sk-Br-3. FIG. **24***a* shows a bar graph illustrating ADCC at 1 ng/ml antibody. Results indicate that V2641 and V264I/I332E trastuzumab provide substantially enhanced ADCC compared to WT trastuzumab, with the relative ADCC enhancements proportional to their binding improvements to FcγRIIa as indicated by AlphaScreen assay and SPR. FIGS. **24***b* and **24***c* show the dose dependence of ADCC on antibody concentration for select Fc variants. The EC50s obtained from the fits of these data and the relative fold-improvements in ADCC are provided in Table 6 below. Significant ADCC improvements are observed for I332E trastuzumab when combined with A330L and A330Y. Furthermore, S239D/A330L/I332E provides a substantial ADCC enhancement, greater than 300-fold for PBMCs expressing homozygous F158/F158 FcγRIIIa, relative to WT trastuzumab and S298A/E333A/K334A, consistent with the FcγR binding data observed by the AlphaScreen assay and SPR.

TABLE 6

	log (EC50)	EC50 (ng/ml)	Fold WT
FIG. 24b			
WT	1.1	11.5	
I332E	0.34	2.2	5.2
A330Y/I332E	−0.04	0.9	12.8
A330L/I332E	0.04	1.1	10.5
FIG. 24c			
WT	−0.15	0.71	
S298A/E333A/K334A	−0.72	0.20	3.6
S239D/A330L/I332E	−2.65	0.0022	323

[0378] ADCC assays were run on V264I/I332E, WT, and S298A/D333A/K334A rituximab using WIL2-S lymphoma

target cells. FIG. **25***a* presents a bar graph showing the ADCC of these proteins at 1 ng/ml antibody. Results indicate that V264I/I332E rituximab provides substantially enhanced ADCC relative to WT rituximab, as well as superior ADCC to S298A/D333A/K334A, consistent with the FcγRIIIa binding improvements observed by AlphaScreen assay and SPR. FIGS. **25***b* and **25***c* show the dose dependence of ADCC on antibody concentration for select Fc variants. The EC50s obtained from the fits of these data and the relative fold-improvements in ADCC are provided in Table 7 below. As can be seen S239D/I332E/A330L rituximab provides greater than 900-fold enhancement in EC50 over WT for PBMCs expressing homozygous F158/F158 FcγRIIIa. The differences in ADCC enhancements observed for alemtuzumab, trastuzumab, and rituximab are likely due to the use of different PBMCs, different antibodies, and different target cell lines.

TABLE 7

	log (EC50)	EC50 (ng/ml)	Fold WT
FIG. 25b			
WT	0.23	1.7	
S298A/E333A/K334A	−0.44	0.37	4.6
V264I/I332E	−0.83	0.15	11.3
FIG. 25c			
WT	0.77	5.9	
S239D/I332E/A330L	−2.20	0.0063	937

[0379] Thus far, ADCC data has been normalized such that the lower and upper baselines of each Fc polypeptide are set to the minimal and maximal fluorescence signal for that specific Fc polypeptide, typically being the fluorescence signal at the lowest and highest antibody concentrations respectively. Although presenting the data in this matter enables a straightforward visual comparison of the relative EC50s of different antibodies (hence the reason for presenting them in this way), important information regarding the absolute level of effector function achieved by each Fc polypeptide is lost. FIGS. **26***a* and **27***b* present cell-based ADCC data for trastuzumab and rituximab respectively that have been normalized according to the absolute minimal lysis for the assay, provided by the fluorescence signal of target cells in the presence of PBMCs alone (no antibody), and the absolute maximal lysis for the assay, provided by the fluorescence signal of target cells in the presence of Triton X1000. The graphs show that the antibodies differ not only in their EC50, reflecting their relative potency, but also in the maximal level of ADCC attainable by the antibodies at saturating concentrations, reflecting their relative efficacy. Thus far these two terms, potency and efficacy, have been used loosely to refer to desired clinical properties. In the current experimental context, however, they are denoted as specific quantities, and therefore are here explicitly defined. By "potency" as used in the current experimental context is meant the EC50 of an Fc polypeptide. By "efficacy" as used in the current experimental context is meant the maximal possible effector function of an Fc polypeptide at saturating levels. In addition to the substantial enhancements to potency described thus far, FIGS. **26***a* and **26***b* show that the Fc variants of the present invention provide greater than 100% enhancements in efficacy over WT trastuzumab and rituximab.

Example 4

Cross-Validation of Fc Variants

[0380] Select Fc variants were validated for their FcγR binding and ADCC improvements in the context of two antibodies—alemtuzumab and trastuzumab. Binding to human V158 FcγRIIIa was measured using both AlphaScreen and SPR as described above. Exemplary AlphaScreen data measuring FcγRIIIa binding are provided in FIG. **27**. ADCC was carried out in the context of trastuzumab using Sk-Br-3 target cells and LDH detection as described above. Exemplary ADCC data are provided in FIG. **28**. Table 8 provides a summary of the fold FcγRIIIa binding affinities to relative to WT as determined by AlphaScreen and SPR, and the fold ADCC relative to WT for a series of Fc variants in the context of alemtuzumab (alem) and trastuzumab (trast).

TABLE 8

Variant	Variant		Fold WT V158 FcγRIIIa		
Substitution	Number	Context	AlphaScreen	SPR	ADCC
G236S	719	trast	2.78	1.34	0.37
G236S	719	alem	6.22	6.69	
S239E	43	trast	29.99	4.17	7.6
S239E	43	alem	2.64	3.28	
S239D	86	trast	16.9	3.5	6.1
S239D	86	alem	36.56	16.61	
K246H	812	trast	17.91	2.67	2
K246H	812	alem	13.58	22.36	
K246Y	813	trast	17.44	2.39	1.36
K246Y	813	alem	4.32	7.07	
R255Y	818	trast	21.14	2.75	1.6
R255Y	818	alem	0.92	1.41	
E258H	820	trast	1.18	0.77	0.76
E258H	820	alem	2.35	5.5	
E258Y	821	trast	2.82	1.69	0.92
E258Y	821	alem	0.64	1.77	
T260H	824	trast	35.32	2.82	
T260H	824	alem	1	1.86	
S267E	338	alem	9.33	2.62	
H268D	350	trast	45.27	4.76	4.59
H268D	350	alem	10.55	5.66	
E272I	237	trast	5.86	1.63	1.38
E272I	237	trast	3.24	1.99	
E272R	634	alem		1.38	
E272H	636	trast	1.02	0.65	1.28
E272H	636	alem	187.1	383.88	
E272P	642	trast	0.005	0.522	0.39
E272P	642	alem	1.46	1.41	
E283H	839	trast	0.99	0.71	1.4
E283H	839	alem		2.31	
E283L	840	trast	19.88	3.68	5.2
E283L	840	alem	1.36	2.56	
V284E	844	trast	2.82	1.26	0.84
V284E	844	alem		1.51	
E293R	555	trast	1.15	0.94	0.47
S298D	364	trast	3.48	1.49	0.58
S304T	879	trast	6.33	1.65	1.02
S304T	879	alem		12.85	
S324I	267	trast	5.26	1.46	2.21
S324G	608	trast	3.04	1.76	3.23
S324G	608	alem	13.62	14.17	
K326E	103	trast	6.12	2.12	2.87
K326E	103	alem	1.86	3.13	
A327D	274	trast	2.44	1.31	1.04
I332E	22	trast			
I332D	62	trast	19	2.57	5
I332D	62	alem	21.65	11.16	
E333Y	284	trast	8.24	1.94	2.23
K334I	285	trast	15.24	7.1	1.2
K334T	286	trast	15.73	6.79	3.14
K334F	287	trast	10.46	5.82	1.92

Example 5

ADCC at Varying Target Antigen Expression Levels

[0381] A critical parameter governing the clinical efficacy of anti-cancer antibodies is the expression level of target antigen on the surface of tumor cells. Thus a major clinical advantage of Fc variants that enhance ADCC may be that it enables the targeting of tumors that express lower levels of antigen. In order to test this hypothesis, WT and Fc variant trastuzumab antibodies were tested for their ability to mediate ADCC against different cell lines expressing varying levels of the Her2/neu target antigen using the DELFIA EuTDA method. Four cell lines cell lines expressing amplified to low levels of Her2/neu receptor were used, including Sk-Br-3 (1×10^6 copies), SkOV3 ($\sim1\times10^5$), OVCAR3($\sim1\times10^4$), and MCF-7 ($\sim3\times10^3$ copies) (FIG. **29***a*). Target cells were loaded with BATDA in batch for 25 minutes, washed multiple times with medium and seeded at 10,000 cells per well in 96-well plates. Target cells were opsonized for 15 minutes with various antibodies and concentrations (final conc. ranging from 100 ng/ml to 0.0316 ng/ml in ½ log steps, including no treatment control). Human PBMCs, isolated from buffy-coat and allotyped as homozygous F158/F158 FcγRIIIa were then added to opsonized cells at 25-fold excess and co-cultured at 37° C. for 4 hrs. Thereafter, plates were centrifuged, supernatants were removed and treated with Eu3+ solution, and relative fluorescence units (correlating to the level of cell lysis) were measured using a Packard Fusion™ α-FP HT reader (PerkinElmer, Boston, Mass.). The experiment was carried out in triplicates. FIG. **29***b* shows the ADCC data comparing WT and Fc variant trastuzumab against the four different Her2/neu$^+$ cell lines. The S239D/I332E and S239D/I332E/A330L variants provide substantial ADCC enhancements over WT trastuzumab at high, moderate, and low expression levels of target antigen. This result suggests that the Fc variants of the present invention may broaden the therapeutic window of anti-cancer antibodies.

Example 6

ADCC with NK Cells as Effector Cells

[0382] Natural killer (NK) cells are a subpopulation of cells present in PBMCs that are thought to play a significant role in ADCC. Select Fc variants were tested in a cell-based ADCC assay in which natural killer (NK) cells rather than PBMCs were used as effector cells. In this assay the release of endogenous lactose dehydrogenase (LDH), rather than EuTDA, was used to monitor cell lysis. FIG. **30** shows that the Fc variants show substantial ADCC enhancement when NK cells are used as effector cells. Furthermore, together with previous assays, the results indicate that the Fc variants of the present invention show substantial ADCC enhancements regardless of the type of effector cell or the detection method used.

Example 7

ADCP of Fc Variants

[0383] Another important FcγR-mediated effector function is ADCP. Phagocytosis of target cancer cells may not only lead to the immediate destruction of target cells, but because phagocytosis is a potential mechanism for antigen uptake and processing by antigen presenting cells, enhanced ADCP may also improve the capacity of the Fc polypeptide to elicit an adaptive immune response. The ability of the Fc variants of the present invention to mediate ADCP was therefore investigated. Monocytes were isolated from heterozygous V158/F158 FcγRIIIa PBMCs using a Percoll gradient. After one week in culture in the presence of 0.1 ng/ml, differentiated macrophages were detached with EDTA/PBS—and labeled with the lipophilic fluorophore, PKH26, according to the manufacturer's protocol (Sigma, St Louis, Mo.). Sk-Br-3 target cells were labeled with PKH67 (Sigma, St Louis, Mo.), seeded in a 96-well plate at 20,000 cells per well, and treated with designated final concentrations of WT or Fc variant trastuzumab. PKH26-labeled macrophages were then added to the opsonized, labeled Sk-Br-3 cells at 20,000 cells per well and the cells were co-cultured for 18 hrs before processing cells for analysis of dual label flow cytometry. Percent phagocytosis was determined as the number of cells co-labeled with PKH76 and PKH26 (macrophage+Sk-Br-3) over the total number of Sk-Br-3 in the population (phagocytosed+non-phagocytosed) after 10,000 counts. FIG. **31** shows data comparing WT and Fc variant trastuzumab at various antibody concentrations. The results indicate that the S239D/I332E/A330L variant provides a significant enhancement in ADCP over WT trastuzumab.

Example 8

Complement Binding and Activation by Fc Variants

[0384] Complement protein C1q binds to a site on Fc that is proximal to the FcγR binding site, and therefore it was prudent to determine whether the Fc variants have maintained their capacity to recruit and activate complement. The AlphaScreen assay was used to measure binding of select Fc variants to the complement protein C1q. The assay was carried out with biotinylated WT alemtuzumab antibody attached to streptavidin donor beads as described in Example 2, and using C1q coupled directly to acceptor beads. Binding data of V2641, 1332E, S239E, and V264I/I332E rituximab shown in FIG. **32***a* indicate that C1q binding is uncompromised. Cell-based CDC assays were also performed on select Fc variants to investigate whether Fc variants maintain the capacity to activate complement. Alamar Blue was used to monitor lysis of Fc variant and WT rituximab-opsonized WIL2-S lymphoma cells by human serum complement (Quidel, San Diego, Calif.). The data in FIG. **32***b* show that CDC is uncompromised for the Fc variants S239E, V264I, and V264I/I332E rituximab. In contrast, FIG. **32***c* shows that CDC of the Fc variant S239D/I332E/A330L is completely ablated, whereas the S239D/I332E variant mediates CDC that is comparable to WT rituximab. These results indicate that protein engineering can be used to distinguish between different effector functions. Such control will not only enable the generation of Fc polypeptides, including antibodies and Fc fusions, with properties tailored for a desired clinical outcome, but also provide a unique set of reagents with which to experimentally investigate effector function biology.

Example 9

Enhanced B Cell Depletion in Macaques

[0385] In order to evaluate the capacity of the Fc variants to enhance effector function in vivo, a pre-clinical study was carried out wherein B cell depletion was used to measure antibody cytotoxicity in cynomogus monkeys (*Macaca fascicularis*). Three monkeys per sample were injected intravenously with WT or S239D/I332E rituximab antibody, with

injections given once daily over days 1-4 in approximate dose ranges of 40 μg/kg (WT control) or 1, 4, 10, or 40 μg/kg (S239D/I332E and/or WT). Actual concentrations were determined experimentally. B cell and natural killer cell levels were monitored from days 5 to 28, and cell populations were counted using flow cytometry using B cell markers CD20+ and CD40+, and natural killer cell markers CD3−/CD16+ and CD3−/CD8+.

[0386] FIG. **33***a* shows the percent of CD20+ B cells remaining in monkeys dosed with antibodies comprising WT or S239D/I332E rituximab. The S239D/I332E variant and WT control at the lower dosage (1.8 and 2.1 ug/kg) show the greatest difference in B cell counts on day 5. NK cell populations were monitored to evaluate the impact of the effector function enhancement on this cell type; FIG. **33***b* shows that the increased CD20+ B cell killing of S239D/I332E variant does not affect natural kill cell population. The reduction in B cell level is also dose-dependant, as is shown in FIG. **33***c* for day 5.

Example 10

Capacity for Testing Fc Variants in Mice

[0387] Optimization of Fc to nonhuman FcγRs may be useful for experimentally testing Fc variants in animal models. For example, when tested in mice (for example nude mice, SCID mice, xenograft mice, and/or transgenic mice), antibodies and Fc fusions that comprise Fc variants that are optimized for one or more mouse FcγRs may provide valuable information with regard to clinical efficacy, mechanism of action, and the like. In order to evaluate whether the Fc variants of the present invention may be useful in such experiments, affinity of select Fc variants for mouse FcγRIII was measured using the AlphaScreen assay. The AlphaScreen assay was carried out using biotinylated WT alemtuzumab attached to streptavidin donor beads as described in Example 2, and GST-tagged mouse FcγRIII bound to glutathione chelate acceptor beads, expressed and purified as described in Example 2. These binding data are shown in FIG. **34***a* for Fc variants in the context of alemtuzumab, and in FIGS. **34***b* and **34***c* in the context of trastuzumab. Results show that some Fc variants that enhance binding to human FcγRIIIa also enhance binding to mouse FcγRIII. The enhancement of mouse effector function by the Fc variants was investigated by performing the aforementioned cell-based ADCC assays using mouse rather than human PBMC's. FIG. **35** shows that the S239D/I332E/A330L trastuzumab variant provides substantial ADCC enhancement over WT in the presence of mouse immune cells. This result indicates that the Fc variants of the present invention, or other Fc variants that are optimized for nonhuman FcγRs, may find use in experiments that use animal models.

Example 11

Validation of Fc Variants Expressed in CHO Cells

[0388] Whereas the Fc variants of the present invention were expressed in 293T cells for screening purposes, large scale production of antibodies is typically carried out by expression in Chinese Hamster Ovary (CHO) cell lines. In order to evaluate the properties of CHO-expressed Fc variants, select Fc variants and WT alemtuzumab were expressed in CHO cells and purified as described in Example 1. FIG. **36** shows AlphaScreen data comparing binding of CHO- and 293T-expressed Fc variant and WT alemtuzumab to human V158 FcγRIIIa. The results indicate that the Fc variants of the present invention show comparable FcγR binding enhancements whether expressed in 293T or CHO.

Example 12

Enhancement of Fc Variants in Fucose Minus Strain

[0389] Combinations of the Fc variants of the present invention with other Fc modifications are contemplated with the goal of generating novel Fc polypeptides with optimized properties. It may be beneficial to combine the Fc variants of the present invention with other Fc modifications, including modifications that alter effector function or interaction with one or more Fc ligands. Such combination may provide additive, synergistic, or novel properties in Fc polypeptides. For example, a number of methods exist for engineering different glycoforms of Fc that alter effector function. Engineered glycoforms may be generated by a variety of methods known in the art, many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region. One method for engineering Fc glycoforms is to express the Fc polypeptide in a cell line that generates altered glycoforms, for example Lec-13 CHO cells. In order to investigate the properties of Fc variants combined with engineered glycoforms, WT and V209 (S239D/I332E/A330L) trastuzumab were expressed in Lec-13 CHO cells and purified as described above. FIG. **37***a* shows AlphaScreen binding data comparing the binding to human V158 FcγRIIIa by WT and V209 trastuzumab expressed in 293T, CHO, and Lec-13 cells. The results show that there is substantial synergy between the engineered glycoforms produced by this cell line and the Fc variants of the present invention. The cell-based ADCC assay, shown in FIG. **37***b*, supports this result. Together these data indicate that other Fc modifications, particularly engineered glycoforms, may be combined with the Fc variants of the present invention to generate Fc polypeptides, for example antibodies and Fc fusions, with optimized effector functions.

Example 13

Aglycosylated Fc Variants

[0390] As discussed, one goal of the current experiments was to obtain optimized aglycosylated Fc variants. Several Fc variants provide significant progress towards this goal. Because it is the site of glycosylation, substitution at N297 results in an aglycosylated Fc. Whereas all other Fc variants that comprise a substitution at N297 completely ablate FcγR binding, N297D/I332E has significant binding affinity for FcγRIIIa, shown in FIG. **41** and illustrated in FIG. **38**. The exact reason for this result is uncertain in the absence of a high-resolution structure for this variant, although the computational screening predictions suggest that it is potentially due to a combination of new favorable Fc/FcγR interactions and favorable electrostatic properties. Indeed other electrostatic substitutions are envisioned for further optimization of aglycosylated Fc. FIG. **41** shows that other aglycosylated Fc variants such as N297D/A330Y/I332E and S239D/N297D/I332E provide binding enhancements that bring affinity for FcγRIIIa within as much as 0.4- and 0.8-respectively of glycosylated WT alemtuzumab. Combinations of these variants with other Fc variants that enhance FcγR binding are contemplated, with the goal of obtaining aglycosylated Fc variants

that bind one or more FcγRs with affinity that is approximately the same as or even better than glycosylated parent Fc. Preferred Fc variants for enhancing Fc ligand binding and/or effector function in an aglycosylated Fc polypeptide include but are not limited to: N297D, N297D/I332E, N297D/I332D, S239D/N297D, S239D/N297D/I332E, N297D/A330Y/I332E, and S239D/N297D/A330Y/I332E. The present invention of course contemplates combinations of these aglycosylated variants with other Fc variants described herein which also enhance Fc ligand binding and/or effector function.

[0391] An additional set of promising Fc variants provide stability and solubility enhancements in the absence of carbohydrate. Fc variants that comprise substitutions at positions 241, 243, 262, and 264, positions that do not mediate FcγR binding but do determine the interface between the carbohydrate and Fc, ablate FcγR binding, presumably because they perturb the conformation of the carbohydrate. In deglycosylated form, however, Fc variants F241E/F243R/V262E/V264R, F241E/F243Q/V262T/V264E, F241R/F243Q/V262T/V264R, and F241E/F243Y/V262T/V264R show stronger binding to FcγRIIIa than in glycosylated form, as shown by the AlphaScreen data in FIG. **39**. This result indicates that these are key positions for optimization of the structure, stability, solubility, and function of aglycosylated Fc. Together these results suggests that protein engineering can be used to restore the favorable functional and solution properties of antibodies and Fc fusions in the absence of carbohydrate, and pave the way for aglycosylated antibodies and Fc fusions with favorable solution properties and full functionality that comprise substitutions at these and other Fc positions.

Example 14

Preferred Variants

[0392] Taken together, the data provided in the present invention indicate that Fc variants that provide optimized FcγR binding properties also provide enhanced effector function. Substitutions at a number of positions, including but not limited to 236, 239, 246, 246, 249, 255, 258, 260, 264, 267, 268, 272, 274, 281, 283, 304, 324, 326, 327, 330, 332, 333, 334, and 334 provide promising candidates for improving the effector function and therefore the clinical properties of Fc polypeptides, including antibodies and Fc fusions. Because combinations of Fc variants of the present invention have typically resulted in additive or synergistic binding improvements, and accordingly additive or synergistic enhancements in effector function, it is anticipated that as yet unexplored combinations of the Fc variants provided in FIG. **41** will also provide favorable results. Preferred Fc variants of the present invention for enhancing Fc ligand binding and/or effector function are provided in Table 9.

TABLE 9

G236S	S239D/I332E	S239D/K246H/I332E	S239D/K246H/T260H/I332E
G236A	S239D/G236A	S239D/V264I/I332E	S239D/K246H/H268D/I332E
S239D	S239D/G236S	S239D/S267E/I332E	S239D/K246H/H268E/I332E
S239E	S239D/V264I	S239D/H268D/I332E	S239D/H268D/S324G/I332E
S239N	S239D/H268D	S239D/H268E/I332E	S239D/H268E/S324G/I332E
S239Q	S239D/H268E	S239D/S298A/I332E	S239D/H268D/K326T/I332E
S239T	S239D/S298A	S239D/S324G/I332E	S239D/H268E/K326T/I332E
K246H	S239D/K326E	S239D/S324I/I332E	S239D/H268D/A330L/I332E
K246Y	S239D/A330L	S239D/K326T/I332E	S239D/H268E/A330L/I332E
D249Y	S239D/A330Y	S239D/K326E/I332E	S239D/H268D/A330Y/I332E
R255Y	S239D/A330I	S239D/K326D/I332E	S239D/H268E/A330Y/I332E
E258Y	I332E/V264I	S239D/A327D/I332E	S239D/S298A/S267E/I332E
T260H	I332E/H268D	S239D/A330L/I332E	S239D/S298A/H268D/I332E
V264I	I332E/H268E	S239D/A330Y/I332E	S239D/S298A/H268E/I332E
S267E	I332E/S298A	S239D/A330I/I332E	S239D/S298A/S324G/I332E
H268D	I332E/K326E	S239D/K334T/I332E	S239D/S298A/S324I/I332E
H268E	I332E/A330L		S239D/S298A/K326T/I332E
E272Y	I332E/A330Y		S239D/S298A/K326E/I332E
E272I	I332E/A330I		S239D/S298A/A327D/I332E
E272H	I332E/G236A		S239D/S298A/A330L/I332E
K274E	I332E/G236S		S239D/S298A/A330Y/I332E
G281D	I332D/V264I		S239D/K326T/A330Y/I332E
E283L	I332D/H268D		S239D/K326E/A330Y/I332E
E283H	I332D/H268E		S239D/K326T/A330L/I332E
S304T	I332D/S298A		S239D/K326E/A330L/I332E
S324G	I332D/K326E		
S324I	I332D/A330L		
K326T	I332D/A330Y		
A327D	I332D/A330I		
A330Y	I332D/G236A		
A330L	I332D/G236S		
A330I			
I332D			
I332E			
I332N			
I332Q			
E333Y			
K334T			
K334F			

[0393] This list of preferred Fc variants is not meant to constrain the present invention. Indeed all combinations of the any of the Fc variants provided in FIG. **41** are embodiments of the present invention. Furthermore, combinations of any of the Fc variants of the present invention with other discovered or undiscovered Fc variants may also provide favorable properties, and these combinations are also contemplated as embodiments of the present invention. Finally, it is anticipated from these results that other substitutions at positions mutated in present invention may also provide favorable binding enhancements and specificities, and thus substitutions at all positions in FIG. **41** are contemplated.

Example 15

Therapeutic Application of Fc Variants

[0394] A number of Fc variants described in the present invention have significant potential for improving the therapeutic efficacy of anticancer antibodies. For illustration purposes, a number of Fc variants of the present invention have been incorporated into the sequence of the antibody rituximab. The WT rituximab light chain and heavy chain, described in U.S. Pat. No. 5,736,137, are provided in FIGS. **40***a* and **40***b*. The improved anti-CD20 antibody sequences are provided in FIG. **40***c*. The improved anti-CD20 antibody sequences comprise at least non-WT amino acid selected from the group consisting of X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, and X_9. These improved anti-CD20 antibody sequences may also comprise a substitution Z_1 and/or Z_2. The use of rituximab here is solely an example, and is not meant to constrain application of the Fc variants to this antibody or any other particular Fc polypeptide.

[0395] Table 10 depicts the positions of human Fc, the wild type residue, and the variants that are included in particular embodiments of the invention. Table 10 is based on IgG1, although as will be appreciated by those in the art, the same thing can be done to any Ig, particularly IgG2, IgG3 and IgG4.

TABLE 10

Position	Wild Type (Human)	Variants including wild type
118-220	FX	see FIG. 3a
Vb(221)	D	D, K, Y
Vb(222)	K	K, E, Y
Vb(223)	T	T, E, K
Vb(224)	H	H, E, Y
Vb(225)	T	T, E, K, W
Fx(226)	WT	C
Vb(227)	P	P, E, G, K, Y
Vb(228)	P	P, E, G, K, Y
Fx(229)	(OPEN)(WT)	C
Vb(230)	P	P, A, E, G, Y
Vb(231)	A	A, E, G, K, P, Y
Vb(232)	P	P, E, G, K, Y
Vb(233)	E	A, D, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
Vb(234)	L	L, A, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W, Y
Vb(235)	L	L, A, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W, Y
Vb(236)	G	G, A, D, E, F, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
Vb(237)	G	G, D, E, F, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
Vb(238)	P	P, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
Vb(239)	S	S, D, E, F, G, H, I, K, L, M, N, P, Q, R, T, V, W, Y
Vb(240)	V	V, A, I, M, T
Vb(241)	F	F, D, E, L, R, S, W, Y
Fx(242)	WT	L
Vb(243)	F	F, E, H, L, Q, R, W, Y
Vb(244)	P	P, H
Vb(245)	P	P, A
Vb(246)	K	K, D, E, H, Y
Vb(247)	P	P, G, V
Vb(248)	WT	K
Vb(249)	D	D, H, Q, Y
Fx(250-254)	WT	-(T-L-M-I-S)-
Vb(255)	R	R, E, Y
Fx(256-257)	WT	-(T-P)-
Vb(258)	E	E, H, S, Y
Fx(259)	WT	V
Vb(260)	T	T, D, E, H, Y
Fx(261)	WT	C
Vb(262)	V	V, A, E, F, I, T
Vb(263)	V	V, A, I, M, T
Vb(264)	V	V, A, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, W, Y
Vb(265)	D	D, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y
Vb(266)	V	V, A, I, M, T
Vb(267)	S	S, D, E, F, H, I, K, L, M, N, P, Q, R, T, V, W, Y
Vb(268)	H	H, D, E, F, G, I, K, L, M, N, P, Q, R, T, V, W, Y
Vb(269)	E	E, F, G, H, I, K, L, M, N, P, R, S, T, V, W, Y

TABLE 10-continued

Position	Wild Type (Human)	Variants including wild type
Vb(270)	D	D, F, G, H, I, L, M, P, Q, R, S, T, W, Y
Vb(271)	A	A, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
Vb(272)	E	E, D, F, G, H, I, K, L, M, P, R, S, T, V, W, Y
Vb(273)	V	V, I
Vb(274)	K	K, D, E, F, G, H, L, M, N, P, R, T, V, W, Y
Vb(275)	F	F, L, W
Vb(276)	N	N, D, E, F, G, H, I, L, M, P, R, S, T, V, W, Y
Fx(277)	WT	W
Vb(278)	Y	Y, D, E, G, H, I, K, L, M, N, P, Q, R, S, T, V, W
Fx(279)	WT	V
Vb(280)	D	D, G, K, L, P, W
Vb(281)	G	G, D, E, K, N, P, Q, Y
Vb(282)	V	V, E, G, K, P, Y
Vb(283)	E	E, G, H, K, L, P, R, Y
Vb(284)	V	V, D, E, L, N, Q, T, Y
Vb(285)	H	H, D, E, K, Q, W, Y
Vb(286)	N	N, E, G, P, Y
Fx(287)	WT	A
Vb(288)	K	K, D, E, Y
Fx(289)	WT	T
Vb(290)	K	K, D, H, L, N, W
Vb(291)	P	P, D, E, G, H, I, Q, T
Vb(292)	R	R, D, E, T, Y
Vb(293)	E	E, F, G, H, I, L, M, N, P, R, S, T, V, W, Y
Vb(294)	E	E, F, G, H, I, K, L, M, P, R, S, T, V, W, Y
Vb(295)	Q	Q, D, E, F, G, H, I, M, N, P, R, S, T, V, W, Y
Vb(296)	Y	Y, A, D, E, G, H, I, K, L, M, N, Q, R, S, T, V
Vb(297)	N	N, D, E, F, G, H, I, K, L, M, P, Q, R, S, T, V, W, Y
Vb(298)	S	S, D, E, F, H, I, K, M, N, Q, R, T, W, Y
Vb(299)	T	T, A, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, V, W, Y
Vb(300)	Y	Y, A, D, E, G, H, K, M, N, P, Q, R, S, T, V, W
Vb(301)	R	R, D, E, H, Y
Vb(302)	V	V, I
Vb(303)	V	V, D, E, Y
Vb(304)	S	S, D, H, L, N, T
Vb(305)	V	V, E, T, Y
Fx(306-312)	WT	-(L-T-V-L-H-Q-D)-*
Vb(313)	W	W, F
Fx(314-316)	WT	-(L-N-G)-
Vb(317)	K	K, E, Q
Vb(318)	E	E, H, L, Q, R, Y
Fx(319)	WT	Y
Vb(320)	K	K, D, F, G, H, I, L, N, P, S, T, V, W, Y
Fx(321)	WT	C
Vb(322)	K	K, D, F, G, H, I, P, S, T, V, W, Y
Vb(323)	V	V, I
Vb(324)	S	S, D, F, G, H, I, L, M, P, R, T, V, W, Y
Vb(325)	N	N, A, D, E, F, G, H, I, K, L, M, P, Q, R, S, T, V, W, Y
Vb(326)	K	K, I, L, P, T
Vb(327)	A	A, D, E, F, H, I, K, L, M, N, P, R, S, T, V, W, Y
Vb(328)	L	L, A, D, E, F, G, H, I, K, M, N, P, Q, R, S, T, V, W, Y
Vb(329)	P	P, D, E, F, G, H, I, K, L, M, N, Q, R, S, T, V, W, Y
Vb(330)	A	A, E, F, G, H, I, L, M, N, P, R, S, T, V, W, Y
Vb(331)	P	P, D, F, H, I, L, M, Q, R, T, V, W, Y
Vb(332)	I	I, A, D, E, F, H, K, L, M, N, P, Q, R, S, T, V, W, Y
Vb(333)	E	E, F, H, I, L, M, N, P, T, Y
Vb(334)	K	K, F, I, L, P, T
Vb(335)	T	T, D, F, G, H, I, L, M, N, P, R, S, V, W, Y
Vb(336)	I	I, E, K, Y
Vb(337)	S	S, E, H, N

Example 16

Novel Methods for Inhibiting FcγRIIb$^+$ Cells

[0396] FcγRIIb is expressed on a variety of immune cells, including B cells, plasma cells, dendritic cells, monocytes, and macrophages, where it plays a critical role in immune regulation. In its normal role on B cells, FcγRIIb serves as a feedback mechanism to modulate B cell activation through the B cell receptor (BCR). Engagement of B cell antigen receptor (BCR) by immune complexed antigen on mature B cells activates an intracellular signaling cascade, including calcium mobilization, which leads to cell proliferation and differentiation. However, as IgG antibodies with specificity to the antigen are produced, the associated immune complexes

(ICs) can crosslink the BCR with FcγRIIb, whereupon the activation of BCR is inhibited by engagement of FcγRIIb and associated intracellular signaling pathways that interfere with the downstream pathways of BCR activation.

[0397] B cells function not only to produce antibodies and cytokines that control immune response, they are also antigen presenting cells (APCs). Internalization of antigen by BCR into a B cell can play a role in presentation to and activation of T cells. Regulation of B cell activation through the BCR is also potentially regulated by antibody engagement of FcγRIIb. Other APCs such as dendritic cells, macrophages, and monocytes, are capable of internalizing antibody-bound antigen through activating receptors such as FcγRIIa, FcγRIIIa, and FcγRI. Expression of FcγRIIb on these cell types, particularly dendritic cells, can inhibit activation of these cell types and subsequent presentation to and activation of T cells (Desai et al., 2007, J Immunol).

[0398] A novel strategy for inhibiting activation of the aforementioned cell types it to use a single immunoglobulin to coengage FcγRIIb with surface antigen present on the FcγRIIb+ cell. In the case of B cells, based on the natural biological mechanism, this would potentially involve dual targeting of FcγRIIb and BCR, with the goal of mimicking immune complex-mediated suppression of B cell activation. FIG. **44** illustrates one such potential mechanism, in which an antibody is used to coengage both FcγRIIb via its Fc region, and a target antigen associated with BCR complex, in this example CD19, via its Fv region.

Example 16.2

Engineering Immunoglobulins with Selectively Enhanced Affinity for FcγRIIb

[0399] Under physiological conditions, bridging of the BCR with FcγRIIb and subsequent B cell suppression occurs via immune complexes of IgGs and cognate antigen. The design strategy was to reproduce this effect using a single crosslinking antibody. Human IgG binds human FcγRIIb with weak affinity (approximately 1 μM for IgG1), and FcγRIIb-mediated inhibition occurs in response to immune-complexed but not monomeric IgG. It was reasoned that increasing Fc affinity to this receptor would be required for maximal inhibition of B cell activation. Protein engineering methods were used to design and screen Fc variants for enhanced FcγRIIb binding.

[0400] In addition to this primary design goal (maximal Fc affinity to FcγRIIb), a secondary design goal was to reduce interaction of the Fc region with activating FcγRs. FcγR affinity profiles that may be optimal for inhibiting FcγRIIb cells include not only high affinity for the inhibitory receptor FcγRIIb, but also potentially high FcγRIIb affinity coupled with reduced affinity for one or more activating receptors, including, for example, FcγRI, FcγRIIa, and/or FcγRIIa. Reduced affinity to activating receptors may lead to reduced toxicity associated with an antibody treatment. For example, reduced affinity to FcγRIIIa, present on NK cells, should reduce the level of NK cell-mediated ADCC. Similarly, reduced affinity to FcγRIIa, present on a variety of effector cells including macrophages and neutrophils, should reduce the level of phagocytosis (ADCP) mediated by these cells. In addition, for monocytes, macrophages, dendritic cells, and the like, reduced interaction with activating FcγRs would mean that immunoglobulin would be more free to interact with FcγRIIb on the cell surface.

[0401] Using solved structures of the human Fc/FcγRIIIb complex (and the sequences of the human FcγRs, structural and sequence analysis were used to identify FcγR positions that contribute to FcγRIIb affinity and selectivity relative to the activating receptors. The design strategy employed two steps. First, FcγR positions that are determinants of FcγRIIb and FcγRIIIa binding selectivity were identified by accounting for proximity to the FcγR/Fc interface and amino acid dissimilarity between FcγRIIb and FcγRIIIa. The results of this analysis are presented in FIG. **45**. Second, sequence positions in the Fc region proximal to these FcγR positions were identified. The results of this analysis are presented in FIG. **46**. Fc variants were designed that incorporate substitutions at these positions.

[0402] A library of Fc variants was generated and screened to explore amino acid modifications at these positions. Variants were generated and screened in the context of an antibody targeting the antigen CD19, a regulatory component of the BCR coreceptor complex. The Fv region of the this antibody is a humanized and affinity matured version of antibody 4G7, and is referred to herein as HuAM4G7. The amino acid sequences of this antibody are provided in FIG. **95**. The Fv genes for this antibody were subcloned into the mammalian expression vector pTT5 (National Research Council Canada). Mutations in the Fc domain were introduced using site-directed mutagenesis (QuikChange, Stratagene, Cedar Creek, Tex.). In addition, control knock out variants with ablated affinity for Fc receptors were generated that comprise the substitution L328R, and either a G236R substitution or an Arg inserted after position 236. These variants (G236R/L328R and ^236R/L328R) are referred to as Fc-KO or FcγR knockout. To serve as non-CD19 Fc isotype controls, anti-respiratory syncytial virus (RSV) and anti-FITC antibodies were constructed in the pTT5 vector by fusing the appropriate V_L and V_H regions to the CLκ and CH1-3 domains with Fc changes. Heavy and light chain constructs were cotransfected into HEK293E cells for expression, and antibodies were purified using protein A affinity chromatography (Pierce Biotechnology, Rockford, Ill.).

[0403] Human Fc receptor proteins FcγRI and FcγRIIb for binding and competition studies were obtained from R&D Systems (Minneapolis, Minn.). Genes encoding FcγRIIa and FcγRIIa receptor proteins were obtained from the Mammalian Gene Collection (ATCC), and subcloned into pTT5 vector (National Research Council Canada) containing 6×His and GST-tags. Allelic forms of the receptors (H131 and R131 for FcγRIIa and V158 and F158 for FcγRIIIa) were generated using QuikChange mutagenesis. Vectors encoding the receptors were transfected into HEK293T cells, and proteins were purified using nickel affinity chromatography.

[0404] Variants were screened for receptor affinity using Biacore™ technology, also referred to as Biacore herein, a surface plasmon resonance (SPR) based technology for studying biomolecular interactions in real time. SPR measurements were performed using a Biacore 3000 instrument (Biacore, Piscataway, N.J.). A protein A/G (Pierce Biotechnology) CM5 biosensor chip (Biacore) was generated using a standard primary amine coupling protocol. All measurements were performed using HBS-EP buffer (10 mM HEPES pH 7.4, 0.15 M NaCl, 3 mM EDTA, 0.005% vol/vol surfactant P20, Biacore). Antibodies at 20 nM or 50 nM in HBS-EP buffer were immobilized on the protein A/G surface and FcγRs were injected. After each cycle, the surface was regenerated by injecting glycine buffer (10 mM, pH 1.5). Data were

processed by zeroing time and response before the injection of FcγR and by subtracting appropriate nonspecific signals (response of reference channel and injection of running buffer). Kinetic analyses were performed by global fitting of binding data with a 1:1 Langmuir binding model using BIAevaluation software (Biacore).

[0405] A representative set of sensorgrams for binding of select variant anti-CD19 antibodies to FcγRIIb is shown in FIG. **47**. The affinities (equilibrium Kds) of all variants and WT (native) IgG1 to all of the FcγRs, obtained from fits of the Biacore binding data, are presented in FIG. **48**. Whereas WT IgG1 Fc binds with FcγRIIb with μM affinity (Kd=1467 nM in FIG. **48**), a large number of variants have been engineered that bind more tightly. Because all of the antibodies tested have specificity for CD19 (via their Fv region), the binding results in FIG. **48** are due solely to binding to FcγRIIb by the Fc region. This is supported by the lack of detectable binding by the Fc-KO variants (G236R/L328R and A236R/L328R), which are ablated for binding to all FcγRs.

[0406] A useful quantity for analysis of the variants is their fold affinity relative to WT IgG1, which is generated by dividing the Kd for binding of WT IgG1 by the Kd for binding of variant for each receptor. These fold affinity results are provided in FIG. **49**. A number of variants have FcγRIIb binding enhancements over 2 logs, and substantially reduced or ablated affinities for the activating receptors. In particular, S267E (single substitution) as well as L235Y/S267E, G236D/S267E, S239D/S267E, S267E/H268E, and S267E/L328F (double substitutions) have markedly higher affinity for FcγRIIb. In addition, these variant have affinity for the activating receptor FcγRIIIa that is either comparable to native IgG1, modestly enhanced, or even significantly reduced.

[0407] FIG. **50** shows a plot of the FcγR affinities of select variants on a log scale, compared with those of WT IgG1. The variant with the highest affinity for FcγRIIb, S267E/L328F, shows over 2 orders of magnitude improvement in affinity to FcγRIIb, and significantly reduced affinity to the activating receptors, including FcγRIIIa, FcγRI, and H131 FcγRIIa.

[0408] The data in FIGS. **50** and **51** indicate that the properties of the variants are highly dependent not only on the position that is mutated, but also the precise amino acid that is substituted at each position. For example, one of the strongest positions for controlling FcγRIIb affinity and selectivity relative to activating FcγRs is position 267. Yet modification at this position can yield dramatically different results depending on the particular amino acid that is substituted In particular, as shown in FIG. **51**, whereas affinity of S267E for FcγRIIb is greatly enhanced relative to WT IgG1 and provides substantial selectivity improvement relative to FcγRIIIa, other substitutions such as S267A and S267G provide either marginal or no FcγRIIb enhancement, and/or little or no selectivity improvement relative to FcγRIIIa. The importance of the precise modification is further supported by the fact that two of the best positions for selectively enhancing FcγRIIb affinity, 236 and 328 (for example 236D and 328F) are also the same positions that are modified to generate the Fc-KO variant (236R and 328R). These results illustrate the complexity of the FcγR interface, and highlight the challenge of engineering modifications that precisely control desired FcγR properties.

[0409] Many of the Fc combination variants, including double and triple combinations of single substitutions, exhibited unexpected synergy (non-additivity) when compared against the single substitutions alone. This was determined (for all combination variants for which data was available) by comparing the actual fold improvement in affinity as measured by Biacore versus the expected fold improvement in affinity as calculated by the product of the fold improvements of the single substitutions (FIG. **52**). As can be seen from the data, double substitutions at the following pairs of positions resulted in a greater than expected affinity for one or more FcγRs: 234/267, 235/267, 236/267, 236/268, 239/267, 239/268, 266/267, 267/328, and 268/327.

[0410] In order to validate the Biacore data and evaluate receptor binding of the variants on the cell surface, binding of select antibodies to cells expressing FcγRIIb was measured. Since HEK293T cells do not express CD19 or FcγRs, transfection of these cells with FcγRIIb allowed an analysis of antibody binding to Fc receptors in an isolated system on a cell surface. HEK293T cells in DMEM with 10% FBS were transfected with human FcγRIIb cDNA in pCMV6 expression vector (Origene Technologies, Rockville, Md.), cultured for 3 days, harvested, washed twice in PBS, resuspended in PBS with 0.1% BSA (PBS/BSA), and aliquoted at 2×105 cells per well into 96-well microtiter plates. Fc variant antibodies were serially diluted in PBS/BSA then added to the cells and incubated with mixing for 1 h at room temperature. After extensive washing with PBS/BSA, phycoerythrin (PE)-labeled anti-human-Fab-specific goat F(ab')2 fragment was added for detection. Cells were incubated for 30 min at room temperature, washed, and resuspended in PBS/BSA. Binding was evaluated using a FACSCanto II flow cytometer (BD Biosciences, San Jose, Calif.), and the mean fluorescence intensity (MFI) was plotted as a function of antibody concentration using GraphPad Prism software (GraphPad Software, San Diego, Calif.) from which half-maximal binding (EC50) values were determined by sigmoidal dose response modeling.

[0411] Receptor expression levels were assessed prior to binding of antibodies, and half-maximal effective concentration (EC50) values of the MFI at different antibody concentrations were determined. FIG. **53** shows the results of this experiment. The EC50 values of the variants tested showed a similar rank order as the Biacore results. The cell-surface binding confirmed that the S267E/L328F variant of those tested has the highest affinity for FcγRIIb, with an EC50 approximately 320-fold relative to WT IgG1. The strong agreement between these cell surface binding data and the Biacore binding data support the accuracy of the affinity measurements.

[0412] Because of the importance of animal models in drug development, select variants were screened further for binding to mouse and cynomolgous monkey receptors. The extracellular regions of mouse and cynologous monkey (*Macaca fascicularis*) FcγRs were expressed and purified. The extracellular regions of these receptors were obtained by PCR from clones obtained from the Mammalian Gene Collection (MGC), or generated de novo using recursive PCR. To enable purification and screening, receptors were fused C-terminally with a His- and GST-tag. Tagged FcγRs were transfected into 293T cells, and media containing secreted receptor were harvested 3 days later and purified using Nickel chromatography.

[0413] Variant antibodies were tested for their affinity to mouse or cynologous monkey FcγRs using Biacore SPR as described above. Specifically, antibodies were first immobilized on a protein A/G chip to high density, and then followed by injections of the extracellular domain of the mouse or

cynologous monkey FcγR of interest. Both association and dissociation phases were tracked in real time using the Biacore technology. FIG. **54** shows the fold improvements (compared to WT IgG1) for binding of select variants to mouse and cynologous monkey FcγRs as determined from Biacore.

[0414] Although the variants were screened in the context of human IgG1, it is contemplated that the variants could be used in the context of other antibody isotypes, for example including but not limited to human IgG2, human IgG3, and human IgG4 (FIG. **3**). In order to explore the transferability of the variants to other antibody isotypes, the S267E/L328F variant was constructed and tested in the context of a IgG1/2 ELLGG antibody, which is a variant of an IgG2 Fc region (U.S. Ser. No. 11/256,060, herein expressly incorporated by reference). The mutations were constructed, antibodies purified, and binding data carried out as described above. FIG. **55** shows affinities of the IgG1 and IgG1/2 variant antibodies to the human FcγRs as determined by Biacore. The data indicate that the greatly enhanced FcγRIIb affinity and the overall FcγR binding profile are maintained in the variant IgG2 Fc region, thus supporting the use of the variants in other isotype contexts.

[0415] Collectively, the above data indicate that a number of engineered variants, at specific Fc positions, provide the targeted properties, namely enhanced affinity for FcγRIIb, and selectively enhanced FcγRIIb affinity relative to the activating receptors FcγRI, FcγRIIa, and FcγRIIIa. Substitutions to enhance affinity to FcγRIIb include: 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332. In some embodiments, substitutions are made to at least one or more of the nonlimiting following positions to enhance affinity to FcγRIIb: 235, 236, 239, 266, 267, 268, and 328.

[0416] Nonlimiting combinations of positions for making substitutions to enhance affinity to FcγRIIb include: 234/239, 234/267, 234/328, 235/236, 235/239, 235/267, 235/268, 235/328, 236/239, 236/267, 236/268, 236/328, 237/267, 239/267, 239/268, 239/327, 239/328, 239/332, 266/267, 267/268, 267/325, 267/327, 267/328, 267/332, 268/327, 268/328, 268/332, 326/328, 327/328, and 328/332. In some embodiments, combinations of positions for making substitutions to enhance affinity to FcγRIIb include, but are not limited to: 235/267, 236/267, 239/268, 239/267, 267/268, and 267/328.

[0417] Substitutions for enhancing affinity to FcγRIIb include: L234D, L234E, L234W, L235D, L235F, L235R, L235Y, G236D, G236N, G237D, G237N, S239D, S239E, V266M, S267D, S267E, H268D, H268E, A327D, A327E, L328F, L328W, L328Y, and I332E. In some embodiments, combination of positions for making substitutions for enhancing affinity to FcγRIIb include, but are not limited to: L235Y, G236D, S239D, V266M, S267E, H268D, H268E, L328F, L328W, and L328Y.

[0418] Combinations of substitutions for enhancing affinity to FcγRIIb include: L234D/S267E, L234E/S267E, L234F/S267E, L234E/L328F, L234W/S239D, L234W/S239E, L234W/S267E, L234W/L328Y, L235D/S267E, L235D/L328F, L235F/S239D, L235F/S267E, L235F/L328Y, L235Y/G236D, L235Y/S239D, L235Y/S267D, L235Y/S267E, L235Y/H268E, L235Y/L328F, G236D/S239D, G236D/S267E, G236D/H268E, G236D/L328F, G236N/S267E, G237D/S267E, G237N/S267E, S239D/S267D, S239D/S267E, S239D/H268D, S239D/H268E, S239D/A327D, S239D/L328F, S239D/L328W, S239D/L328Y, S239D/I332E, S239E/S267E, V266M/S267E, S267D/H268E, S267E/H268D, S267E/H268E, S267E/N325L, S267E/A327D, S267E/A327E, S267E/L328F, S267E/L328I, S267E/L328Y, S267E/I332E, H268D/A327D, H268D/L328F, H268D/L328W, H268D/L328Y, H268D/I332E, H268E/L328F, H268E/L328Y, A327D/L328Y, L328F/I332E, L328W/I332E, and L328Y/I332E. In some embodiments, combinations of substitutions for enhancing affinity to FcγRIIb include, but are not limited to: L235Y/S267E, G236D/S267E, S239D/H268D, S239D/S267E, S267E/H268D, S267E/H268E, and S267E/L328F.

Example 16.3

Immunoglobulins Inhibit BCR-Mediated Primary Human B Cell Viability

[0419] Although normal B cells have a long in vivo half life of approximately five weeks, their lifespan is greatly reduced in vitro. BCR stimulation by crosslinking antibodies such as anti-IgM or anti-CD79b counteracts this in vitro predisposition towards apoptosis, leading to B cell activation and increased B cell viability. To demonstrate this, an ATP-dependent B cell viability assay was performed. Human peripheral blood mononuclear cells (PBMCs) were purified from leukapheresis of anonymous healthy volunteers (HemaCare, Van Nuys, Calif.) using Ficoll-Paque Plus density gradients (Amersham Biosciences, Newark, N.J.). Primary human B cells were purified from PBMCs using a B cell enrichment kit (StemCell Technologies, Vancouver, British Columbia). Murine anti-human CD79b (clone SN8) was purchased from Santa Cruz Biotechnology (Santa Cruz, Calif.). Polyclonal anti-mu F(ab')2 was purchased from Jackson Immunoresearch Lab (West Grove, Pa.). Anti-mu or anti-CD79b antibody serial dilutions were performed in triplicate in 96-well microtiter plates containing RPM11640 with 10% FBS. Purified primary human B cells (5-7.5×104 per well) were added to a final volume of 100 μl, and incubated at 37° C. for 3 days. ATP-dependent luminescence was quantified to determine cell viability (Cell Titer-Glo Cell Viability Assay, Promega, Madison, Wis.) and a Topcount luminometer (PerkinElmer, Waltham, Mass.) was used for data acquisition. FIGS. **56**A and **56**B show the results of the assay, demonstrating the survival of primary human B cells upon BCR activation, here carried out by crosslinking with anti-mu (A) or anti-CD79b (B) antibodies. In vivo such activation would occur via immune complexed antigen, which for example could be an infectious agent, or in the cause of an autoimmune or allergic reaction could be an anutoimmune antigen or allergen.

[0420] The ATP-dependent luminescence assay was used to examine if BCR activation-mediated viability of primary human B cells could be suppressed by an anti-CD19 antibody having enhanced Fc affinity for FcγRIIb. The above experiment was repeated, except that antibody serial dilutions of WT, variant, and control antibodies were performed in triplicate in 96-well microtiter plates containing RPMI1640 with 10% FBS, plus anti-CD79b at 1 pg/ml to stimulate BCR. The results are shown in FIG. **57**. Again, B cells possessed low viability in the absence of BCR crosslinking, and addition of 10 μg/ml anti-CD79b antibody stimulated survival by about 6-fold (cells alone vs. anti-CD79b). Anti-CD19-S267E/L328F, the variant with the highest FcγRIIb affinity, inhibited BCR-stimulated viability in a dose-dependent manner. In contrast, control antibodies including anti-CD19-IgG1 (Fv control) and anti-RSV-S267E/L328F (Fc control) minimally suppressed viability. To assess if this inhibitory effect required coengagement of CD19 and FcγRIIb, as opposed to

simultaneous binding of each receptor by different antibodies, the anti-CD19-S267E/L328F variant was compared to a combination of anti-CD19-IgG1 and anti-RSV-S267E/L328F controls at equal concentrations. The combination of these antibodies should simultaneously bind to both CD19 and FcγRIIb but, unlike anti-CD19-S267E/L328F, is unable to crosslink these receptors. As shown in FIG. **57**, the combination failed to suppress BCR activation-induced survival, indicating that coengagement of FcγRIIb and CD19 by a single molecule is required to inhibit BCR-mediated viability. Not all variants were capable of inhibiting B cell activation. As demonstrated in FIG. **58**, variants with moderately increased affinity relative to WT IgG1 (S267A, 408 nM, 3.6-fold relative to native IgG1) do not inhibit B cell activation. In contrast, that data in FIG. **59** demonstrate that variants with high affinity, here the weakest affinity being the S267E variant (71.9 nM, 20.4-fold relative to native IgG1), do indeed inhibit activation. Together the results in FIGS. **59**, **60**, and **61** suggest that a certain high affinity for FcγRIIb, approximately 100 nM, is needed to mediate inhibitory activity upon coengagement of FcγRIIb and BCR co-receptor target antigen.

Example 16.4

Immunoglobulins Inhibit BCR Activation of Calcium Mobilization in Primary Human B Cells Via Coengagement of FcγRIIb and CD19

[0421] Signals through the B-cell receptor complex ultimately result in calcium release, and this pathway can be inhibited by FcγRIIb (Nielsen et al., 2005, Transfus Med Hemother 32:339-347, incorporated entirely by reference). Intracellular calcium mobilization was used as a quantitative measure of BCR-mediated B cell activation to further evaluate the impact of the immunoglobulins. The current study used primary B cells from normal human donors as a more physiologically relevant model of calcium signaling. In addition, rather than stimulating primarily naive B cells via an anti-IgM antibody, an anti-human CD79b (Igβ) antibody was used in order to induce BCR activation in both naive and memory B cells.

[0422] Intracellular free calcium concentration ([Ca2+]) was measured by flow cytometry using a Fluo-4 NW calcium assay (Molecular Probes, Eugene, Oreg.). Purified human B cells were resuspended at 5×105 cells/ml in calcium assay buffer and pre-loaded with Fluo-4 dye for 30 min at room temperature. After incubation with anti-CD19 or Fc and Fv control antibodies, cells were stimulated by addition of 10 pg/ml of anti-CD79b antibody. Calcium flux kinetics was recorded using a FACSCanto II flow cytometer and data were analyzed using FlowJo software (Tree Star, Ashland, Oreg.).

[0423] Calcium mobilization in the presence of 10 μg/ml anti-CD19 native IgG1 Fc antibody (α-CD19-native-IgG1) was increased relative to the vehicle control (FIG. **60**), as expected from coengagement of CD19 and BCR. In contrast, IIbE variants of anti-CD19 IgG1 (also at 10 pg/ml) inhibited calcium mobilization induced by BCR crosslinking, with the two highest-affinity variants showing greatest activity. To determine the importance of CD19 binding for this effect, an Fc isotype control antibody was used that binds with high affinity to FcγRIIIb but not to CD19; this antibody, referred to as α-FITC-S267E/L328F in FIG. **60**, has the S267E/L328F IgG1 heavy chain, but an Fv region that binds the hapten FITC (which is not on B cells). Relative to vehicle, this antibody had minimal effect on calcium mobilization, indicating that CD19 binding is required to inhibit calcium mobilization. A dose-response extension of this experiment was carried out in which each point represents the area under the curve of a single calcium mobilization response as in FIG. **60**. The data show that potency and efficacy of IIbE variants correlated with affinity for FcγRIIIb, consistent with the B cell viability assay, with anti-CD19-Native-IgG1 showing no dose response (FIG. **61**). The relationship between the EC50 of calcium inhibition and affinity for FcγRIIb is shown in FIG. **62**.

[0424] To assess if the observed inhibition of calcium flux required engagement of both FcγRIIb and CD19 by a single antibody, a competition experiment was performed. Because FcγRI has the highest affinity among all the FcγRs (FIG. **50**) and competes with FcγRIIb for IgG binding (data not shown), a 24-fold molar excess soluble FcγRI (solFcγRI) to block the interaction of the highest affinity antibody (α-CD19-S267E/L328F) with FcγRIIb (FIG. **63**). BCR-induced calcium mobilization was again effectively inhibited by 10 pg/ml α-CD19-S267E/L328F, but not by α-CD19-Native-IgG1. Notably, inhibition by the IIbE variant was completely abolished in the presence of soluble FcγRI, indicating that FcγRIIb engagement is required. These results indicate that BCR-induced calcium mobilization can be inhibited by a single antibody that binds with high affinity to both FcγRIIb and CD19 surface receptors.

[0425] Together the B cell viability and calcium mobilization results suggest that Fc variant antibodies with high affinity for FcγRIIb may be useful in methods for inhibiting activation of B cells. The data provided indicate that amino acid modification at positions 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332 may be useful for such inhibitory methods. In particular, the data provided indicate that substitutions 234D, 234E, 234W, 235D, 235F, 235R, 235Y, 236D, 236N, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, and I332E may be useful for such inhibitory methods.

Example 16.5

Immunoglobulins Induce SHIP Phosphorylation

[0426] SHIP activation is an FcγRIIb-dependent downstream component of ITIM-associated signaling. The capacity of the anti-CD19-S267E/L328F antibody to stimulate SHIP phosphorylation (PSHIP) in the context of BCR activation by anti-CD79b crosslinking antibody was assessed using western analysis. Purified primary human B cells (1×107) were incubated for 10 min at 22° C. with 20 pg/ml anti-CD79b and 10 pg/ml anti-CD19 antibodies, and then ice-cold PBS was added. For the positive control, 10 pg/ml of anti-FcγRII-specific antibody (AT10) (AbD Serotec (Raleigh, N.C.) was used to crosslink FcγRIIb, and 20 pg/ml anti-mouse IgG Fcγ-specific antibody was used to crosslink AT10 and anti-CD79b. Cells were lysed in cold RIPA buffer (Cell Signaling, Beverly, Mass.) containing protease (Roche, Indianapolis, Ind.) and phosphatase (Calbiochem, San Diego, Calif.) inhibitor cocktails with 2 nM microcystin (Calbiochem), and incubated for 30 min on ice. Lysates were centrifuged at 10,000 g for 30 min at 4° C. to remove debris, fractionated by SDS-PAGE (NuPAGE Novex, Invitrogen Life Technologies, Carlsbad, Calif.) and transferred to polyvinylidene difluoride membrane (Invitrogen Life Technologies). Western analysis was performed with phospho-SHIP (Cell Signaling Technologies, Beverly, Mass.) and GAPDH-

specific primary antibodies (Biovision, Mountain View, Calif.) using HRP-conjugated anti-mouse IgG secondary antibody with enhanced chemiluminescence imaging (Amersham Bioscience, Newark, N.J.) and a UVP Bioimaging image capturing system (Upland, Calif.).

[0427] The data are presented in FIG. **64**. The western blot of cell extracts from purified primary human B cells showed that the anti-CD19 IIbE variant stimulated a substantial increase in pSHIP level compared to anti-CD19 IgG1 and other controls (anti-RSV-S267E/L328F and anti-CD19-Fc-KO) (FIG. **64**, lane 1 vs. lanes 2-4). As expected, direct crosslinking of FcγRIIb with BCR by anti-FcγRII antibody also showed an increase in pSHIP level (lane 5). These results indicate that suppression of B cell function by the anti-CD19 IIbE antibody stimulates SHIP phosphorylation, which is consistent with a known signaling pathway of BCR-FcγRIIb coengagement.

Example 16.6

Immunoglobulins Inhibit BCR-Dependent Anti-Apoptotic Effect in Primary Human B Cells

[0428] Although normal B cells in vivo have a long half life of approximately ~5 weeks, in vitro this lifespan is greatly reduced, with increased apoptosis due to the lack of appropriate niche. B cell activation via stimulation via the BCR induces an anti-apoptotic effect and prolongs viability, as demonstrated in FIG. **56**. In order to determine whether the antiproliferative activity of the IIbE variant was a result of neutralizing BCR-mediated survival signals, thereby allowing in vitro apoptosis to proceed, an annexin-V staining assay was performed. 1×105 purified primary human B cells were incubated for 24 h at 37° C. in triplicate with 1 pg/ml anti-CD79b and serial dilutions of anti-CD19 or control antibodies in 100 μl RPMI1640 with 10% FBS. After incubation, cells were harvested and stained with PE-conjugated annexin-V (Biovision, Mountain View, Calif.) and 7-amino-actinomycin D (7-AAD, Invitrogen, Carlsbad, Calif.) at 5 μg/ml. The annexin-V-positive/7-AAD-negative cells were acquired using a FACSCanto II flow cytometer, and analyzed with FACSDiva 5 analysis software (BD Biosciences).

[0429] The data are shown in FIG. **65**. Annexin-V staining of primary human B cells cultured in the presence or absence of anti-CD79b confirmed that apoptosis was suppressed by BCR activation (FIG. **65**, cells alone vs. anti-CD79b). This survival signal was neutralized in a dose-dependent manner by anti-CD19-S267E/L328F, but not by anti-RSV-S267E/L328F Fc control or anti-CD19-IgG1 Fv control antibodies. Inhibition of the anti-apoptotic effect, like inhibition of calcium mobilization and cell proliferation, requires coengagement of CD19 and FcγRIIb by a single antibody, because the combination of anti-CD19-IgG1 and anti-RSV-S267E/L328F (Fv and Fc controls, respectively) did not stimulate apoptosis. These data indicate that the anti-CD19 IIbE variant inhibits BCR-induced B cell proliferation by suppressing anti-apoptotic survival signals.

Example 16.7

Immunoglobulins do not Mediate Effector Functions

[0430] In order to evaluate the effect of modulating FcγRIIIa affinity, the immunoglobulins were examined for their ADCC activity. Antibody serial dilutions were carried out in 96 well microtiter plates in triplicates and incubated with Ramos target cells (10,000 total) to opsonize the target cells for ~15 minutes. Ramos is an immortal huma B cell line derived from Burkitt's lymphoma cells. Purified NK cells (50,000 total) using negative selection kit from frozen PBMC prepared from leukophoresis pack using standard Ficoll density gradient were added to appropriate concentration. The final working ADCC reaction was in 100 ul of 1% FBS/RPMI1640 for 4 hours at 37° C. after which, the amount of LDH released from the target cells was detected using fluorescent detection system. The percentage of ADCC was determined by normalizing the background LDH activity (target and NK together without antibody) adjusted experimental LDH activity against the total LDH activity present in the target cells (spontaneous LDH activity present in the target cells alone adjusted TritonX100 lysed target cells). As shown in FIG. **66**, many of the variants with enhanced FcγRIIb affinity, yet lower or equivalent FcγRIIIa affinity compared with wild-type IgG1, including S267E, G236D/S267E, and S267E/L328F, lack ADCC activity. This is attributed to their reduced or ablated affinity for the activating FcγRs, particularly FcγRIIIa which is the sole FcγR expressed on NK cells.

[0431] Immunoglobulins were also tested for their capacity to mediate phagocytosis by macrophages. Target cells were RS4; 11 cells, an immortal human B cell line derived from leukemia cells. Macrophages express a variety of FcγRs, including FcγRI, FcγRIIa, FcγRIIb, and FcγRIIIa. Purified monocytes were differentiated in the presence of macrophage-colony stimulating factor for 5 days into macrophages. Macrophages were mixed with fluorescently labeled (PKH26) RS4; 11 cells in 10% human AB serum in RPMI followed by the addition of anti-CD19 antibodies and incubated for 4 hours at 37° C. APC conjugated antibodies to CD14 and CD11b were added to the cell mixture, washed and fixed. Phagocytosis was determined by the percentage CD14+CD11b+ and PKH26 double positive population divided by the total number of stained tumors. The data are shown in FIG. **67**. Anti-CD19 IgG1 and the variant S239D/I332E demonstrated phagocytosis. In contrast, variants with enhanced FcγRIIb affinity yet reduced affinity for activating receptors, including S267E/L328F and G236D/S267E, had little or not phagocytic activity, comparable to control antibody that targeted RSV.

[0432] Immunoglobulins were also tested for their capacity to mediate CDC. Release of Alamar Blue was used to monitor lysis of a target B cell line by human serum complement. Raji cells (an immortal B cell line) were washed in 10% FBS medium by centrifugation and resuspension, and loaded into 96-well plates at 40,000 cells per well. Variant anti-CD19 antibodies or Rituxan anti-CD20 control were added in ½ fold dilutions to the indicated final concentrations. Human serum complement (Quidel) was diluted 1 to 5 with medium and added to antibody-opsonized target cells. Plates were incubated for 2 hrs at 37° C., Alamar Blue was added, cells were cultured overnight, and fluorescence was measured. Data from this assay are shown in FIG. **68**. In contrast to the anti-CD20 control, the variant anti-CD19 antibodies do not mediate CDC activity against B cells.

Example 16.8

In Vivo Data Demonstrating Potential for Treating Autoimmune or Inflammatory Disorder

[0433] A hallmark of autoimmunity in mouse and human is dysregulation of FcγRIIb expression resulting in lower sur-

face level of this inhibitory receptor, leading to an elevated level of B cell activation and consequential failure of self-reactive B cell inhibition and production of plasma cells secreting self-antigen specific immunoglobulins. Such self-reactive immunoglobulin immune complexes are etiologic agents in various organ failures in systemic autoimmunity and other arthritic inflammations such as systemic lupus erythematosus (SLE) and rheumatoid arthritis (RA. The immunoglobulins disclosed herein were assessed using a huPBL-SCID mouse model as a proxy, by examining B cell activity measured by the number of B cells and plasma cell development by detecting the antigen specific immunoglobulins. In this method, human PBLs from normal or diseased (e.g., SLE or RA) donors are engrafted to immune-deficient SCID mice and treated with the inhibitory immunoglobulin described herein, then challenged with an antigen to examine the course of B cell development into plasma cells. In such case, the production of antigen-specific immunoglobulins is inhibited from which can be inferred inhibition of both B cell activation and differentiation.

[0434] The protocol for this study is provided in FIG. **69**A. Four different groups of mice with five mice in each group were engrafted with human PBLs from a healthy donor. At day 16, test articles consisting of PBS (vehicle control), anti-CD19 with native IgG1 Fc (anti-CD19 IgG1 WT), anti-CD19 with IgG1 Fc of enhanced affinity for FcγRIIb (anti-CD19 S267E/L328F) or Rituximab IgG1 anti-CD20 were given 10 mg/kg twice weekly for a total of 6 doses. At day 24, antigen challenge with tetanus toxoid fragment C was given, and mice were sacrificed at days 31 and 38. Tetanus toxoid (TT) specific antibody production was examined. The results of this experiment are shown in FIG. **69**B. The data shows that before the antigen challenge, the level of anti-TT specific antibody was very low in all the groups. After immunization, the untreated PBS control group showed the highest level of anti-TT specific antibody level. In comparison, the B cell depleting anti-CD20 antibody produced low level of antigen specific antibody level. After immunization, the anti-CD19 S267E/L328F group showed the lowest level of antigen specific antibodies, whereas the anti-CD19 IgG1 WT produced a higher level of antigen specific antibody. These in vivo data show that the anti-CD19 antibody with enhanced FcγRIIb affinity is capable of inhibiting B cell activation and immunoglobulin secreting plasma cell differentiation, and thus support the potential of the immunoglobulins disclosed herein for treating autoimmune and inflammatory disorders.

Example 16.9

Co-Engagement of FcγRIIb and Other Target Antigens

[0435] The use of antibodies to coengage CD19 and FcγRIIb is an example of how simultaneous high affinity engagement of a B cell antigen and FcγRIIb may be used to inhibit activation or proliferation of FcγRIIb+ cells. As discussed above, FcγRIIb is a negative regulator of a number of cell types, including but not limited to B cells, plasma cells, monocytes, macrophages, dendritic cells, neutrophils, basophils, eosinophils, and mast cells. A variety of antigens expressed on these FcγRIIb+ cell types may be also be co-targeted with high affinity FcγRIIb binding to inhibit cellular activation and/or proliferation. FIG. **70** provides a number of examples of antigens and cell types that may be targeted by the immunoglobulins disclosed herein.

[0436] At the outset, it is not clear which antigens may serve as effective co-targets with FcγRIIb for modulation of cellular activity. A likely key aspect of a potential co-target is its functional role in the cell, and in particular whether its intracellular signaling pathways (if any) overlap with those of FcγRIIb. CD19 is a co-receptor of the BCR complex, and thus the capacity of high affinity co-engagement of CD19 and FcγRIIb to inhibit B cell activation is likely related to the association of CD19 with BCR and the negative regulatory role of FcγRIIb in inhibiting BCR-stimulated activation. Importantly, however, CD19 is not involved in antigen recognition, which is the specific function of the μ (IgM) component of the BCR. Rather CD19, and other proteins such as CD21, CD22, CD72, CD81, and Leu13, are BCR co-receptors. Of course, targeting of other components of the BCR, including the antigen recognition domain (μ, also referred to as IgM), and the signaling domains CD79a (Igα) and CD79b (Igβ), is also supported by the data herein. However, given the complex biochemical pathways involved in regulating cellular activation and proliferation of these cell types, evaluating which antigens (FIG. **70**) may serve as effective co-targets with FcγRIIb for modulation of cellular activity requires experimentation.

[0437] In order to evaluate which antigens may be effective co-targets with FcγRIIb for modulating cellular activity, the S267E/L328F (high FcγRIIb affinity) variant, along with WT IgG1 and Fc-KO variant(s) (ˆ236R/L328R and/or G236R/L328R) were cloned into antibodies specific for a variety of other antigens expressed on FcγRIIb+ cells, including CD19, CD20, CD22, CD23, CD40, CD52, and CD79b. In several cases, multiple Fv's targeting the same antigen were constructed in order to assess the epitope-dependence of the effects. FIG. **95** lists the heavy and light chain variable regions (V_H and V_L) of the antibodies used. The V_H and V_L genes targeting these antigens were constructed by gene synthesis, and variants were constructed, expressed, and purified as described above.

[0438] The effect of high affinity co-engagement of these antigens with FcγRIIb was evaluated using the ATP-dependent luminescence B cell viability assay as described above. FIGS. **71**-**76** show the results of these experiments. The data indicate that CD79b is also an effective co-target for using high affinity FcγRIIb co-engagement to inhibit B cell activation. This is consistent with its role as the signaling component of the BCR complex. Results using two additional anti-CD19 antibodies again confirmed the amenability of this antigen to controlling B cell activation using high affinity FcγRIIb co-ligation, irrespective of the specific epitope targeted. In contrast, no effect of high affinity FcγRIIb co-engagement was observed for antibodies with specificity for CD20, CD23, and CD52. Unexpectedly, dual targeting of FcγRIIb using antibodies having specificity for CD22 and CD40 resulted in enhanced B cell activation. In the case of CD22, this may be the result of its role as a negative regulator of BCR activation. In the case of CD40, this may be the result of its role as a positive regulator of B cell activation via engagement at the T cell interface. It is known that some of the antibodies used are agonist, that is to say that their binding of CD40 on B cells and other cells promotes positive signaling and activation of B cells. In a sense these antibodies are mimicking the co-activation signal of a T cell. The antibody (and thus epitope) dependence of this activation is likely related to the capacity of the antibodies to agonize. The reason for the enhanced agonism and stimulation of the B cells upon

high affinity (S267E/L328F) engagement of FcγRIIb, but not using WT IgG1 or Fc-KO, is not currently clear, and requires further study.

[0439] Select antibodies targeting other antigens were tested further for their capacity to inhibit intracellular calcium mobilization using the assay described above. The results in FIG. **77** agree well with the data from the B cell viability assay. Whereas high affinity co-ligation of FcγRIIb and CD23 had no effect on calcium mobilization, CD79b is an effective co-target for inhibition of calcium. High affinity FcγRIIb co-ligation with CD22 and CD40 resulted in an increase in calcium mobilization, again consistent with the viability results.

[0440] In order to screen a larger set of antigens using commercial reagents, a novel method was developed for evaluating the capacity of FcγRIIb/antigen co-engagement to inhibit of cellular activity. This approach uses a haptenized version of an antibody or ligand that has specificity for the target antigen, together with variant versions of an anti-hapten antibody. This concept is illustrated in FIG. **78**. A variety of haptens are known in the art that may be used for this approach, including but not limited to FITC, biotin, and nitrophenyl.

[0441] The VH and VL genes of the anti-FITC antibody 44-20 were constructed by gene synthesis, and variants were constructed with enhanced affinity for FcγRIIb (S267E/L328F), along with WT IgG1 and FcγR knockout variant(s) (ˆ236R/L328R and/or G236R/L328F). Antibodies were constructed, expressed and purified as described above. Commercial antibodies targeting antigens mu (μ), CD19, CD20, CD21, CD24, CD35, CD45RA, CD72, CD79a, CD79b, CD80, CD81, CD86, and HLA-DR were purchased from Beckman Coulter (Fullerton, Calif.), BD Pharmingen (San Jose, Calif.), AbD Serotec (Raleigh, N.C.), or GenTex, Inc. (San Antonio, Tex.). FITC labeling reagent (Pierce Biotech, Inc., Rockford, Ill.) was used to label commercial antibodies according to the supplied protocol at either room temperature or 37° C. for 1 hour. After labeling, un-reacted label was removed using BioSpin P-6 or P-30 columns from BioRad (Hercules, Calif.) and used with varying concentrations of anti-FITC antibodies in proliferation experiments as described above.

[0442] The effectiveness of the hapten approach for screening antigens was first confirmed using anti-μ and anti-CD19 antibodies, two antigens that are known to mediate inhibitory activity upon high affinity co-engagement with FcγRIIb. FIGS. **79** and **80** show anti-FITC antibody variants with high affinity for FcγRIIb, but not WT IgG1 or Fc-KO variants, are able to inhibit B cell activation in the presence of FITC-labeled anti-mu and anti-CD19 antibodies. These data are consistent with the above approach wherein variants were incorporated directly into the antibody with specificity for CD19 or mu, and thus confirm the use of the hapten approach for screening target antigens for capacity to modulate cellular activity upon high affinity co-engagement with FcγRIIb.

[0443] FIGS. **81-93** show data from the ATP-dependent luminescence B cell viability using Fc variant versions of anti-FITC antibodies and antibodies targeting CD20, CD21, CD24, CD35, CD45RA, CD72, CD79a, CD79b, CD80, CD81, CD86, and HLA-DR. Inhibitory activity was observed for targeting of CD79a and CD79b, consistent with their role in BCR signaling. Targeting of CD81 and HLA-DR resulted in possible inhibition. The role of CD81 as a BCR co-receptor would seem to support the result for this antigen. The amenability of these antigens as co-targets for controlling cellular activation using high affinity FcγRIIb binding requires further study. Stimulatory activity was observed for co-targeting of CD72 with high affinity FcγRIIb affinity.

[0444] FIG. **94** provides a summary of the results from the target antigen screening by both the Fc variant and hapten approaches. The data indicate that immunoglobulins that coengage with high affinity both FcγRIIb and μ, CD19, CD79a, Cd79b, CD81, and HLA-DR have potential for inhibiting the activation of FcγRIIb+ cells. The data also indicate that immunoglobulins that coengage with high affinity both FcγRIIb and CD22, CD40, and CD72 have potential for stimulating FcγRIIb+ cells. Overall, the results of this work suggest that simultaneous high affinity engagement of FcγRIIb and antigens involved or associated with the BCR complex, including μ, CD79a, CD79b, CD19, CD21, CD22, CD72, CD81, and Leu13, are methods for controlling the activation, proliferation, and/or viability of B cells.

[0445] All references are herein expressly incorporated by reference.

[0446] Whereas particular embodiments of the invention have been described above for purposes of illustration, it will be appreciated by those skilled in the art that numerous variations of the details may be made without departing from the invention as described in the appended claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 44

<210> SEQ ID NO 1
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 VL

<400> SEQUENCE: 1

Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Lys Ser Leu Gln Asn Val
20 25 30

-continued

```
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Ser
35                  40                  45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Asn Ser Gly Val Pro
50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65                  70                  75                  80

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Met Gln His
85                  90                  95

Leu Glu Tyr Pro Ile Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
100                 105                 110


<210> SEQ ID NO 2
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 VH

<400> SEQUENCE: 2

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20                  25                  30

Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35                  40                  45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50                  55                  60

Gln Gly Arg Val Thr Ile Ser Ser Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85                  90                  95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Thr Arg Val Phe Asp Tyr Trp Gly
100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115                 120


<210> SEQ ID NO 3
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85                  90                  95
```

-continued

```
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100                 105


<210> SEQ ID NO 4
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100                 105                 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115                 120                 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325                 330


<210> SEQ ID NO 5
```

-continued

<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: S267E/L328F IgG1 constant chain

<400> SEQUENCE: 5

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Glu His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> SEQ ID NO 6
<211> LENGTH: 330
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: G236D/S267E IgG1 constant chain

<400> SEQUENCE: 6

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Asp Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Glu His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> SEQ ID NO 7
<211> LENGTH: 219
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 light chain (VH-Ck)

-continued

<400> SEQUENCE: 7

Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Lys Ser Leu Gln Asn Val
20 25 30

Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Gln Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Asn Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Ile Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> SEQ ID NO 8
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 IgG1 heavy chain

<400> SEQUENCE: 8

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Ser Ser Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Thr Arg Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

-continued

```
115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435                 440                 445

Pro Gly Lys
450


<210> SEQ ID NO 9
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 S267E/L328F heavy chain

<400> SEQUENCE: 9

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
```

-continued

```
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20                  25                  30

Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35                  40                  45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50                  55                  60

Gln Gly Arg Val Thr Ile Ser Ser Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85                  90                  95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Thr Arg Val Phe Asp Tyr Trp Gly
100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Glu His
260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Phe Pro Ala Pro Ile
325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405                 410                 415
```

-continued

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435                 440                 445

Pro Gly Lys
450


<210> SEQ ID NO 10
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: HuAM4G7 G236D/S267E heavy chain

<400> SEQUENCE: 10

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20                  25                  30

Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35                  40                  45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50                  55                  60

Gln Gly Arg Val Thr Ile Ser Ser Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85                  90                  95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Thr Arg Val Phe Asp Tyr Trp Gly
100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Asp
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Glu His
260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290                 295                 300
```

-continued

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435                 440                 445

Pro Gly Lys
450


<210> SEQ ID NO 11
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-RSV Numax VL

<400> SEQUENCE: 11

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
20                  25                  30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35                  40                  45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50                  55                  60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65                  70                  75                  80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85                  90                  95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100                 105


<210> SEQ ID NO 12
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-RSV Numax VH

<400> SEQUENCE: 12

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
```

-continued

```
20                  25                  30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35                  40                  45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
50                  55                  60

Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85                  90                  95

Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
100                 105                 110

Gly Thr Thr Val Thr Val Ser Ser
115                 120


<210> SEQ ID NO 13
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-FITC VL

<400> SEQUENCE: 13

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20                  25                  30

Asn Gly Asn Thr Tyr Leu Arg Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35                  40                  45

Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85                  90                  95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100                 105                 110


<210> SEQ ID NO 14
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-FITC VH

<400> SEQUENCE: 14

Glu Val Lys Leu Asp Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Arg
1               5                   10                  15

Pro Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20                  25                  30

Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
35                  40                  45

Ala Gln Ile Arg Asn Lys Pro Tyr Asn Tyr Glu Thr Tyr Tyr Ser Asp
50                  55                  60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
65                  70                  75                  80
```

-continued

Val Tyr Leu Gln Met Asn Asn Leu Arg Val Glu Asp Met Gly Ile Tyr
85 90 95

Tyr Cys Thr Gly Ser Tyr Tyr Gly Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ser Val Thr Val Ser Ser
115

<210> SEQ ID NO 15
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 15

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Phe Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Leu Thr Phe Gly Ala Gly Thr Glu Leu Glu Leu Lys
100 105 110

<210> SEQ ID NO 16
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 16

Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Gly Gly Asp Thr Asn Tyr Asn Glu Ile Phe
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Thr Arg Arg Val Pro Val Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Ser
100 105 110

Val Thr Val Ser Ser
115

<210> SEQ ID NO 17
<211> LENGTH: 106
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

-continued

<223> OTHER INFORMATION: anti-CD20 Pro70769 VL

<400> SEQUENCE: 17

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr
35 40 45

Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 18
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-CD20 Pro70769 VH

<400> SEQUENCE: 18

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 19
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-CD52 Campath VL

<400> SEQUENCE: 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Ile Asp Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

-continued

```
35                  40                  45

Tyr Asn Thr Asn Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln His Ile Ser Arg Pro Arg
85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100                 105


<210> SEQ ID NO 20
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: anti-CD52 Campath VH

<400> SEQUENCE: 20

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Phe Thr Asp Phe
20                  25                  30

Tyr Met Asn Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35                  40                  45

Gly Phe Ile Arg Asp Lys Ala Lys Gly Tyr Thr Thr Glu Tyr Asn Pro
50                  55                  60

Ser Val Lys Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln
65                  70                  75                  80

Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
85                  90                  95

Tyr Cys Ala Arg Glu Gly His Thr Ala Ala Pro Phe Asp Tyr Trp Gly
100                 105                 110

Gln Gly Ser Leu Val Thr Val Ser Ser
115                 120


<210> SEQ ID NO 21
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 21

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Tyr Tyr
20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35                  40                  45

Tyr Val Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Val Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Val Tyr Ser Thr Pro Arg
85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100                 105
```

-continued

<210> SEQ ID NO 22
<211> LENGTH: 118
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 22

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe Thr Phe Asn
20 25 30

Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
35 40 45

Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp Tyr Ala Asp
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Asn Asn Thr
65 70 75 80

Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly Gln Gly Val
100 105 110

Leu Val Thr Val Ser Ser
115

<210> SEQ ID NO 23
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 23

Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly
1 5 10 15

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile
65 70 75 80

Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95

Val Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 24
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 24

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

-continued

```
Trp Met Ser Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
35                  40                  45

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50                  55                  60

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr
85                  90                  95

Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100                 105                 110

Ser Ser


<210> SEQ ID NO 25
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 25

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35                  40                  45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100                 105


<210> SEQ ID NO 26
<211> LENGTH: 123
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 26

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                   10                  15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20                  25                  30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35                  40                  45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85                  90                  95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Thr Ser Ala
```

-continued

115 120

<210> SEQ ID NO 27
<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Tyr Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ile Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> SEQ ID NO 28
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asp Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Asn Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gln Pro Leu Gly Tyr Cys Thr Asn Gly Val Cys Ser Tyr
100 105 110

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> SEQ ID NO 29
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 29

Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Ala Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

-continued

```
Asn Gly Asn Thr Phe Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35                  40                  45

Pro Lys Leu Leu Ile Tyr Thr Val Ser Asn Arg Phe Ser Gly Val Pro
50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Thr
85                  90                  95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Gln
100                 105                 110


<210> SEQ ID NO 30
<211> LENGTH: 114
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 30

Glu Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20                  25                  30

Tyr Ile His Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35                  40                  45

Gly Arg Val Ile Pro Asn Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe
50                  55                  60

Lys Gly Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85                  90                  95

Ala Arg Glu Gly Ile Tyr Trp Trp Gly His Gly Thr Thr Leu Thr Val
100                 105                 110

Ser Ser


<210> SEQ ID NO 31
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 31

Asp Ala Val Met Thr Gln Asn Pro Leu Ser Leu Pro Val Ser Leu Gly
1               5                   10                  15

Asp Glu Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Glu Asn Ser
20                  25                  30

Asn Gly Asn Thr Phe Leu Asn Trp Phe Phe Gln Lys Pro Gly Gln Ser
35                  40                  45

Pro Gln Leu Leu Ile Tyr Arg Val Ser Asn Arg Phe Ser Gly Val Pro
50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Leu Gln Val
85                  90                  95

Thr His Val Pro Tyr Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Lys
100                 105                 110
```

-continued

<210> SEQ ID NO 32
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 32

Asp Ile Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Thr Asn
20 25 30

Tyr Asn Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Arg Tyr Asp Gly Thr Ser Glu Tyr Thr Pro Ser Leu
50 55 60

Lys Asn Arg Val Ser Ile Thr Arg Asp Thr Ser Met Asn Gln Phe Phe
65 70 75 80

Leu Arg Leu Thr Ser Val Thr Pro Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Leu Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
100 105 110

<210> SEQ ID NO 33
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 33

Glu Leu Gln Leu Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Asn Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 34
<211> LENGTH: 113
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 34

Gln Val Lys Leu Glu Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Arg Tyr
20 25 30

Ser Val Tyr Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Met Met Trp Gly Gly Gly Ser Thr Asp Tyr Asn Ser Ala Leu Lys

-continued

50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Phe Leu
65 70 75 80

Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Met Tyr Tyr Cys Val
85 90 95

Arg Thr Asp Gly Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
100 105 110

Ser

<210> SEQ ID NO 35
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 35

Asp Ile Leu Leu Thr Gln Thr Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser Gly Ile Pro Pro
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65 70 75 80

Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Thr
85 90 95

Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> SEQ ID NO 36
<211> LENGTH: 124
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 36

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ser
1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Ser Ser Tyr
20 25 30

Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn Gly Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr Ala Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 37

-continued

<211> LENGTH: 107
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 37

Ala Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> SEQ ID NO 38
<211> LENGTH: 120
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 38

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Ser Ser
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Arg Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg His Val Thr Met Trp Gly Val Ile Ile Asp Phe Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> SEQ ID NO 39
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 39

Asp Ile Val Met Thr Gln Ala Ala Pro Ser Ile Pro Val Thr Pro Gly
1 5 10 15

Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Asn Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Arg Pro Gly Gln Ser
35 40 45

-continued

Pro Gln Leu Leu Ile Tyr Arg Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln His
85 90 95

Leu Glu Tyr Pro Phe Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> SEQ ID NO 40
<211> LENGTH: 121
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 40

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Ile Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Tyr Tyr Tyr Gly Ser Arg Val Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> SEQ ID NO 41
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Anti-CD20 heavy chain comprising possible Fc variants
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (243)..(243)
<223> OTHER INFORMATION: X is D, E, N, Q or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (244)..(244)
<223> OTHER INFORMATION: X is I or M
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (268)..(268)
<223> OTHER INFORMATION: X is I, T or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (272)..(272)
<223> OTHER INFORMATION: X is Dor E
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (276)..(276)
<223> OTHER INFORMATION: X is Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (278)..(278)
<223> OTHER INFORMATION: X is E

-continued

<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (301)..(301)
<223> OTHER INFORMATION: X is D
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (302)..(302)
<223> OTHER INFORMATION: X is A or D
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (330)..(330)
<223> OTHER INFORMATION: X is E or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (334)..(334)
<223> OTHER INFORMATION: X is Y, L, or I
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (336)..(336)
<223> OTHER INFORMATION: X is D, E, N, or Q

<400> SEQUENCE: 41

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100 105 110

Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Xaa Xaa Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Xaa Asp Val Ser Xaa
260 265 270

Glu Asp Pro Xaa Val Xaa Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

-continued

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Xaa Xaa Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Xaa Ala Leu Pro Xaa Pro Xaa
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> SEQ ID NO 42
<211> LENGTH: 213
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Anti-CD20 light chain

<400> SEQUENCE: 42

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

-continued

```
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195                 200                 205

Asn Arg Gly Glu Cys
210


<210> SEQ ID NO 43
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Anti-CD20 heavy chain

<400> SEQUENCE: 43

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20                  25                  30

Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile
35                  40                  45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85                  90                  95

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly
100                 105                 110

Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser
115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195                 200                 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys
210                 215                 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290                 295                 300
```

-continued

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325                 330                 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435                 440                 445

Pro Gly Lys
450


<210> SEQ ID NO 44
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Fc Variants
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: X is D,K or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: X is K,E, or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (3)..(3)
<223> OTHER INFORMATION: X is T,E or K
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (4)..(4)
<223> OTHER INFORMATION: X is H,E or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (5)..(5)
<223> OTHER INFORMATION: X is T,E,K or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (7)..(7)
<223> OTHER INFORMATION: X is P,E,G,K or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (8)..(8)
<223> OTHER INFORMATION: X is P,E,G,K or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (10)..(10)
<223> OTHER INFORMATION: X is P,A,E,G or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (11)..(11)
<223> OTHER INFORMATION: X is A,E,G,K,P or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
```

-continued

<222> LOCATION: (12)..(12)
<223> OTHER INFORMATION: X is P,E,G,K or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (13)..(13)
<223> OTHER INFORMATION: X is A,D,F,G,H,I,K,L,M,N,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: X is L,A,D,E,F,G,H,I,K,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (15)..(15)
<223> OTHER INFORMATION: X is L,A,D,E,F,G,H,I,K,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (16)..(16)
<223> OTHER INFORMATION: X is G,A,D,E,F,H,I,K,L,M,N,P,Q,R,S,T,V, or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (17)..(17)
<223> OTHER INFORMATION: X is G,D,E,F,H,I,K,L,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (18)..(18)
<223> OTHER INFORMATION: X is P,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: X is S,D,E,F,G,H,I,K,L,M,N,P,Q,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (20)..(20)
<223> OTHER INFORMATION: X is V,A,I,M or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (21)..(21)
<223> OTHER INFORMATION: X is F,D,E,L,R,S,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (23)..(23)
<223> OTHER INFORMATION: X is F,E,H,L,Q,R,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (24)..(24)
<223> OTHER INFORMATION: X is P or H
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (25)..(25)
<223> OTHER INFORMATION: X is P or A
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (26)..(26)
<223> OTHER INFORMATION: X is K,D,E,H or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (27)..(27)
<223> OTHER INFORMATION: X is P,G or V
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (29)..(29)
<223> OTHER INFORMATION: X is D,H,Q or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (35)..(35)
<223> OTHER INFORMATION: X is R,E or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (38)..(38)
<223> OTHER INFORMATION: X is E,H,S or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (40)..(40)
<223> OTHER INFORMATION: X is T,D,E,H or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE

-continued

<222> LOCATION: (42)..(42)
<223> OTHER INFORMATION: X is V,A,E,F,I or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (43)..(43)
<223> OTHER INFORMATION: X is V,A,I,M or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (44)..(44)
<223> OTHER INFORMATION: X is V,A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (45)..(45)
<223> OTHER INFORMATION: X is D,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (46)..(46)
<223> OTHER INFORMATION: X is V,A,I,M or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (47)..(47)
<223> OTHER INFORMATION: X is S,D,E,F,H,I,K,L,M,N,P,Q,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (48)..(48)
<223> OTHER INFORMATION: X is H,D,E,F,G,I,K,L,M,N,P,Q,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (49)..(49)
<223> OTHER INFORMATION: X is E,F,G,H,I,K,L,M,N,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (50)..(50)
<223> OTHER INFORMATION: X is D,F,G,H,I,L,M,P,Q,R,S,T,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (51)..(51)
<223> OTHER INFORMATION: X is A,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (52)..(52)
<223> OTHER INFORMATION: X is E,D,F,G,H,I,K,L,M,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (53)..(53)
<223> OTHER INFORMATION: X is V or I
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (54)..(54)
<223> OTHER INFORMATION: X is K,D,E,F,G,H,L,M,N,P,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: X is F,L or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (56)..(56)
<223> OTHER INFORMATION: X is N,D,E,F,G,H,I,L,M,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (58)..(58)
<223> OTHER INFORMATION: X is Y,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (60)..(60)
<223> OTHER INFORMATION: X is D,G,K,L,P or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (61)..(61)
<223> OTHER INFORMATION: X is G,D,E,K,N,P,Q or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (62)..(62)
<223> OTHER INFORMATION: X is V,E,G,K,P or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE

-continued

<222> LOCATION: (63)..(63)
<223> OTHER INFORMATION: X is E,G,H,K,L,P,R or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (64)..(64)
<223> OTHER INFORMATION: X is V,D,E,L,N,Q,T or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (65)..(65)
<223> OTHER INFORMATION: X is H,D,E,K,Q,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (66)..(66)
<223> OTHER INFORMATION: X is N,E,G,P or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: X is K,D,E or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (70)..(70)
<223> OTHER INFORMATION: X is K,D,H,L,N or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (71)..(71)
<223> OTHER INFORMATION: X is P,D,E,G,H,I,Q or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (72)..(72)
<223> OTHER INFORMATION: X is R,D,E,T or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (73)..(73)
<223> OTHER INFORMATION: X is E,F,G,H,I,L,M,N,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: X is E,F,G,H,I,K,L,M,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (75)..(75)
<223> OTHER INFORMATION: X is Q,D,E,F,G,H,I,M,N,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (76)..(76)
<223> OTHER INFORMATION: X is Y,A,D,E,G,H,I,K,L,M,N,Q,R,S,T or V
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (77)..(77)
<223> OTHER INFORMATION: X is N,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (78)..(78)
<223> OTHER INFORMATION: X is S,D,E,F,H,I,K,M,N,Q,R,T,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (79)..(79)
<223> OTHER INFORMATION: X is T,A,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (80)..(80)
<223> OTHER INFORMATION: X is Y,A,D,E,G,H,K,M,N,P,Q,R,S,T,V or W
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (81)..(81)
<223> OTHER INFORMATION: X is R,D,E,H or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: X is V or I
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (83)..(83)
<223> OTHER INFORMATION: X is V,D,E or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE

-continued

<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: X is S,D,H,L,N or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (85)..(85)
<223> OTHER INFORMATION: X is V,E,T or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: X is W or F
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: X is K,E or Q
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (98)..(98)
<223> OTHER INFORMATION: X is E,H,L,Q,R or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: X is K,D,F,G,H,I,L,N,P,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (102)..(102)
<223> OTHER INFORMATION: X is K,D,F,G,H,I,P,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (103)..(103)
<223> OTHER INFORMATION: X is V or I
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (104)..(104)
<223> OTHER INFORMATION: X is S,D,F,G,H,I,L,M,P,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (105)..(105)
<223> OTHER INFORMATION: X is N,A,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (106)..(106)
<223> OTHER INFORMATION: X is K,I,L,P or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (107)..(107)
<223> OTHER INFORMATION: X is A,D,E,F,H,I,K,L,M,N,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (108)..(108)
<223> OTHER INFORMATION: X is L,A,D,E,F,G,H,I,K,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (109)..(109)
<223> OTHER INFORMATION: X is P,D,E,F,G,H,I,K,L,M,N,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (110)..(110)
<223> OTHER INFORMATION: X is A,E,F,G,H,I,L,M,N,P,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (111)..(111)
<223> OTHER INFORMATION: X is P,D,F,H,I,L,M,Q,R,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (112)..(112)
<223> OTHER INFORMATION: X is I,A,D,E,F,H,K,L,M,N,P,Q,R,S,T,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (113)..(113)
<223> OTHER INFORMATION: X is E,F,H,I,L,M,N,P,Tor Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (114)..(114)
<223> OTHER INFORMATION: X is K,F,I,L,P or T
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE

-continued

<222> LOCATION: (115)..(115)
<223> OTHER INFORMATION: X is T,D,F,G,H,I,L,M,N,P,R,S,V,W or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (116)..(116)
<223> OTHER INFORMATION: X is I,E,K or Y
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (117)..(117)
<223> OTHER INFORMATION: X is S,E,H or N

<400> SEQUENCE: 44

Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Lys Xaa Thr Leu Met
20 25 30

Ile Ser Xaa Thr Pro Xaa Val Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Val Xaa Xaa Xaa Xaa Xaa
50 55 60

Xaa Xaa Ala Xaa Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Leu Thr Val Leu His Gln Asp Xaa Leu Asn Gly
85 90 95

Xaa Xaa Tyr Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa
115

We claim:

1. A method of inhibiting proliferative effects of at least one cell comprising

contacting the cell with an Fc variant, and

wherein said Fc variant coengages a target antigen on the cell's surface and an FcγR on the cell's surface.

2. The method of claim **1**, wherein said FcγR is FcγRIIb.

3. The method of claim **2**, wherein said Fc variant has enhanced binding affinity to FcγRIIb relative to a parent polypeptide.

4. The method of claim **3**, wherein said Fc variant comprises at least one amino acid modification in the Fc region compared to a parent polypeptide, wherein said modification is at a position selected from 234, 235, 236, 237, 239, 266, 267, 268, 298, 327, 328, 329, 330, and 332, wherein numbering is according to the EU index.

5. The method of claim **4**, wherein said modification is at least one amino acid substitution or combination of amino acid substitutions selected from the group consisting of 234F, 234G, 234I, 234K, 234N, 234P, 234Q, 234S, 234V, 234W, 234Y, 235H, 235I, 235N, 235P, 235Q, 235R, 235S, 235W, 235Y, 236D, 236F, 236H, 236I, 236K, 236L, 236M, 236P, 236Q, 236R, 236S, 236T, 236V, 236W, 236Y, 237E, 237H, 237K, 237L, 237P, 237Q, 237S, 237V, 237Y, 239D, 239E, 239N, 239Q, 266I, 266M, 267D, 267E, 268D, 268E, 268Q, 298D, 298E, 298M, 298Q, 327D, 327L, 327N, 328E, 328F, 329E, 330H, 330S, 267E/327D, 239D/267E, 239D/268D, 239D/332E, and 239D/267E/332E.

* * * * *